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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION  
Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

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Tom Wehrman, Radoje T. Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

- x This is a new application for a  
x Utility patent.  
☐ Design patent.  
x Applicants claim small entity status (See 37 CFR 1.27)

2. Application Papers Enclosed

- 1 Title Page  
142 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)  
4 Page(s) of Claims  
1 Page(s) of Abstract  
0 Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal  
723 Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on November 17, 2000, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EK415382545US

Sandy Fong

**3. Oath or Declaration**

- ☐ Enclosed
- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
- ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
- ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
- ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- x Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

**4. Additional Papers Enclosed**

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- x Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- x Statement Under 37 CFR § 1.821
- x Paper copy of sequence listing identical to computer copy (723 pages)
- ☐ Microfiche computer program
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- x Return receipt postcard
- ☐ Other \_\_\_\_\_

**5. Priority Applications Under 35 USC 119**

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.



6. Filing Fee Calculation (37 CFR 1.16)

A. ☒ Utility Application

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$355.00		\$710.00
TOTAL	30-20	= 10	X 9 =	\$90.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 40 =	\$00.00	X 80 =	\$0.00
First Presentation of Multiple Dependent Claim			+ 135 =	\$135.00	+ 270 =	\$0.00
FILING FEE:				\$580.00	OR	\$0.00

B. ☐ Design Application (\$160.00/\$320.00) Filing Fee: \$ \_\_\_\_\_

C. ☐ Plant Application (\$245.00/\$490.00) Filing Fee: \$ \_\_\_\_\_

D. Other fees

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ \_\_\_\_\_

☐ Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached [Fee -- \$130.00] \$ \_\_\_\_\_

☐ Other \$ \_\_\_\_\_

**TOTAL FEES ENCLOSED \$ 580.00**

**7. Method of Payments of Fees**

- ☐ Enclosed check
- ☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

**8. Deposit Account and Refund Authorization**

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Leslie A. Mooi at the address below.

Respectfully submitted,

Date: November 17, 2000

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Our Ref. No.: 797

**NOVEL NUCLEIC ACIDS AND POLYPEPTIDES**

Express Mail Label No.: EF415382545US

# NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

## 1. BACKGROUND OF THE INVENTION

### 5 1.1 TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

### 10 1.2 BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

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## 2. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 362 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 – 362 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 – 362. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 – 362 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 – 362. The sequence

information can be a segment of any one of SEQ ID NO: 1 – 362 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 – 362.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1–362; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1–362; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1–362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under

stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-362; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-362; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These

techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form



the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 1); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

### 3. DETAILED DESCRIPTION OF THE INVENTION

#### 3.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules.

The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells.

PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil).

Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of

oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-362.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-362. The sequence information can be a segment of any one of SEQ ID NOs: 1-362 that uniquely identifies

or represents the sequence information of that sequence of SEQ ID NO: 1-362. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1 \div 4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol)

and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions,

deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation.

Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of



glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted"

proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

5           Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

10           The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

15           In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

20           As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences.

Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no

more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and

the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

5

### 3.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

10 The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1 – 362; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 – 362; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1 – 362; (b) 15 nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 362. Domains of 20 interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include 25 receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

30 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known

methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1 - 362 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1 - 362 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1 - 362 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1 - 362, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can

differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 362, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 362 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 362, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably

constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by

the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis

5 techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA  
10 sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

15 The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate  
20 polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-362, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in  
25 appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor  
30 Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and



the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell.

- 5 Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a  
10 nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof is inserted, in a forward or reverse orientation. In the  
15 case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of  
20 example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an  
25 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein  
30 "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the

protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT

(chloramphenicol transferase) vectors or other vectors with selectable markers. Two

5 appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will

10 include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat

15 shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired

20 characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of

25 replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

30 As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived

from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

### 3.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous

promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7

lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed  
5 primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking  
10 nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion  
15 chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

20 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella*  
25 *typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

30 In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the

invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this

purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No.

5 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

### 10 3.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-362 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 362 or the corresponding full length or mature protein. Polypeptides of the  
15 invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NOs: 1 – 362 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-362 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization  
20 conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-362 or the corresponding full length or mature protein; and “substantial equivalents” thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least  
25 about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-362.

Fragments of the proteins of the present invention which are capable of exhibiting  
30 biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for

example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments



of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

5           The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level.

10       One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

15           The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded  
20       polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

25           In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes,  
30       *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in*

*Molecular Biology.* Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-362.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in

the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin

(TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

- 5 One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or  
10 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces  
15 fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity  
20 and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be  
25 fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

#### 30 **3.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

### 3.5 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient

expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human

5 disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of

10 antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to

15 express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of

20 cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein

25 encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron

30 DNA may be inserted along with the heterologous promoter DNA. If linked to the desired

protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting

sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

5           The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by  
10       reference herein in its entirety.

### 3.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed  
15       or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals,  
20       preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals,  
25       are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using  
30       homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased



protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

### 3.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of

5 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the  
10 invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein  
15 expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular  
20 antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

### 25 3.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either  
30 constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when

labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology:

Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

### 3.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

### 3.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION

#### ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

- 5            Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 15           Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- 25           Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter
- 30

6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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#### 3.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of

5 mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

10 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to  
15 create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present  
20 invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and  
25 neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

30 Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a

specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

### 3.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation



of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I.

Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

### 5           **3.7.6 TISSUE GROWTH ACTIVITY**

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

10           A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an  
15           osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

20           A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

25           Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing  
30           damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising

such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

### **3.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY**

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes

viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul et al., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected

cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$  microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.



Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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### 3.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

### 3.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

### 3.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assays for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

### 3.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases,

blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl,

Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

*In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

### 3.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of

such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and

5 receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of

10 receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek,

15 D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,

20 Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

25 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in

30 Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of

colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

### 5                    3.7.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One  
10 method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One  
15 may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include  
20 (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or  
25 compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.  
30 Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).



Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 3.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind

polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

### **3.7.15 ANTI-INFLAMMATORY ACTIVITY**

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or

promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### **3.7.16 LEUKEMIAS**

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### **3.7.17 NERVOUS SYSTEM DISORDERS**

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases

or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple

sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive

bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

### 3.7.18 OTHER ACTIVITIES

5 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue  
10 pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional  
15 factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case  
20 of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is  
25 cross-reactive with such protein.

### 3.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for  
30 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving

inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

### 3.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963,

Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

### 3.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 3.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically,



the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

### 3.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF),

platelet-derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

### **3.9.1 ROUTES OF ADMINISTRATION**

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome

coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

### 3.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol,

propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

5           When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to  
10       pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other  
15       vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal  
20       administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills,  
25       dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including  
30       lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose,

hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose,

5 concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

10 Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds  
15 may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

20 For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be  
25 determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit  
30 dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or

aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without

destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T



cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with  
5 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a  
10 liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids,  
15 and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and  
20 severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response.

25 Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1  $\mu$ g to about 10 mg, more  
30 preferably about 0.1  $\mu$ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are

useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering

agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final

composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

### 3.9.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical

procedures in cell cultures or experimental animals, *e.g.*, for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>.

5 Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of  
10 administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration  
15 (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should  
20 be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the  
25 invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the  
30 subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

### 3.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

### 3.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab', F(ab')<sub>2</sub>, and F<sub>v</sub>, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), *Antibodies A Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988),

Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell,



A.M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al., Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding, J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

### 3.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 362 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NOs: 1 - 362 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence

information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs)

5 within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence  
10 information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present  
15 invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded  
20 thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which  
25 match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily  
30 recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based

systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

### 3.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

### 3.13 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays*:

Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

### 3.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

### 3.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NOs: 1 - 362, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives

expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspiczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a



skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA.

- 5 Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple  
10 helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization  
15 blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present  
20 invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

### 3.16 USE OF NUCLEIC ACIDS AS PROBES

25 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 362. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from  
30 of any of the nucleotide sequences SEQ ID NOs: 1 - 362 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes.

Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

### 3.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987;

Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond

joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of

Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

### 3.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to

the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI\*\**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI\*\** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI\*\** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

### 3.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the

density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or  
5 may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays  
10 may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell  
15 plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is  
20 intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the  
25 invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 4.0 EXAMPLES

### 4.1 EXAMPLE 1

#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

### 4.2 EXAMPLE 2

#### Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.



Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genepet release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1- 362.

Table 1 shows the various tissue sources of SEQ ID NO: 1-362.

The homology for SEQ ID NO: 1-362 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1-362 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1-362 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren

Brunak, and Gunnar von Heijne in the publication “ Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites” Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al as reference, was obtained for the

5 polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

TABLE 1

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	4 18 39-40 83 88 98 110 112-113 136 168-169 201-203
adult brain	GIBCO	ABD003	7 15-16 31-32 39-41 45 54 58 63 70 73-75 82-84 92 98 106 110 114 116-117 126 128 130 139 144 155 164 168-169 191-192 195 198 204-215 239-240 249 252 258 272-274
adult brain	Clontech	ABR001	10-11 15 19 39-40 88 106 120 144 168 215-216 258
adult brain	Clontech	ABR006	13 17 20 23 33 39-40 50 58 62 75 82 84 88 100 104 121-122 129 149 168 208 216 223 232-233 239 256 269 277 287-288 353 360
adult brain	Clontech	ABR008	4 10-11 13 17 20 23 25 28-30 32 34-35 39-41 48 50 53-54 58 61 63 68-69 74 76 78 80 84-89 91 98 104 107 112-114 118 121-122 130 134-136 143 153-155 158-160 163-166 168 172-173 184-188 199-200 203 212-213 215-216 219-220 226-227 234 239 242 244 251-252 255-257 263 268 271-272 277-280 287 291 300-301 305-306 316 322 338 346-347 360
adult brain	Clontech	ABR011	157 306
adult brain	BioChain	ABR012	36 247
adult brain	Invitrogen	ABR013	176
adult brain	Invitrogen	ABR014	50 53 100 269
adult brain	Invitrogen	ABR015	19 38 74 161-162
brain	Invitrogen	ABR016	53 74 137 139 239
adult brain	Invitrogen	ABT004	8 15 19-20 28 30 35 75 78 100 106-107 113 134 160 179 181 184 198-199 210 216 224 227 252 254-255 288 340
adipocytes	Stratagene	ADP001	9 13 19 45 74 98 121-122 131 164 187 189-190 217 239
adrenal gland	Clontech	ADR002	9 15 18-19 24-25 31-32 46 56 77-78 112 114-115 117-119 121-122 124 139 170 182 192 209 213 218 220 225 249 276 306
adult heart	GIBCO	AHR001	2 4 7 17 19-22 26-27 34 38 45-46 50 53-54 58 60-61 63 74 76-77 86-87 91 96 98 108 112 114 121-122 131 133 136-140 144 155 160 165-168 184 188 217 226 239 241-242 251 259 265 277-278 290 306
adult kidney	GIBCO	AKD001	4 6-11 13 15-17 19-20 24 30-32

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			34 36-38 47 53-54 60-63 66 69 73-75 78 82-85 87 89-92 96 98 100 103 106 108 110 112-113 116 121-123 126 129 131 134 136 139-142 144 153 155 158- 159 169-170 176 181 207 237 239 266-267 271-272 306
adult kidney	Invitrogen	AKT002	7-8 10-11 13 15 19 25-27 32 37-38 53 55-56 66 75 86 90 92 108 123 144 165-166 172 182 199 218 225 233 236 238 260 266-267 332
adult lung	GIBCO	ALG001	8 22 26-28 38-40 47 54 78 91 98 104 110 112 117 139 148 168 189 196 225 239 248 351-352
lymph node	Clontech	ALN001	7 26-27 32 35 38-40 79 82 120 127 152 158-159 169 171 219 239 244
young liver	GIBCO	ALV001	7 14 16-17 19 33 37 53 72 77 107 113 116 118 134 152 168 212 249
adult liver	Invitrogen	ALV002	12 14 17 24 28 32-33 36 58 73 75-76 84 101 116 131 138 140 158-160 182 194 212 238 275 284 323 342-343
adult liver	Clontech	ALV003	271 284 358
ovary	Invitrogen	AOV001	4 6-11 13 15-16 18-21 25-27 31-32 34 36 38-40 46 48 50 53- 54 56 58 60 65 70 73-78 80 83- 84 86 91-92 95 98 100-101 103- 106 108 110-112 115 117-118 124 126-127 129-131 136 139- 142 144 148 155 157-161 163- 167 169 173-174 178 180-186 188-189 191-193 196 199-200 204-208 210-211 220-223 233 236 239 249-252 260-263 266- 270 287-288 306 315 351-352
placenta	Clontech	APL001	30 50 74 82 230
placenta	Invitrogen	APL002	45 50 59 70 75 103 163 223
adult spleen	GIBCO	ASP001	7 19 30 38 45 54 58 62 74 81 83 91 106 110 112-113 116 131 144 151 155 162 165-166 172 176 189 191 215 230 236 239 249 329
testis	GIBCO	ATS001	4 15 19-20 30 48 53 74 89 94 110 126 140 158-159 173 214- 215 220 239 245 306
bladder	Invitrogen	BLD001	30 35 59 61 74-75 123 164 221 241 318
bone marrow	Clontech	BMD001	3 6-7 9 13 17 20 26-27 30-31 34 38-40 42 46 53-54 63-79 82- 83 85 91 93-98 101 105 110 115 121-122 126 128-129 133-134

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			143 145 154 161-162 176 192 205-206 234 236 239 243 264 289 306 322
bone marrow	Clontech	BMD002	3-4 7 9 13 16-17 19-20 23 30 32 34 36 38-40 47-48 54-56 58 61 68-69 74-75 79 84 108 118- 119 121-122 125 128-129 131 133 140 144 147 149 153-154 158-159 161 163 167 171 174 176 185-187 200 211 218 232 239 241 247 252 277-278 285 296 303 310 320 324 329 339 341 353 356 359
bone marrow	Clontech	BMD004	64
colon	Invitrogen	CLN001	18 32 100 106 110 143 153 163- 164 178 213 247 266-267 284
cervix	BioChain	CVX001	4 6 8-9 19 22 24-25 28 32 45- 46 53 55-56 63 74-75 77-78 83 87 91-92 95 102 105 108 110 123 127 136-137 140 169 172 182 184-186 189-191 199 211 238 249 266-267 274 283 306- 308 317 354
endothelial cells	Stratagene	EDT001	2 4 6-7 9 15 17-21 25-28 30 32 36 39-40 45 47-48 53 55-57 60 62-63 69-70 74-76 78 83 85-87 98 101-104 106 108 112-113 119 121-123 130-131 136-137 139- 142 155-156 158-159 161 174 189-192 204 208 218 220 223 230 239 251 280 306
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM001	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM003	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM004	223
fetal brain	Clontech	FBR001	32 227
fetal brain	Clontech	FBR004	319
fetal brain	Clontech	FBR006	7 10-11 13 17 20 23-25 28-29 32 35 41-42 48 50 53 63 75 80 89 91 104 112 121-122 125 130 154 163 165-166 168 171 173 191 199 210 215-216 218 226 232 239 256 272 277 290 300 306 309 319-320 333 353 360
fetal brain	Invitrogen	FBT002	15 17 19 35 69 75 87 104 109 140 163 174 192-193 198-199

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			207 220 228 239 252 256-258
fetal heart	Invitrogen	FHR001	3 8 19 32 41 48 77-79 91 114 119 126 163 165-166 172 174 176 200 218 232 244 263 331 351-352 360-361
fetal kidney	Clontech	FKD001	16-17 36 46 53 74 82 95 104 111 117 169 189
fetal kidney	Clontech	FKD002	26-27 165-166 218 220 232 238 263 306
fetal kidney	Invitrogen	FKD007	38 74
fetal lung	Clontech	FLG001	32 48 139 173 217
fetal lung	Invitrogen	FLG003	10-11 19 36 58 61 69 74 134 163 168 178 194 249 263 266- 267 351-352
fetal liver- spleen	Columbia University	FLS001	1-19 21-38 41-62 68 70 72 74- 78 87 90-91 93 100-104 106-121 123-125 127 130-131 133-134 141-142 144 149 155-156 161 163 165-167 169 176 194-196 200 207 210 221 224-225 227 231-233 236 238 263 303 306 313 324 336 342
fetal liver- spleen	Columbia University	FLS002	2 5 7-9 12 14 16-18 22-24 30- 33 35-40 43-46 48-50 52-53 57 70 72 76-78 84-85 87 90 92 101-102 106-108 110 112 114 116-120 124 127-128 130-131 134-135 140-142 144 155 163 172 174 187 189-190 192 195- 196 199 205-207 210 220-221 223-224 230-234 244 251 258 260-261 263 265 275 296 313- 315 331 337-338 345 362
fetal liver- spleen	Columbia University	FLS003	19 30 33 139 174 265 313 339 355
fetal liver	Invitrogen	FLV001	10-11 14 17 19 21 37 46 50 61 63 156 163 165-166 172 200 210 238 253
fetal liver	Clontech	FLV002	19 32 74 163 356
fetal liver	Clontech	FLV004	3 14 19 32-33 37 42 47-48 50 58 60 82 85 121-122 129 131 152 171 193 272 353
fetal muscle	Invitrogen	FMS001	28 32 39-40 45 48 50 57 74 107 121-122 131 137 139-140 147 173 204 230 281
fetal muscle	Invitrogen	FMS002	19 23 32 34 55-56 80-81 98 121-122 124 131-132 158-159 199 212 230 280-281 353 357 360
fetal skin	Invitrogen	FSK001	2 4 14-15 17-19 22 41 46 50 53 59 72 75-76 81-82 84 94 103 106 113 128 135 140 144 156 164 167 170 174 188 209-210 220 227 230 238-239 254 306

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			321-322 333-335
fetal skin	Invitrogen	FSK002	4 34 47 54 79 84 113 126-127 129 134 156 192-193 208 223 230 241 277 285 333
fetal spleen	BioChain	FSP001	32 104
umbilical cord	BioChain	FUC001	4 19 22-23 32 38-40 46 55-56 58 61 73-75 91 98-99 103 106 110 112 116 120 123 129-130 139 160 165-166 175 182 230 234 249 251 302
fetal brain	GIBCO	HFB001	6 9 16 19-20 25 32 35-36 39-41 45 48 53-54 56 60 73 80-81 83- 92 98 107 112 114 157-159 163 165-166 172 191 197-198 211 226-227 239 350
infant brain	Columbia University	IB2002	6-8 13 15-17 19 21 32 35 41-42 48 50 60-61 77 81 84-85 88 92 104-106 112-113 116 119 134 139 144 160 165-166 168-169 173 176 191 196 199-201 215 223 225 227-228 239 261 285 290 329 339-340 348
infant brain	Columbia University	IB2003	7-9 13 32 39-41 58 92 103 105- 106 144 160 162 199 205-206 219 227-228 271 357
infant brain	Columbia University	IBM002	32 88 340
infant brain	Columbia University	IBS001	6 26-27 32 164 199 340
lung, fibroblast	Stratagene	LFB001	2 4 18-19 25 39-40 46 53 55-56 106 112 124 129 136 139 146 150 164 169 189-190 215 230 239 260 349
adult lung	Invitrogen	LGT002	2 6 8-11 15-16 19 26-28 30 32 39-40 46 48 50 53-56 60-61 66 72 74-75 85 87 92 94 96 98 103-104 108 110 112-113 117 119-120 124 130-131 139-140 149 152-153 155 158-159 167 169 174 176 178 184 189-190 195-196 217 220 229-230 234- 239 248-250 263 265-267 280 286 310 329-330 351-352
lymphocyte	ATCC	LPC001	7 13 16 19 32 39-40 54 63 74 82 96 113 120 126 130-131 133 144 150 178 184-186 223 239 241 260 262 294 305 339
leukocytes	GIBCO	LUC001	1 3-4 7-9 13 16-20 26-27 30 32 34-35 38-40 46 48 51 53-56 63 66 70 72-76 78 82 84-85 87 89 91-92 95-96 101 106 108 110- 112 114 116 120-122 126-127 129-133 136 139 144 146-152 164 175-179 187 192 232 236

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			239 241 266-267 292-294 306 325-327 329 339 359
leukocytes	Clontech	LUC003	7-8 17 55-56 76 84 112 129 131 161-162 176 180 185-186 329
melanoma	Clontech	MEL004	4 13 17 28 30-31 39-40 83 85 92 113 126 129 139 160 162 182 198 232 239 303 324
mammary gland	Invitrogen	MMG001	8-11 16-21 28 30 32 35 41 45 58-59 61 72 74-75 78 84 87 92 103-104 106-107 110 113 115- 116 123 128 131 134-135 144 152 163 176 181 183 210 212 220-221 230 234 236 238-239 248 251 260 272-273 275-276 306 331 351-352 360
neuron	Stratagene	NTD001	18-19 39-40 45 74 78 85 91
neuron	Stratagene	NTR001	19 21 57 246 265
neuronal cells	Stratagene	NTU001	8-9 18-19 21 32 81 85 87 128 164 174 184
pituitary gland	Clontech	PIT004	13 47 82 87 98 112 288 354
placenta	Clontech	PLA003	13 48 50 58 77 100 106 112 126 129 152 178 232
prostate	Clontech	PRT001	16 19 22 26-27 32 34 46-47 76- 77 92 98 106 112 124 172 214 239 260 280 294
rectum	Invitrogen	REC001	8 10-11 18 30 54 74-76 106 113 123-124 143 163 172 213 220 232 237 260 322-323 340
salivary gland	Clontech	SAL001	8 19 36 74 83 104 118 124 150 176 260 295 304
skin fibroblast	ATCC	SFB002	239
small intestine	Clontech	SIN001	9 17 19 22 32 34 54 57 59-60 73 75 84-85 96 99 107 113 118 134 139 144 149 151 185-187 189 197 199 217 219 221 230- 231 248 250 253-254 260 266- 267 295 304 356
skeletal muscle	Clontech	SKM001	17 19 39-40 48 89 104 116 131 281
spinal cord	Clontech	SPC001	8 19 32 34 38-40 47 58 61 74 80 83-84 89 104 108 131 139- 140 168 187 213 226 236 239 300 350
adult spleen	Clontech	SPLc01	1 46 54 134 236
stomach	Clontech	STO001	7 32 38-40 51 66 74 76 89 117 124 128 169 229 239 253 280 294 296
thalamus	Clontech	THA002	24 30 50 87 124 127 143 163 201 207 220 223 230 266-267 269 279
thymus	Clontech	THM001	7 13 19 25 32 36 39-40 54-56 72 74 82 96 108 113 119 127



TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			137 139 141-142 146 169 184 192 260 276 296
thymus	Clontech	THMc02	9 17 28 30 32 39-40 48 53 61 72 74-75 77 79 82 91 107 112 119-122 125-126 131 139-142 153 171 175-176 178 184 187 205-206 222-223 227 235-236 269 278 289 297 305 310-311 325 327-329 336
thyroid gland	Clontech	THR001	7-11 15 17 19-20 25-27 32 34 36 46 48 53 59 72 82-87 89 91 96 98-99 104 106 110 118-119 121-122 127 130 136 139 144 151-152 158-159 165-167 179 187 204 208 220 239 249 281 283 295 298-299 312 316 344
trachea	Clontech	TRC001	62-63 73 75 86-87 89 101 147 192 239 266-267 282-283
uterus	Clontech	UTR001	4 8 17 19 22 26-27 32 39-40 46 63 82 98 110 130 151

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	L29075	Dictyostelium discoideum G-box binding factor	173	21
2	AL359215	Streptomyces coelicolor A3(2) putative phosphoglycerate mutase.	133	28
3	AF228713	Homo sapiens EDAG-1	1671	100
4	AC007130	Homo sapiens similar to 3-hydroxyisobutyrate dehydrogenase ; similar to P29266 (PID:g416873)	1557	100
5	AB040926	Homo sapiens KIAA1493 protein	1973	98
6	AF193016	Homo sapiens methyltransferase COQ3	1609	99
7	U95825	Homo sapiens androgen-induced prostate proliferative shutoff associated protein	2968	63
8	AL390081	Homo sapiens SEMA4B, Semaphorin 4B	3560	99
9	AC002130	Arabidopsis thaliana F1N21.9	258	50
10	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	323	27
11	D88733	Equine herpesvirus 1 membrane glycoprotein	284	24
13	M80783	Homo sapiens B12 protein	1144	70
14	U72678	Mus musculus EF-9	792	92
15	AK026486	Homo sapiens unnamed protein product	427	83
16	AK025813	Homo sapiens unnamed protein product	1010	100
17	AF151036	Homo sapiens HSPC202	722	84
18	AY007148	Homo sapiens similar to Homo sapiens HSPC197 mRNA with GenBank Accession Number AF151031.1	984	100
19	X57432	Rattus rattus ribosomal protein S2	956	97
20	AF164793	Homo sapiens protein x 013	386	100
21	J02642	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	1639	95
22	M34573	Homo sapiens alpha-2 collagen type VI-a	515	100
23	AL109928	Homo sapiens dJ551D2.5 (novel protein)	1999	100
24	AF111858	Homo sapiens dimethylglycine dehydrogenase precursor	3918	99
25	U64854	Caenorhabditis elegans partial CDS	184	25
26	AF151072	Homo sapiens HSPC238	838	99
27	AF151072	Homo sapiens HSPC238	393	96
28	AK024825	Homo sapiens unnamed protein product	1794	99
29	AF285631	Rattus norvegicus secretory carrier membrane protein 4	894	75
30	AK024113	Homo sapiens unnamed protein	3672	99

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
31	AL161515	Arabidopsis thaliana putative protein	146	52
32	AJ007798	Homo sapiens stromal antigen 3, (STAG3)	6320	99
33	D31856	Bacillus subtilis HutI protein, imidazolone-5-propionate hydrolase	667	39
34	AL391145	Arabidopsis thaliana putative protein	423	24
35	AF134726	Homo sapiens G7A	1591	46
36	AJ276485	Homo sapiens integral membrane transporter protein	1502	100
37	J05158	Homo sapiens carboxypeptidase N (EC 3.4.17.3)	2274	88
38	X57351	Homo sapiens l-8D	673	97
39	AF230904	Homo sapiens c-Cbl-interacting protein	3437	100
40	AF230904	Homo sapiens c-Cbl-interacting protein	2615	99
41	AF276893	Homo sapiens p21-activated protein kinase 6	3550	100
42	AF269255	Homo sapiens lysosomal apyrase-like protein 1	3198	100
43	S85655	Homo sapiens prohibitin	742	84
44	AB040926	Homo sapiens KIAA1493 protein	1973	98
45	AF151063	Homo sapiens HSPC229	1012	100
46	X68277	Homo sapiens protein-tyrosine phosphatase	1886	100
47	Z98745	Homo sapiens dJ29K1.2	889	51
48	AF032668	Rattus norvegicus rsec15	3738	92
50	AF195534	Rattus norvegicus GERp95	4513	99
51	AF161368	Homo sapiens HSPC105	513	98
52	W73147	Amino acid sequence of the soluble complement receptor 1	651	81
53	AF271212	Homo sapiens disrupter of silencing SAS10	2431	100
54	AF116646	Homo sapiens PRO0082	598	100
55	AF145613	Drosophila melanogaster BcDNA.GH03108	817	46
56	AF145613	Drosophila melanogaster BcDNA.GH03108	884	38
57	AL023803	Homo sapiens dJ616B8.3 (novel gene)	2287	100
59	AC024877	Caenorhabditis elegans contains similarity to Pfam families PF00621 (Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases, score=58.2, E=1.7e-13, N=10 and PF00169 (PH (pleckstrin homology) domain, score=17.0, E=0.00071, N=1)	296	31
60	AL390114	Leishmania major probable proteophosphoglycan	154	30
61	AL031427	Homo sapiens dJ167A19.1 (novel	732	51

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
		protein)		
62	AL390935	Leishmania major possible CG17807 protein	151	43
63	J04067	Canis familiaris microsomal signal peptidase	930	99
64	AF062378	Mus musculus calmodulin-binding protein SHA1	1782	60
65	AE001002	Archaeoglobus fulgidus ATP-dependent RNA helicase, putative	195	29
66	X69065	Erythroid ankyrin [Mus musculus]	181	30
68	AF017807	Homo sapiens Arp2/3 complex 16kDa subunit	371	100
69	AC007660	Arabidopsis thaliana putative translation initiation factor	173	29
70	AJ243177	Xenopus laevis Xenopus RPA interacting protein alpha	447	42
71	AF226055	Homo sapiens HTGN29	1367	100
72	AF090930	Homo sapiens PRO0478	180	89
73	AF118084	Homo sapiens PRO1914	350	98
74	AB028893	Homo sapiens ribosomal protein S11	824	100
75	AK024500	Homo sapiens FLJ00109 protein	1514	100
76	AF238866	Mus musculus LNR42	1041	99
77	AC026875	Arabidopsis thaliana T6D22.6	129	30
78	U42436	Caenorhabditis elegans Hypothetical protein C49H3.3	130	32
79	M80902	Homo sapiens AHNAK nucleoprotein	8529	99
80	W90962	Human CSGP-2 protein [homo sapiens]	2346	99
81	AF206661	Gallus gallus neuronal tetraspanin	1066	81
82	S73591	Homo sapiens brain-expressed HHCPA78 homolog VDUP1	800	42
83	AF116650	Homo sapiens PRO0786	302	100
84	L26335	Cavia porcellus zinc finger protein	1493	99
85	AF209198	Homo sapiens zinc finger protein 277	2357	100
86	AE001399	Plasmodium falciparum GAF domain protein (cyclic nt signal transduct.)	178	35
87	Y48226	Human prostate cancer-associated protein 12 [Homo sapiens]	1204	96
88	M94389	Loligo pealei neurofilament protein	165	23
89	AF121775	Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16	903	58
90	AF116675	Homo sapiens PRO1942	257	100
91	AE002760	Drosophila melanogaster CG14464 gene product	195	43
92	AK000100	Homo sapiens unnamed protein product	841	100
93	AB020236	Homo sapiens ribosomal protein L27A	754	99
94	AF119865	Homo sapiens PRO2176	470	97
96	AF138863	Homo sapiens PRO1677	868	99
97	X14361	Homo sapiens CR-1 receptor SCR9 (or	135	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		16) C-term. (21 is 3rd base in codon) (106 is 1st base in codon)		
98	Z24725	Homo sapiens mitogen inducible gene mig-2	3576	99
99	U64598	Caenorhabditis elegans weakly similar to S. cerevisiae PTM1 precursor (SP:P32857)	398	45
100	AC004770	Homo sapiens BC269730 4	1527	84
101	AL139075	Campylobacter jejuni NOL1\NOP2\sun family protein	312	35
102	AF113694	Homo sapiens PRO1359	416	100
103	U15158	Homo sapiens ESP-2	564	41
104	AL020996	Homo sapiens dJ317E23.3 (novel protein)	1818	99
105	AF161370	Homo sapiens HSPC107	824	100
106	AK000161	Homo sapiens unnamed protein product	284	100
107	AK001784	Homo sapiens unnamed protein product	684	100
108	AE000913	Methanobacterium thermoautotrophicum conserved protein	221	25
109	AF165527	Homo sapiens DGCR8	859	100
110	AF230200	Homo sapiens OVN6-2	358	95
111	Z72516	Caenorhabditis elegans T25G3.1	180	36
112	AF201940	Homo sapiens DC6	505	100
113	AK001301	Homo sapiens unnamed protein product	2040	98
114	U23515	Caenorhabditis elegans weakly similar to gastrula zinc finger protein	205	47
115	AF228021	Bos taurus cyclophilin I	345	91
116	AF166124	Homo sapiens selenoprotein X	527	100
117	AF079445	Dictyostelium discoideum TipC	529	30
118	AB032179	Homo sapiens similar to mouse Ehm2	2255	100
119	U89867	Homo sapiens nuclear matrix protein 55	2449	98
120	U29056	Mus musculus Src-like adapter protein	352	47
121	U22015	Mus musculus retinoid X receptor interacting protein	2190	73
122	AF113538	Homo sapiens retinoid x receptor interacting protein	1800	100
123	AK000158	Homo sapiens unnamed protein product	740	100
124	AF260924	Mus musculus UFD2/D4COLE1E fusion protein	1222	82
125	U12465	Homo sapiens ribosomal protein L35	591	97
126	AJ277591	Homo sapiens p15-2a protein	749	100
127	AF205599	Mus musculus transposase-like protein	2406	74
128	U58975	Homo sapiens proto-oncogene	659	90

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
129	X98374	Rattus norvegicus KIS	2193	99
130	AF151049	Homo sapiens HSPC215	627	100
131	M59807	Homo sapiens putative	907	99
132	U12979	Homo sapiens PC4	563	99
133	AF076642	Homo sapiens regulator of G-protein signaling 13	1218	100
134	AF116718	Homo sapiens PRO2900	396	100
135	AC018758	Homo sapiens GPI-anchored metastasis-associated protein homolog	213	31
136	AC025416	Arabidopsis thaliana F5011.12	135	36
137	M83186	Homo sapiens cytochrome c oxidase subunit VIIa	247	100
138	AF232937	Mus musculus thymic stroma derived lymphopoietin	247	41
139	M15841	Homo sapiens U2 small nuclear ribonucleoprotein B''	638	100
140	AK026916	Homo sapiens unnamed protein product	2612	99
141	Y05317	Human secreted protein bn97_1 [Homo sapiens]	1508	100
142	Y05317	Human secreted protein bn97_1 [Homo sapiens]	851	99
143	AF041083	Rattus norvegicus RoBo-1	139	25
144	AC024260	Arabidopsis thaliana cell division control protein, putative; 15914-18846	194	25
146	AL022398	Homo sapiens dJ434014.3.2 (putative protein) (isoform 2)	575	100
147	AF212842	Homo sapiens immunoglobulin-like transcript 11 protein	1280	99
148	AB042827	Rattus norvegicus Nadrin	477	66
149	AK001841	Homo sapiens unnamed protein product	1916	100
150	AJ278120	Homo sapiens putative ankyrin-repeat containing protein	540	98
151	AL135959	Homo sapiens dJ233G16.1 (novel protein)	770	100
152	Y58196	[Homo sapiens] Human STRAP-3 protein, encoded by testis EST AI139607	671	100
153	U41060	Homo sapiens LIV-1 protein	373	50
154	AJ007590	Homo sapiens XRP2 protein	1766	100
155	AB046868	Xenopus laevis beta-catenin-interacting protein	125	46
156	AB027258	Homo sapiens basal transcriptional activator hABT1	1408	100
157	AF039656	Homo sapiens neuronal tissue-enriched acidic protein	1109	96
158	AK001425	Homo sapiens unnamed protein product	1695	99
159	AK001425	Homo sapiens unnamed protein	858	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
		product		
160	AK002030	Homo sapiens unnamed protein product	1029	100
161	X79417	Sus scrofa 40S ribosomal protein S12	510	83
162	X12597	Homo sapiens HMG-1 protein (AA 1-215)	1140	99
163	AK001159	Homo sapiens unnamed protein product	764	100
164	AK000020	Homo sapiens unnamed protein product	1613	100
165	AK001322	Homo sapiens unnamed protein product	1207	100
166	AK001322	Homo sapiens unnamed protein product	892	98
167	AE003822	Drosophila melanogaster CG8493 gene product	357	36
168	AF023451	Bos taurus guanine nucleotide-exchange protein	187	21
169	AK000154	Homo sapiens unnamed protein product	673	100
170	AJ132702	Mus musculus ATFa-associated factor	435	64
172	AL022311	Homo sapiens dJ1014D13.3 (novel protein)	405	38
174	AB017634	Mus musculus ENP	770	65
175	U40407	synthetic construct T cell receptor alpha chain	1119	80
176	AF043179	Homo sapiens T cell receptor beta chain	681	73
177	AF116678	Homo sapiens PRO1995	587	100
178	AF217522	Homo sapiens uncharacterized bone marrow protein BM046	262	42
179	AB046074	Macaca fascicularis unnamed protein product	515	83
180	X79417	Sus scrofa 40S ribosomal protein S12	429	84
181	AF002668	Homo sapiens MLD	1235	65
182	AB036422	Bos taurus molybdopterin cofactor sulfurase	3509	79
184	AF036696	Caenorhabditis elegans contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632)	662	42
185	AJ277276	Homo sapiens rapa-2	5155	99
186	AJ277275	Homo sapiens rapa-1	5086	100
187	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform	1444	93
188	AE003750	Drosophila melanogaster CG9996 gene product	468	44
189	Z97056	Homo sapiens dJ434P1.2 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum	1103	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein retention receptor 3)		
190	AF081126	Drosophila melanogaster ER lumen protein retaining receptor	409	75
192	AF226047	Homo sapiens GL002	863	100
193	AF269167	Homo sapiens arsenite related gene 1	906	60
195	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor	162	26
197	AL357374	Homo sapiens bA353C18.2 (novel protein)	404	97
199	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	964	42
202	AF230201	Homo sapiens OVC10-2	396	100
203	AK001984	Homo sapiens unnamed protein product	658	100
204	AK000530	Homo sapiens unnamed protein product	691	100
205	U37134	Drosophila melanogaster inturnd protein	248	23
206	U37134	Drosophila melanogaster inturnd protein	244	23
208	AB033130	Mus musculus testis-specific gene	871	85
209	AK000464	Homo sapiens unnamed protein product	221	100
210	AJ277557	Homo sapiens mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2)	617	100
211	AF127564	Arabidopsis thaliana ubiquitin-protein ligase 1	854	42
213	Y17108	Homo sapiens rhomboid-related protein	485	39
214	AL132776	Homo sapiens dJ393D12.2 (novel LIM domain protein)	1660	99
215	U73819	Mus musculus polypeptide GalNAc transferase-T4	1039	42
216	AL035406	Homo sapiens dJ233K16.1 (KIAA0444, a putative chromodomain helicase DNA binding protein 3 (CHD3))	3844	100
217	M15800	Homo sapiens MAL protein	308	42
218	L29554	Rattus norvegicus alpha 2,6-sialyltransferase	942	80
219	AL137315	Homo sapiens hypothetical protein	983	100
220	AK026027	Homo sapiens unnamed protein product	647	100
221	AL137584	Homo sapiens hypothetical protein	246	97
223	AC005498	Homo sapiens R31665 1	1752	78
225	AC010155	Arabidopsis thaliana F3M18.5	171	34
226	AL080276	Homo sapiens dJ101K10.2 (regulator of G-protein signaling 17 (RGS17) (RGSZ2))	1126	100
227	AF042345	Homo sapiens truncated EVI5	1815	64
228	J04214	Bos taurus retinaldehyde-binding protein precursor	504	39



SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
230	AF181263	Homo sapiens EH domain containing 2	2816	99
231	AP001660	Homo sapiens putative gene, multidrug resistance associated protein like	1424	100
232	AB000910	Sus scrofa ribosomal protein	542	100
233	AL133404	Homo sapiens dJ238023.9 (novel protein similar to rat SAC (soluble adenylyl cyclase))	298	100
234	X51397	Mus musculus MyD88 protein (AA 1-243)	136	25
235	X01403	Homo sapiens T-cell receptor alpha-chain	840	90
236	X14254	Rattus rattus invariant chain (AA 1-280)	745	77
238	U23084	Saccharomyces cerevisiae Ynl0470p	344	35
239	X03342	Homo sapiens rpl32 (aa 1-135)	152	96
240	AF116669	Homo sapiens PRO1828	237	100
241	U23181	Caenorhabditis elegans final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein	135	25
242	AF263913	Mus musculus fidgetin	3864	97
243	AF090892	Homo sapiens PRO0106	290	100
244	U21310	Caenorhabditis elegans F40H6.3 gene product	153	27
246	AK001673	Homo sapiens unnamed protein product	3661	100
247	AL022603	Arabidopsis thaliana putative protein	166	43
248	AL023803	Homo sapiens dJ616B8.3 (novel gene)	339	42
249	X52140	Rattus norvegicus precursor polypeptide (AA -28 to 1152)	5429	87
250	AB020755	Arabidopsis thaliana gene id:MZN1.18~unknown protein	139	46
251	AE003619	Drosophila melanogaster CG7224 gene product	186	43
252	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), and C01164 (NID:g1433394); alternatively spliced form of H_DJ130H16.1a (C-terminal truncation confirmed by C01164)	388	67
254	AE003588	Drosophila melanogaster CG13947 gene product	115	42
256	Y50934	Human fetal brain cDNA clone vc30_1 derived protein #1 [Homo sapiens]	498	100
257	AF242768	Homo sapiens mesenchymal stem cell protein DSC43	1554	100
259	M95779	Bos taurus G protein gamma-5 subunit	333	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
260	AL035521	Arabidopsis thaliana putative protein	145	28
261	AF247501	Drosophila melanogaster PINEAPPLE EYE	333	36
263	AL034548	Homo sapiens dJ1103G7.2 (novel protein)	262	100
264	AF119851	Homo sapiens PRO1722	143	63
265	L41834	Ensis minor nuclear protein	173	26
266	X97966	Homo sapiens calcyphosine	963	100
267	X97966	Homo sapiens calcyphosine	660	95
269	AF022383	Homo sapiens complexin I	668	99
271	Y10054	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase	224	67
274	AF153201	Homo sapiens zinc finger protein dp	179	36
275	X85738	Bos taurus novel brain-specific protein	326	55
277	AF250342	Arabidopsis thaliana SMC-related protein MSS2	266	39
278	AL080242	Homo sapiens bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	131	100
279	Z83760	Ciona intestinalis COS41.4	1162	62
280	U41534	Caenorhabditis elegans similar to yeast MAK16 protein (SP:MK16 YEAST,P10962)	721	54
281	AF272975	Gallus gallus smoothelin-C	543	37
282	AL035414	Homo sapiens dJ667H12.2.2 (novel protein (isoform 2))	588	100
283	AF116661	Homo sapiens PRO1438	145	62
285	AK001757	Homo sapiens unnamed protein product	1300	100
287	U20897	Homo sapiens melanoma ubiquitous mutated protein	2133	100
289	U09847	Homo sapiens zinc finger protein	880	100
290	AJ000079	Trypanosoma cruzi glycosylphosphatidylinositol-specific phospholipase C	225	26
291	AF156549	Mus musculus putative E1-E2 ATPase	2108	49
293	AF161345	Homo sapiens HSPC082	439	100
294	AF116694	Homo sapiens PRO2219	351	88
295	M74027	Homo sapiens mucin	461	39
298	AL133640	Homo sapiens hypothetical protein	2149	100
299	M17886	Homo sapiens acidic ribosomal phosphoprotein (P1)	161	76
300	Y99368	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100 [Homo sapiens]	300	32
303	AE003708	Drosophila melanogaster CG6171 gene product	144	27
304	M32639	Homo sapiens statherin precursor	276	87
305	Z83844	Homo sapiens dJ37E16.2 (SH3-domain binding protein 1)	897	96

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
306	AE003791	Drosophila melanogaster CG18065 gene product	120	32
307	AF135026	Homo sapiens kallikrein-like protein 3 splice variant 1	1392	100
310	AF198257	Felis catus immunoglobulin kappa light chain	678	76
311	X57725	Homo sapiens TCR Vbeta 22a	626	100
312	AC018513	Homo sapiens unknown	818	100
313	X03249	Bos taurus epsilon-4 beta-globin	321	79
314	AB046099	Macaca fascicularis unnamed protein product	395	88
315	AC006033	Homo sapiens T cell receptor gamma chain; match to S08328 (PID:g106470)	1017	95
316	AB046103	Macaca fascicularis unnamed protein product	801	94
317	U88895	Homo sapiens ORF2	399	81
318	U09848	Homo sapiens zinc finger protein	242	49
319	AB003184	Homo sapiens ISLR	880	59
320	AB036921	Chrysophrys major maturation-inducing protein	797	69
322	AF284422	Homo sapiens cation-chloride cotransporter-interacting protein	4694	100
325	AE000659	Homo sapiens TCRAV8S2	577	100
327	R59748	T cell receptor Valpha2.3 chain [homo sapiens]	636	100
328	AJ004871	Homo sapiens TCR alpha chain	1328	94
329	AF043179	Homo sapiens T cell receptor beta chain	1286	92
330	AF090930	Homo sapiens PRO0478	140	50
332	AF077043	Homo sapiens 60S ribosomal protein L36	275	87
333	AL121988	Homo sapiens dJ34M23.3 (gap junction protein, beta 4 (connexin 30.3))	1457	100
334	D86424	Mus musculus high-sulfur keratin protein	521	87
335	AF090434	Fundulus heteroclitus cytochrome P450 2N1	760	40
336	AF116688	Homo sapiens PRO2133	370	98
337	X85372	Homo sapiens Sm protein F	222	84
338	D87009	Homo sapiens putative	1822	99
339	AE000860	Methanobacterium thermoautotrophicum conserved protein	631	35
340	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	1305	98
341	AE000004	Mycoplasma pneumonia MG207 homolog, from M. genitalium	141	27
342	AF151076	Homo sapiens HSPC242	135	100
343	AB037902	Homo sapiens truncated aldo-keto reductase	670	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
345	M33014	Drosophila melanogaster ubiquitin	153	62
346	AF053356	Homo sapiens leucin rich neuronal protein	580	46
348	AL137512	Homo sapiens hypothetical protein	751	100
349	S68015	Homo sapiens c6.1A	1664	100
350	AF151037	Homo sapiens HSPC203	318	100
351	AB036432	Homo sapiens advanced glycation endproducts receptor	2133	100
352	AB036432	Homo sapiens advanced glycation endproducts receptor	2094	96
353	AC006942	Homo sapiens R31181_2, partial protein	547	100
354	AF125535	Homo sapiens pp21 homolog	502	95
355	AF227130	Homo sapiens candidate taste receptor T2R3	1629	100
357	AB046626	Macaca fascicularis hypothetical protein	291	93
358	Z69597	Canis familiaris Rod transducin alpha subunit	1145	100
359	AE000659	Homo sapiens TCRAV16S1	565	100
360	Y99368	Human PRO1326 (UNQ686) Amino acid sequence SEQ ID NO:100. [Homo sapiens]	2034	100
362	L06499	Homo sapiens ribosomal protein L37a	187	55

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 4.025e-06 60-80
2	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 7.750e-06 208-220
3	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.438e-07 285-319
4	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 7.061e-22 151-190 BL00895C 20.10 8.071e-22 200-236 BL00895A 12.61 1.973e-18 42-63
5	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
7	PF00598	Influenza Matrix protein (M1).	PF00598C 19.35 3.333e-07 531-563
9	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 3.250e-06 287-297
10	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
11	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
12	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775G 10.64 3.487e-07 8-27
13	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 1.000e-05 176-200
14	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.127e-07 159-171 PR00875D 5.00 1.000e-05 158-169
15	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 9.200e-07 181-191 DM01803A 10.51 1.000e-06 178-199 DM01803C 7.00 7.337e-06 214-224
16	PF00803	3A movement protein.	PF00803D 14.15 2.622e-06 41-71
17	PR00170	SODIUM CHANNEL SIGNATURE	PR00170G 7.74 1.000e-05 24-53
18	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 5.684e-06 117-133
20	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 6.063e-06 55-68
21	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL- TERMINAL.	DM01418A 20.83 7.731e-06 64-112
22	BL00616	Histidine acid phosphatases phosphohistidine proteins.	BL00616D 15.83 7.268e-06 117-133

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611A 7.73 5.826e-06 173-181
24	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832D 21.81 5.017e-06 425-449
25	PR00354	7FE FERREDOXIN SIGNATURE	PR00354C 5.72 8.590e-09 543-561
26	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 3.851e-07 89-105
27	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 1.439e-06 168-180
28	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552A 11.97 1.000e-05 130-152
29	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 3.088e-06 102-126
30	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.	DM00060 6.92 3.284e-07 680-690
34	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 6.971e-07 484-496
35	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 4.183e-06 722-744
37	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513C 10.79 8.927e-07 287-304
38	PR00166	AROMATIC AMINO ACID PERMEASE SIGNATURE	PR00166I 11.06 1.000e-05 98-118
39	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
40	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
41	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 8.788e-07 2-14
42	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701F 14.45 7.750e-06 25-46
43	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895B 8.85 4.185e-06 157-167
44	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
45	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519A 8.06 8.984e-06 137-154
46	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 1.828e-07 151-168
47	DM00892	3 RETROVIRAL PROTEINASE.	DM00892B 9.78 2.047e-06 21-27
48	BL00832	2'-5'-oligoadenylate synthetases	BL00832B 15.45 6.836e-07 375-416

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	
49	DM00588	8 kw CHO2 ALPHA ANTIGEN PARAMYOSIN.	DM00588A 10.87 7.128e-06 20-31
50	DM00604	2 SHIGA/RICIN RIBOSOMAL INACTIVATING TOXINS.	DM00604D 13.26 8.250e-06 263-273
51	BL01193	Ribosomal protein S8e proteins.	BL01193A 13.21 1.000e-05 19-50
52	PR00172	GLUCOSE TRANSPORTER SIGNATURE	PR00172F 8.47 9.901e-06 69-90
53	PR00297	10 KD CHAPERONIN SIGNATURE	PR00297A 13.91 4.740e-06 379-395
54	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.710e-06 81-96
55	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
56	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
57	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547E 13.94 4.656e-06 229-252
58	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 3.723e-06 32-68
60	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 7.338e-07 171-185
61	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 3.187e-06 205-244
62	PR00439	11-S SEED STORAGE PROTEIN FAMILY SIGNATURE	PR00439G 17.85 9.239e-07 82-100
63	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652F 11.66 4.767e-06 100-122
64	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785A 14.90 2.196e-06 218-261
65	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 5.104e-06 315-336
67	BL00405	43 Kd postsynaptic protein.	BL00405F 8.07 9.920e-06 13-44
68	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 9.043e-06 44-66
69	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683D 15.87 9.571e-06 46-65
70	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753C 13.93 7.330e-06 192-213
71	PF00602	Influenza RNA- dependant RNA	PF00602J 9.52 9.727e-06 47-102

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polymerase subunit PB1.	
72	DM01855	PROTEIN-GLUTAMATE O-METHYLTRANSFERASE.	DM01855A 11.54 7.594e-06 27-44
74	BL01277	Ribonuclease PH proteins.	BL01277A 17.39 1.000e-05 50-88
75	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517G 16.45 6.919e-06 755-771
77	PF01073	3-beta hydroxysteriod dehydrogenase/isomerase family.	PF01073B 12.26 9.767e-07 102-147
78	PR00351	MAS20 PROTEIN IMPORT RECEPTOR SIGNATURE	PR00351C 7.03 6.182e-06 99-112 PR00351C 7.03 1.000e-05 5-18
79	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 4.549e-06 1489-1501
80	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111C 9.35 2.800e-06 44-73
82	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 1.000e-06 94-111
83	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 9.850e-06 14-44
84	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517F 11.48 7.250e-06 45-62
87	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 3.535e-07 223-237
88	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 8.034e-08 270-320
91	DM01242	3 THREONINE--TRNA LIGASE.	DM01242B 23.57 4.672e-06 71-120
92	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388E 6.66 3.797e-06 124-136
93	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 9.676e-06 15-32
94	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 4.555e-06 16-52
95	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551H 11.29 8.740e-06 21-39
96	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756E 11.91 9.338e-06 68-81
97	PR00547	X OPIOID RECEPTOR SIGNATURE	PR00547B 6.96 3.268e-06 17-36
98	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR	PR00651A 16.53 4.000e-06 653-674



SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
99	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208C 11.51 9.775e-06 54-71
101	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 1.000e-05 152-161
102	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832B 15.45 7.569e-06 1-42
103	BL00405	43 Kd postsynaptic protein.	BL00405J 13.28 6.952e-06 142-176
104	DM01242	3 THREONINE--TRNA LIGASE.	DM01242F 10.61 5.500e-07 187-201
105	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834A 4.96 7.097e-06 53-60
107	PR00101	ASPARTATE CARBAMOYLTRANSFERASE SIGNATURE	PR00101E 5.52 1.000e-05 111-117
109	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 9.922e-06 91-115
110	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259A 9.27 9.716e-06 9-33
111	BL00785	5'-nucleotidase proteins.	BL00785B 10.65 6.507e-06 53-67
112	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652G 10.94 5.429e-06 14-32
113	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 3.661e-06 372-384
114	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637D 7.09 9.449e-07 32-44
115	DM01235	5 kw T4 55.10 METHYLCYTOSINE TRANSCRIPTASE.	DM01235 20.29 9.832e-06 77-108
116	PR00873	ECHINOIDEA (SEA URCHIN) METALLOTHIONEIN SIGNATURE	PR00873C 6.16 9.906e-06 70-81
117	PR00387	3'5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE SIGNATURE	PR00387D 10.81 4.889e-06 155-172
118	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 7.158e-06 211-254
119	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 8.036e-06 428-467
120	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419D 10.62 9.430e-06 18-33
121	DM00396	5 kw INTRON COI ND4L	DM00396B 7.85 3.739e-07 381-389

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		ND5.	
122	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 5.500e-06 135-147
123	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 4.208e-06 93-110
124	BL00405	43 Kd postsynaptic protein.	BL00405G 7.78 6.294e-06 130-167
125	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298D 10.23 3.847e-06 14-40
126	PR00317	EPENDYMIN SIGNATURE	PR00317A 13.39 9.897e-06 79-99
127	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 3.971e-06 277-290
130	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516G 15.11 8.811e-06 18-35
131	PR00828	FORMIN SIGNATURE	PR00828F 8.56 1.000e-05 61-81
132	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.279e-06 28-56
133	PR00586	PROSTANOID EP4 RECEPTOR SIGNATURE	PR00586B 14.97 7.322e-06 10-28 PR00586H 8.65 9.791e-06 16-40
134	PF00954	S-locus glycoprotein family.	PF00954D 18.68 9.843e-06 9-44
135	PR00018	KRINGLE DOMAIN SIGNATURE	PR00018A 14.52 1.000e-05 120-136
136	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115E 14.13 9.921e-06 40-69
137	PR00521	ANDROGEN RECEPTOR SIGNATURE	PR00521A 17.02 9.729e-06 5-25
138	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 5.267e-07 16-40
139	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.085e-08 93-121
140	PR00915	LUTEOVIRUS GROUP 1 COAT PROTEIN SIGNATURE	PR00915D 16.14 1.000e-05 374-392
143	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 4.441e-06 94-104
144	PF00598	Influenza Matrix protein (M1).	PF00598B 13.10 1.623e-06 89-133
145	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 6.250e-06 24-40
147	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 6.049e-06 266-288
148	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513D 11.06 9.920e-06 103-121
149	PF00603	Influenza RNA-dependant RNA polymerase subunit	PF00603D 8.49 9.319e-07 30-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PA.	
150	DM01688	2 POLY-IG RECEPTOR.	DM01688N 11.93 9.920e-08 72-100
151	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637B 10.68 6.906e-06 186-195
152	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461A 15.90 1.764e-08 21-57
153	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554A 6.07 2.565e-06 589-599
154	BL00405	43 Kd postsynaptic protein.	BL00405E 8.84 8.125e-06 109-135
155	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637A 15.49 5.179e-06 42-65
156	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 7.339e-06 85-97
157	DM01688	2 POLY-IG RECEPTOR.	DM01688P 13.54 1.925e-07 44-89 DM01688L 4.36 2.367e-07 123-133
159	PR00933	B-LYTIC METALLOENDOPEPTIDASE (M23) SIGNATURE	PR00933D 13.92 1.000e-05 85-106
161	PR00352	3FE-4S FERREDOXIN SIGNATURE	PR00352A 11.15 6.162e-06 94-106
163	BL00785	5'-nucleotidase proteins.	BL00785E 15.85 4.000e-06 95-111
164	PR00916	2C ENDOPEPTIDASE (C24) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00916C 8.02 2.655e-06 121-133
165	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 154-164
166	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 123-133
167	DM01023	2 GLYCOSYL HYDROLASES FAMILY 5.	DM01023C 13.51 6.486e-06 149-175
168	PF00803	3A movement protein.	PF00803A 15.38 8.088e-06 255-290
169	PR00282	SNAKE CYTOTOXIN SIGNATURE	PR00282D 11.82 9.882e-06 74-85
170	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 5.787e-06 83-100
172	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.804e-06 136-157
173	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 9.724e-06 14-30
174	BL00118	Phospholipase A2 histidine proteins.	BL00118A 16.00 9.842e-06 132-145
175	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 1.825e-06 89-121
176	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 146-159

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
177	PR00510	NEBULIN SIGNATURE	PR00510F 9.88 8.552e-06 34-51
179	PF00432	Prenyltransferase and squalene oxidase repeat proteins.	PF00432A 11.90 1.000e-05 27-39
180	PR00537	MU OPIOID RECEPTOR SIGNATURE	PR00537A 8.17 1.000e-05 27-41
183	PR00536	MELANOCYTE STIMULATING HORMONE RECEPTOR SIGNATURE	PR00536C 8.58 8.833e-06 64-82
184	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973B 17.81 8.261e-06 158-184
185	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
186	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
187	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651A 16.53 6.447e-06 144-165
188	BL01017	Ergosterol biosynthesis ERG4/ERG24 family proteins.	BL01017D 20.82 9.737e-06 21-67
191	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315B 6.84 7.459e-06 95-107
192	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE	PR00930E 5.98 9.740e-06 285-298
193	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794B 22.12 8.967e-06 150-191
194	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 5.853e-06 115-128
196	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.031e-07 11-32
197	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171B 14.73 1.000e-05 15-35
198	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407J 10.55 6.610e-06 69-81
199	PF00604	Influenza RNA-dependant RNA polymerase subunit PB2.	PF00604F 10.21 2.417e-06 276-331
201	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409D 13.02 9.900e-06 43-58
202	BL00660	Band 4.1 family	BL00660A 31.50 9.595e-06 1-54

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		domain proteins.	
203	PR00745	GLYCOSYL HYDROLASE FAMILY 39 SIGNATURE	PR00745D 15.85 9.700e-06 68-83
204	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364A 6.18 9.667e-06 9-16
205	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
206	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
207	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 3.170e-06 241-266
208	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 4.835e-06 59-71
209	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 9.719e-06 20-50
210	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551E 10.27 9.432e-06 19-34
211	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418B 22.51 3.289e-06 527-569
213	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785E 12.98 6.400e-06 165-216
214	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834B 15.29 3.382e-06 64-90
215	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 4.583e-06 407-423
216	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 6.538e-36 628-675 DM00547E 13.94 2.400e-18 387-410 DM00547C 17.30 9.486e-16 266-288 DM00547B 11.28 9.217e-15 237-251 DM00547D 11.60 4.951e-12 357-371 DM00547A 12.38 6.455e-11 216-228
217	BL00407	Connexins proteins.	BL00407D 17.61 1.000e-05 57-87
218	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.481e-06 74-86
219	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 15.47 3.550e-06 90-102
220	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519E 3.58 2.404e-07 184-199
221	PD01313	INTRON PROBABLE MATURASE CHLOROPLAST MR.	PD01313B 23.27 1.000e-05 10-45
222	PR00047	C4-TYPE STEROID	PR00047A 15.70 9.878e-06 99-116

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		RECEPTOR ZINC FINGER SIGNATURE	
223	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554C 11.76 3.571e-06 255-271
224	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 5.206e-06 28-67
226	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 8.630e-07 28-40
227	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 5.173e-06 185-224
229	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 9.794e-06 13-40
230	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651B 9.95 6.416e-06 62-77
231	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 9.113e-06 214-226
232	PR00582	PROSTANOID EP3 RECEPTOR SIGNATURE	PR00582B 9.74 1.000e-05 76-95
233	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407E 13.51 9.438e-06 176-192
234	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.913e-06 6-40
235	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 4.450e-06 94-126 DM01688J 14.69 6.000e-06 34-71
236	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 1.000e-05 80-106
237	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076B 11.24 6.418e-07 14-44
239	PR00243	MUSCARINIC ACETYLCHOLINE RECEPTOR SIGNATURE	PR00243F 16.45 9.182e-06 7-18
240	BL00854	Proteasome B-type subunits proteins.	BL00854B 10.97 1.000e-05 1-9
241	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 5.263e-07 876-889
242	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111I 15.32 2.473e-07 522-552
243	BL00415	Synapsins proteins.	BL00415B 9.91 9.778e-06 53-89
244	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514E 14.28 1.000e-05 221-238
245	PR00187	ARTHROPOD HAEMOCYANIN SIGNATURE	PR00187B 15.70 1.000e-05 37-55

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
246	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637C 27.33 1.184e-06 368-415
247	BL00785	5'-nucleotidase proteins.	BL00785A 9.73 7.557e-06 57-68
248	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651D 12.56 2.615e-06 228-249
249	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 1.811e-06 310-325
250	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461C 18.34 9.495e-06 30-58
251	BL00888	Cyclic nucleotide- binding domain proteins.	BL00888A 18.03 9.667e-06 20-37
252	DM01242	3 THREONINE--TRNA LIGASE.	DM01242E 23.00 6.215e-07 119-161
253	DM00250	kw ANNEXIN ANTIGEN PROLINE TUMOR.	DM00250A 10.52 6.488e-06 16-32
254	BL00291	Prion protein.	BL00291A 4.49 2.469e-07 51-86 BL00291A 4.49 6.878e-07 40-75 BL00291A 4.49 5.330e-06 22-57 BL00291A 4.49 1.000e-05 30-65
255	PF00506	Influenza virus nucleoprotein.	PF00506F 9.40 5.459e-08 17-55
256	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126A 27.56 6.026e-06 25-62
257	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003D 8.10 5.131e-06 291-300
258	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 7.061e-06 10-20
259	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 8.071e-06 3-13
260	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775D 8.91 3.831e-06 147-165
261	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 1.167e-06 75-91
262	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388D 14.87 8.079e-06 69-83
263	PR00023	ZONA PELLUCIDA SPERM-BINDING PROTEIN SIGNATURE	PR00023A 17.17 9.036e-06 24-39
264	BL00024	Hemopexin domain proteins.	BL00024F 11.30 9.894e-06 3-24
265	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 6.294e-06 177-227
266	PR00652	5-HYDROXYTRYPTAMINE	PR00652A 8.92 9.224e-07 69-90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		7 RECEPTOR SIGNATURE	
267	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 9.224e-07 69-90
268	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 1.673e-06 14-35
270	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875C 8.64 9.550e-06 65-77
271	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.308e-06 21-42
272	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 4.383e-06 46-89
273	PR00113	ALKALINE PHOSPHATASE SIGNATURE	PR00113D 6.87 9.260e-06 8-19
274	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841E 18.60 9.446e-06 80-118
275	PF00600	Influenza non- structural protein (NS1).	PF00600A 20.40 1.563e-06 40-67
276	PR00877	PLANT PEC FAMILY METALLOTHIONEIN SIGNATURE	PR00877B 4.74 9.878e-06 31-38
277	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076E 12.73 6.417e-06 71-99
279	BL00101	Hexapeptide-repeat containing- transferases proteins.	BL00101A 10.95 1.000e-05 71-78
280	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111M 10.67 2.629e-06 163-187
282	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.934e-06 35-50
283	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519C 9.73 1.227e-06 22-37
284	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304E 7.79 1.000e-05 54-67
285	BL00197	2Fe-2S ferredoxins, iron-sulfur binding region proteins.	BL00197A 18.23 9.866e-07 49-79
286	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753D 6.85 8.636e-06 61-83
287	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003B 7.64 1.300e-06 166-174
288	BL00940	Gamma-thionins family proteins.	BL00940A 20.51 9.671e-06 16-40
289	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.609e-11 122-135 PD00066 13.92 1.900e-09 94-107 PD00066 13.92 2.703e-07 66-79



SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD00066 13.92 1.000e-05 38-51
291	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516F 10.18 9.609e-07 761-779
293	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 8.487e-06 51-71
296	PR00635	AT1 ANGIOTENSIN II RECEPTOR SIGNATURE	PR00635C 7.44 8.602e-06 28-45
297	PF00915	Calicivirus coat protein.	PF00915E 5.71 1.000e-05 102-112
298	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 3.968e-06 495-512
299	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 9.730e-06 22-40
300	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.273e-06 7-44
301	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.752e-06 42-57
302	BL00283	Soybean trypsin inhibitor (Kunitz) protease inhibitors family.	BL00283B 16.55 1.000e-05 15-30
303	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.	DM01753A 21.93 9.830e-06 59-94
304	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516E 14.87 6.516e-06 20-38
305	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 5.452e-07 20-37
306	PR00331	HAEMAGGLUTININ HA2 CHAIN SIGNATURE	PR00331E 18.67 1.000e-05 75-93
307	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651H 5.59 8.858e-06 152-175
308	BL00208	Plant hemoglobins proteins.	BL00208A 18.41 1.000e-05 5-47
309	PR00240	ALPHA-1A ADRENERGIC RECEPTOR SIGNATURE	PR00240E 9.25 9.391e-06 36-56
310	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701C 10.53 8.255e-06 55-76
311	PR00423	CELL DIVISION PROTEIN FTSZ SIGNATURE	PR00423B 7.15 1.000e-05 5-26
312	PF00602	Influenza RNA-dependant RNA polymerase subunit PB1.	PF00602C 12.16 2.068e-07 26-66
313	PR00246	SOMATOSTATIN RECEPTOR SIGNATURE	PR00246D 7.36 1.000e-05 4-14

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
314	BL00216	Sugar transport proteins.	BL00216A 13.29 9.526e-06 26-38
316	PF00721	Tobacco mosaic virus coat.	PF00721A 14.59 9.845e-06 131-167
317	PD00489	PROTEIN TRANSMEMBRANE TRANSPORT C.	PD00489A 15.57 1.000e-05 55-71
318	PR00163	RUBREDOXIN SIGNATURE	PR00163A 10.47 9.888e-06 59-76
319	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 9.149e-07 205-217
320	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418C 20.48 5.142e-06 377-419
321	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067D 21.49 7.441e-06 9-42
322	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 7.821e-08 52-80
323	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 5.133e-06 43-53
324	PD01672	+ TRANSPORT EXCHANGER NA H TRANS.	PD01672B 15.16 1.000e-05 6-55
325	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 5.538e-06 31-68
327	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372A 19.18 1.000e-05 9-54
328	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 4.308e-06 31-68
329	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 144-157
330	PF00685	Sulfotransferase proteins.	PF00685A 19.12 9.370e-06 49-82
331	PR00347	PATHOGENESIS-RELATED PROTEIN SIGNATURE	PR00347A 13.98 9.649e-06 55-68
332	PR00538	MUSCARINIC M1 RECEPTOR SIGNATURE	PR00538F 10.59 8.667e-06 30-48
334	PR00159	2FE-2S FERREDOXIN SIGNATURE	PR00159A 9.58 1.153e-06 23-32
336	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554B 12.52 9.778e-06 41-50
337	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111G 10.39 7.250e-06 3-44
338	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 7.649e-06 214-229
340	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 5.050e-06 141-160
342	DM01664	kw.	DM01664D 16.63 1.000e-05 22-47

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
343	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841K 14.81 1.000e-05 65-95
344	PR00416	EUKARYOTIC DNA TOPOISOMERASE I SIGNATURE	PR00416D 12.12 9.772e-06 23-40
345	BL00726	AP endonucleases family 1 proteins.	BL00726C 19.90 1.000e-05 7-33
346	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.566e-06 465-507
347	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332A 10.15 9.890e-06 16-33
348	PR00518	5-HYDROXYTRYPTAMINE 5A RECEPTOR SIGNATURE	PR00518A 8.62 7.807e-06 19-36
349	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.736e-06 276-318
350	PR00503	BROMODOMAIN SIGNATURE	PR00503C 19.84 9.731e-06 28-47
351	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
352	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
353	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 5.273e-06 99-147
354	PR00216	OSTEOPONTIN SIGNATURE	PR00216F 11.79 9.913e-06 50-69
356	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895G 3.62 9.913e-06 62-72
357	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 6.329e-06 35-47
358	PR00512	5-HYDROXYTRYPTAMINE 1A RECEPTOR SIGNATURE	PR00512G 6.54 3.139e-06 3-19
359	PD02455	ELEMENT TRANSPOSABLE INSERTION PROTEIN TRANSPOSITION DNA.	PD02455D 18.65 1.000e-05 58-77
360	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 3.250e-07 16-29
361	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 9.702e-06 27-65
362	PR00866	RNA-DEPENDENT DNA-POLYMERASE (MSDNA) SIGNATURE	PR00866B 9.86 9.786e-06 60-73

\* Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TABLE 4

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
2	PGAM	Phosphoglycerate mutase family	2.5e-05	23.4
6	Ubie_methyltran	ubiE/COQ5 methyltransferase family	0.035	-133.9
8	Plexin repeat	Plexin repeat	0.03	18.4
13	K_tetra	K <sup>+</sup> channel tetramerisation domain	2.3e-31	117.6
14	EGF	EGF-like domain	7.8e-14	59.4
16	Armadillo_seg	Armadillo/beta-catenin-like repeats	1.3e-05	32.1
19	Ribosomal S5	Ribosomal protein S5	1.7e-46	167.9
21	gpdh	glyceraldehyde 3-phosphate dehydrogenases	1.3e-230	773.2
24	GCV_T	Glycine cleavage T-protein (aminomethyl tran	9.3e-156	530.9
25	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.015	12.5
26	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	38.4
33	urease	Urease	0.014	11.0
35	tRNA-synt_1e	tRNA synthetases class I (C)	0.0091	12.1
37	LRRNT	Leucine rich repeat N-terminal domain	0.00049	26.8
39	SH3	SH3 domain	3.4e-60	213.4
40	SH3	SH3 domain	3.4e-60	213.4
41	PBD	P21-Rho-binding domain	1e-08	42.4
42	GDA1_CD39	GDA1/CD39 (nucleoside phosphatase) family	9e-94	324.9
43	Band 7	SPFH domain / Band 7 family	1.7e-21	84.9
46	Rhodanese	Rhodanese-like domain	2.9e-24	94.0
47	zf-C2H2	Zinc finger, C2H2 type	6.2e-32	119.5
50	ZAP	ZAP domain	1.6e-50	181.3
52	sushi	Sushi domain (SCR repeat)	9.5e-27	102.3
55	zf-C2H2	Zinc finger, C2H2 type	0.047	20.3
56	zf-C2H2	Zinc finger, C2H2 type	0.00021	28.1
59	PH	PH domain	2.6e-06	27.6
60	PHD	PHD-finger	2e-09	44.8
64	IQ	IQ calmodulin-binding motif	6.4e-42	152.7
66	ank	Ank repeat	2.7e-23	90.8
69	eIF-1a	Eukaryotic initiation factor 1A	0.0047	-2.4
74	Ribosomal S17	Ribosomal protein S17	6e-43	148.6
75	LIM	LIM domain containing proteins	0.00067	19.0
80	Phosphodiect	Type I phosphodiesterase / nucleotide py	2.7e-49	177.2
81	transmembrane4	Transmembrane 4 family	6.6e-61	197.7
84	zf-C2H2	Zinc finger, C2H2 type	1.6e-64	227.8
85	zf-C2H2	Zinc finger, C2H2 type	1.4e-07	38.6
89	ank	Ank repeat	4e-31	116.8
93	L15	Ribosomal protein L15	3.5e-21	61.9

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
98	Band 41	FERM domain (Band 4.1 family)	0.00015	16.7
101	Nol1 Nop2 Sun	NOL1/NOP2/sun family	4.5e-19	68.6
103	LIM	LIM domain containing proteins	1.3e-30	113.2
113	WD40	WD domain, G-beta repeat	0.00018	28.3
115	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	5.3e-34	120.4
116	DUF25	Domain of unknown function DUF25	1.1e-11	46.9
118	Band 41	FERM domain (Band 4.1 family)	3.2e-77	242.4
119	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	1.1e-33	125.4
120	SH3	SH3 domain	3e-05	30.9
125	Ribosomal L29	Ribosomal L29 protein	1.6e-15	65.0
126	NTF2	Nuclear transport factor 2 (NTF2) domain	7.6e-06	32.2
129	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	0.0016	25.2
130	Fork head	Fork head domain	1e-28	108.8
132	PC4	Transcriptional Coactivator p15 (PC4)	2.1e-38	141.0
133	RGS	Regulator of G protein signaling domain	2.6e-45	164.0
137	COX7a	Cytochrome c oxidase subunit VIIa	2.3e-40	147.5
139	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	3.2e-15	64.0
141	lectin c	Lectin C-type domain	5.1e-05	30.0
142	lectin c	Lectin C-type domain	5.1e-05	30.0
147	ig	Immunoglobulin domain	9.1e-07	26.9
150	ank	Ank repeat	8.6e-09	42.6
161	Ribosomal L7Ae	Ribosomal protein L7Ae	0.03	0.8
162	HMG box	HMG (high mobility group) box	8e-53	188.9
163	PH	PH domain	3e-13	52.4
168	Peptidase C6	Helper component proteinase	0.0056	7.9
175	ig	Immunoglobulin domain	2.3e-09	35.2
176	ig	Immunoglobulin domain	9.2e-09	33.3
178	WW	WW domain	0.054	17.2
180	Ribosomal S12e	Ribosomal protein S12e	1.9e-38	141.1
185	myb DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
186	myb DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
187	pkinase	Eukaryotic protein kinase domain	3.4e-26	98.4
189	ER_lumen_recept	ER lumen protein retaining receptor	3.9e-144	492.2
190	ER_lumen_recept	ER lumen protein retaining receptor	2.1e-88	307.1
195	EMP24 GP25L	emp24/gp25L/p24 family	6.9e-06	28.1
199	zf-B box	B-box zinc finger.	5.2e-07	36.7
211	HECT	HECT-domain (ubiquitin-transferase).	1.1e-115	397.8
213	Rhomboid	Rhomboid family	4.2e-42	153.3
214	LIM	LIM domain containing	8.8e-35	127.8

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
		proteins		
215	Ricin_B_lectin	Similarity to lectin domain of ricin	0.0015	19.2
216	chromo	'chromo' (CHRromatin Organization Modifier	2.1e-09	37.1
218	Sialyltransf	Sialyltransferase family	7.3e-20	79.4
219	PG_binding_2	Putative peptidoglycan binding domain	5e-06	33.5
223	zf-C2H2	Zinc finger, C2H2 type	1.5e-104	360.7
226	RGS	Regulator of G protein signaling domain	5.1e-52	186.2
227	TBC	TBC domain	7.2e-35	129.3
228	CRAL TRIO	CRAL/TRIO domain.	4.5e-47	158.6
232	Ribosomal L44	Ribosomal protein L44	1e-48	175.3
235	ig	Immunoglobulin domain	3.5e-08	31.4
236	thyroglobulin 1	Thyroglobulin type-1 repeat	3.9e-24	93.6
238	TBC	TBC domain	1.2e-54	195.0
241	zf-C2H2	Zinc finger, C2H2 type	3.8e-08	40.5
242	AAA	ATPases associated with various cellular act	2.1e-43	157.6
249	integrin_A	Integrin alpha cytoplasmic region	0.091	18.0
256	PAP2	PAP2 superfamily	0.00084	22.8
257	zf-C2H2	Zinc finger, C2H2 type	1.2e-60	214.9
259	G-gamma	GGL domain	5.5e-30	108.3
266	efhand	EF hand	3.4e-07	37.4
267	efhand	EF hand	3.4e-07	37.4
274	zf-C2H2	Zinc finger, C2H2 type	0.00014	28.6
277	RecF	RecF protein	0.036	11.1
281	CH	Calponin homology (CH) domain	7.9e-22	86.0
285	cyclin	Cyclin	3.9e-07	28.5
289	zf-C2H2	Zinc finger, C2H2 type	1.9e-21	84.7
290	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.073	10.8
299	60s ribosomal	60s Acidic ribosomal protein	4.1e-07	25.8
307	trypsin	Trypsin	6.9e-81	257.3
310	ig	Immunoglobulin domain	1.3e-10	39.3
311	ig	Immunoglobulin domain	6.1e-07	27.4
313	globin	Globin	3.8e-21	78.2
315	ig	Immunoglobulin domain	1.6e-05	22.8
318	zf-C2H2	Zinc finger, C2H2 type	9e-19	75.8
319	ig	Immunoglobulin domain	0.01	13.8
320	BTB	BTB/POZ domain	5e-17	70.0
322	aa permeases	Amino acid permease	0.0058	-262.2
325	ig	Immunoglobulin domain	1.6e-10	38.9
327	ig	Immunoglobulin domain	1.9e-09	35.5
328	ig	Immunoglobulin domain	2.9e-09	34.9
329	ig	Immunoglobulin domain	7.4e-14	49.7
332	Ribosomal L36e	Ribosomal protein L36e	6.3e-17	69.7
333	connexin	Connexin	7.6e-148	504.6
335	p450	Cytochrome P450	2.1e-100	347.0
337	Sm	Sm protein	0.00012	28.8
338	zf-C2H2	Zinc finger, C2H2 type	0.0025	24.5

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
343	aldo ket red	Aldo/keto reductase family	2.4e-53	190.7
345	ubiquitin	Ubiquitin family	3.1e-13	45.5
346	CH	Calponin homology (CH) domain	0.0017	23.8
351	ig	Immunoglobulin domain	4.8e-18	63.2
352	ig	Immunoglobulin domain	4.8e-18	63.2
358	G-alpha	G-protein alpha subunit	4.5e-148	505.3
359	ig	Immunoglobulin domain	8.9e-09	33.3
362	Ribosomal_L37ae	Ribosomal L37ae protein family	0.00083	-3.0

**TABLE 5**

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
2	1-29	0.942	0.664
12	1-15	0.909	0.589
14	1-17	0.974	0.943
20	1-22	0.932	0.802
25	1-16	0.988	0.881
28	1-13	0.896	0.771
37	1-21	0.992	0.929
42	1-46	0.978	0.754
52	1-34	0.954	0.756
63	1-31	0.960	0.773
71	1-45	0.981	0.652
80	1-22	0.982	0.882
81	1-42	0.993	0.715
83	1-30	0.966	0.767
95	1-18	0.997	0.971
102	1-13	0.981	0.764
107	1-45	0.890	0.631
110	1-27	0.992	0.969
138	1-33	0.961	0.864
144	1-45	0.987	0.658
145	1-20	0.992	0.967
175	1-20	0.957	0.874
176	1-21	0.989	0.945
179	1-42	0.980	0.577
184	1-20	0.972	0.771
189	1-28	0.941	0.755
190	1-28	0.941	0.755
191	1-12	0.907	0.779
195	1-21	0.958	0.779
200	1-15	0.970	0.875
211	1-20	0.895	0.595
215	1-31	0.987	0.895
218	1-30	0.971	0.889
225	1-17	0.884	0.588
235	1-23	0.965	0.817
237	1-29	0.933	0.725
249	1-28	0.972	0.870
251	1-17	0.966	0.905
260	1-26	0.921	0.587
270	1-20	0.938	0.631
283	1-18	0.901	0.763
288	1-20	0.940	0.693
293	1-26	0.937	0.784
295	1-22	0.972	0.745
296	1-15	0.930	0.748
297	1-35	0.906	0.600
300	1-29	0.981	0.864
307	1-19	0.976	0.916
308	1-27	0.973	0.931



SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
309	1-29	0.950	0.629
310	1-19	0.969	0.913
311	1-21	0.956	0.823
315	1-17	0.976	0.938
317	1-19	0.943	0.837
319	1-18	0.991	0.978
324	1-26	0.968	0.806
325	1-20	0.972	0.828
326	1-27	0.893	0.567
327	1-21	0.994	0.959
328	1-20	0.945	0.891
329	1-21	0.984	0.858
330	1-27	0.891	0.593
333	1-40	0.955	0.703
347	1-22	0.968	0.806
351	1-23	0.982	0.945
352	1-23	0.982	0.945
355	1-32	0.955	0.617
356	1-23	0.936	0.677
359	1-20	0.937	0.859
360	1-29	0.956	0.765
361	1-23	0.968	0.819

## CLAIMS

### WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 362, a mature protein coding portion of SEQ ID NO: 1 – 362, an active domain of SEQ ID NO: 1 – 362, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 – 362.

5 11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:  
10 a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

15 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:  
a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

20 b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

25 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

30 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:  
a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 5 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

10 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- 15 b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-362, a mature protein coding portion of SEQ ID NO: 1-362, an active domain of SEQ ID NO: 1-362, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-362, under conditions sufficient to express the polypeptide in said cell; and
- 20 b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the  
30 mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 362.

5 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

10 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

15 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

20 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



# DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

**Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi, Feiyan Ren,  
Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman,  
Radoje T. Drmanac**

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

  X   is attached hereto.

       was filed on [date] as Application Serial Number [            ]  
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Leslie A. Mooi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

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Express Mail No.: EF415382545US

Docket No.: 797

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant(s): Tang, et al.

Serial No: Not Yet Assigned

Filed: Herewith

For: NOVEL NUCLEIC ACIDS  
AND POLYPEPTIDES

CERTIFICATE OF MAILING  
BY "EXPRESS MAIL" UNDER 37 CFR § 1.10

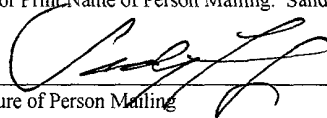
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Date of Deposit November 17, 2000

I hereby certify that this paper and all enclosures are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 CFR § 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231

Type or Print Name of Person Mailing. Sandy Fong

Signature of Person Mailing



**STATEMENT REGARDING SEQUENCE LISTING UNDER 37 CFR §1.821(f)**

BOX PATENT APPLICATION  
Assistant Commissioner for Patents  
Washington, D.C. 20231

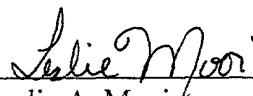
Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Dated: November 17, 2000

By:

  
Leslie A. Mooi  
Attorney for Applicants  
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<110> Tang, Y. Tom  
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 Xue, Aidong J.  
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 Polypeptides

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gcg	gaa	tcc	cat	cta	aaa	cgt	aat	gag	gca	tca	ctg	cca	tca	att	ctt	1817	
Ala	Glu	Ser	His	Leu	Lys	Arg	Asn	Glu	Ala	Ser	Leu	Pro	Ser	Ile	Leu		
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Gln	Tyr	Gln	Pro	Asn	Leu	Ser	Asn	Gln	Met	Thr	Ser	Lys	Gln	Tyr	Thr		
				220					225					230			
gga	aat	tcc	aac	atg	cct	ggg	ggg	ctc	cca	agg	caa	gct	tac	acc	cag	1913	
Gly	Asn	Ser	Asn	Met	Pro	Gly	Gly	Leu	Pro	Arg	Gln	Ala	Tyr	Thr	Gln		
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aaa	aca	aca	cag	ctg	gag	cac	aag	tca	caa	atg	tac	caa	gtt	gaa	atg	1961	
Lys	Thr	Thr	Gln	Leu	Glu	His	Lys	Ser	Gln	Met	Tyr	Gln	Val	Glu	Met		
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aat	caa	ggg	cag	tcc	caa	ggt	aca	gtg	gac	caa	cat	ctc	cag	ttc	caa	2009	
Asn	Gln	Gly	Gln	Ser	Gln	Gly	Thr	Val	Asp	Gln	His	Leu	Gln	Phe	Gln		
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Lys	Pro	Ser	His	Gln	Val	His	Phe	Ser	Lys	Thr	Asp	His	Leu	Pro	Lys		
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Ala	His	Val	Gln	Ser	Leu	Cys	Gly	Thr	Arg	Phe	His	Phe	Gln	Gln	Arg		
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Ala	Asp	Ser	Gln	Thr	Glu	Lys	Leu	Met	Ser	Pro	Val	Leu	Lys	Gln	His		
			315					320					325				
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Leu	Asn	Gln	Gln	Ala	Ser	Glu	Thr	Glu	Pro	Phe	Ser	Asn	Ser	His	Leu		

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ttg caa cat aag cct cat aaa cag gca gca caa aca caa cca tcc cag Leu Gln His Lys Pro His Lys Gln Ala Ala Gln Thr Gln Pro Ser Gln 345 350 355			2249
agt tca cat ctc cct caa aac cag caa cag cag caa aaa tta caa ata Ser Ser His Leu Pro Gln Asn Gln Gln Gln Gln Gln Lys Leu Gln Ile 360 365 370 375			2297
aag aat aaa gag gaa ata ctc cag act ttt cct cac ccc caa agc aac Lys Asn Lys Glu Glu Ile Leu Gln Thr Phe Pro His Pro Gln Ser Asn 380 385 390			2345
aat gat cag caa aga gaa gga tca ttc ttt ggc cag act aaa gtg gaa Asn Asp Gln Gln Arg Glu Gly Ser Phe Phe Gly Gln Thr Lys Val Glu 395 400 405			2393
gaa tgt ttt cat ggt gaa aat cag tat tca aaa tca agc gag ttc gag Glu Cys Phe His Gly Glu Asn Gln Tyr Ser Lys Ser Ser Glu Phe Glu 410 415 420			2441
act cat aat gtc caa atg gga ctg gag gaa gta cag aat ata aat cgt Thr His Asn Val Gln Met Gly Leu Glu Glu Val Gln Asn Ile Asn Arg 425 430 435			2489
aga aat tcc cct tat agt cag acc atg aaa tca agt gca tgc aaa ata Arg Asn Ser Pro Tyr Ser Gln Thr Met Lys Ser Ser Ala Cys Lys Ile 440 445 450 455			2537
cag gtt tct tgt tca aac aat aca cac cta gtt tca gag aat aaa gaa Gln Val Ser Cys Ser Asn Asn Thr His Leu Val Ser Glu Asn Lys Glu 460 465 470			2585
cag act aca cat cct gaa ctt ttt gca gga aac aag acc caa aac ttg Gln Thr Thr His Pro Glu Leu Phe Ala Gly Asn Lys Thr Gln Asn Leu 475 480 485			2633
cat cac atg caa tat ttt cca aat aat gtg atc cca aag caa gat ctt His His Met Gln Tyr Phe Pro Asn Asn Val Ile Pro Lys Gln Asp Leu 490 495 500			2681
ctt cac agg tgc ttt caa gaa cag gag cag aag tca caa caa gct tca Leu His Arg Cys Phe Gln Glu Gln Glu Gln Lys Ser Gln Gln Ala Ser 505 510 515			2729
gtt cta cag gga tat aaa aat aga aac caa gat atg tct ggt caa caa Val Leu Gln Gly Tyr Lys Asn Arg Asn Gln Asp Met Ser Gly Gln Gln 520 525 530 535			2777
gct gcg caa ctt gct cag caa agg tac ttg ata cat aac cat gca aat Ala Ala Gln Leu Ala Gln Gln Arg Tyr Leu Ile His Asn His Ala Asn 540 545 550			2825
gtt ttt cct gtg cct gac cag gga gga agt cac act cag acc cct ccc Val Phe Pro Val Pro Asp Gln Gly Gly Ser His Thr Gln Thr Pro Pro 555 560 565			2873



cag aag gac act caa aag cat gct gct cta agg tgg cat ctc tta cag Gln Lys Asp Thr Gln Lys His Ala Ala Leu Arg Trp His Leu Leu Gln 570 575 580	2921
aag caa gaa cag cag caa aca cag caa ccc caa act gag tct tgc cat Lys Gln Glu Gln Gln Gln Thr Gln Gln Pro Gln Thr Glu Ser Cys His 585 590 595	2969
agt cag atg cac agg cca att aag gtg gaa cct gga tgc aag cca cat Ser Gln Met His Arg Pro Ile Lys Val Glu Pro Gly Cys Lys Pro His 600 605 610 615	3017
gcc tgt atg cac aca gca cca cca gaa aac aaa aca tgg aaa aag gta Ala Cys Met His Thr Ala Pro Pro Glu Asn Lys Thr Trp Lys Lys Val 620 625 630	3065
act aag caa gag aat cca cct gca agc tgt gat aat gtg cag caa aag Thr Lys Gln Glu Asn Pro Pro Ala Ser Cys Asp Asn Val Gln Gln Lys 635 640 645	3113
agc atc att gag acc atg gag cag cat ctg aag cag ttt cac gcc aag Ser Ile Ile Glu Thr Met Glu Gln His Leu Lys Gln Phe His Ala Lys 650 655 660	3161
tcg tta ttt gac cat aag gct ctt act ctc aaa tca cag aag caa gta Ser Leu Phe Asp His Lys Ala Leu Thr Leu Lys Ser Gln Lys Gln Val 665 670 675	3209
aaa gtt gaa atg tca ggg cca gtc aca gtt ttg act aga caa acc act Lys Val Glu Met Ser Gly Pro Val Thr Val Leu Thr Arg Gln Thr Thr 680 685 690 695	3257
gct gca gaa ctt gat agc cac acc cca gct tta gag cag caa aca act Ala Ala Glu Leu Asp Ser His Thr Pro Ala Leu Glu Gln Gln Thr Thr 700 705 710	3305
tct tca gaa aag aca cca acc aaa aga aca gct gct tct gtt ctc aat Ser Ser Glu Lys Thr Pro Thr Lys Arg Thr Ala Ala Ser Val Leu Asn 715 720 725	3353
aat ttt ata gag tca cct tcc aaa tta cta gat act cct ata aaa aat Asn Phe Ile Glu Ser Pro Ser Lys Leu Leu Asp Thr Pro Ile Lys Asn 730 735 740	3401
tta ttg gat aca cct gtc aag act caa tat gat ttc cca tct tgc aga Leu Leu Asp Thr Pro Val Lys Thr Gln Tyr Asp Phe Pro Ser Cys Arg 745 750 755	3449
tgt gta gat cct gta aaa ttt gaa tgt atc tgt ttt aga tca att cgc Cys Val Asp Pro Val Lys Phe Glu Cys Ile Cys Phe Arg Ser Ile Arg 760 765 770 775	3497
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gcg gcc tgc ggg ctg gcc ggg ggc tgc gcc gcc gtg ctc ttc tcg gcc	99	
Ala Ala Cys Gly Leu Ala Gly Gly Ser Ala Ala Val Leu Phe Ser Ala		
10 15 20 25		
gtg gcg gta ggg aag ccg cgc gca ggc ggg gac gcg gag cca cgc ccg	147	
Val Ala Val Gly Lys Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro		
30 35 40		
gct gag ccg ccg gcc tgg gcg ggg ggc gcg ccg ccg gcc ccc ggt gtc	195	
Ala Glu Pro Pro Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val		
45 50 55		
tgg gac ccc aac tgg gac agg cga gaa cca ctg tct ctg atc aac gtg	243	
Trp Asp Pro Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val		
60 65 70		
cgg aag agg aac gtg gaa tct ggg gaa gaa gag ctg gcg tcc aag ctg	291	
Arg Lys Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu		
75 80 85		
gac cac tac aaa gcc aag gcc acg ccg cac atc ttc ctc atc agg cat	339	
Asp His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His		
90 95 100 105		
tcc cag tac cac gtg gat ggc tcc ctg gag aag gac cgc act ctg acc	387	
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu Thr		
110 115 120		
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Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu Ala Ser		
125 130 135		
ttg ggg ttg aag ttt aat aaa atc gtc cat tcg tct atg acg cgc gcc	483	
Leu Gly Leu Lys Phe Asn Lys Ile Val His Ser Ser Met Thr Arg Ala		
140 145 150		
ata gag acc acc gat atc atc agc ccg cac ctg cca ggc gtc tgc aaa	531	
Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro Gly Val Cys Lys		
155 160 165		

gtc agc aca gat ctg ctg cgg gaa ggc gcc ccc atc gag cca gac ccg	579
Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro Ile Glu Pro Asp Pro	
170 175 180 185	
ccc gtg tct cat tgg aag ccg gaa gct gtg cag tat tac gaa gac gga	627
Pro Val Ser His Trp Lys Pro Glu Ala Val Gln Tyr Tyr Glu Asp Gly	
190 195 200	
gcc cgg atc gag gcc gcc ttc cgg aac tac atc cac cgc gca gat gcc	675
Ala Arg Ile Glu Ala Ala Phe Arg Asn Tyr Ile His Arg Ala Asp Ala	
205 210 215	
agg cag gag gag gac agt tac gag atc ttc atc tgt cac gcc aac gtc	723
Arg Gln Glu Glu Asp Ser Tyr Glu Ile Phe Ile Cys His Ala Asn Val	
220 225 230	
atc cgc tac atc gtg tgc aga gca ctg cag ttt cct cct gaa ggc tgg	771
Ile Arg Tyr Ile Val Cys Arg Ala Leu Gln Phe Pro Pro Glu Gly Trp	
235 240 245	
ctc cgg ctc tcc ctc aat aat ggc agc atc acc cac ctg gtg atc cga	819
Leu Arg Leu Ser Leu Asn Asn Gly Ser Ile Thr His Leu Val Ile Arg	
250 255 260 265	
ccc aac ggc cga gtt gcg ctc agg acc ctc ggg gac acg ggg ttc atg	867
Pro Asn Gly Arg Val Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met	
270 275 280	
cct ccc gac aag atc act cga tcc tga gggct ccggcctctc cttccctctg	919
Pro Pro Asp Lys Ile Thr Arg Ser *	
285 290	
tcctccctgc acaggccgca cacacttaac gttttgttcc caaggagacc ggcggaaagt	979
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Figure 1 consists of 12 histograms arranged in a single row. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The values of  $n$  are 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and 120, labeled below each histogram. The x-axis for all histograms is the number of non-zero elements, ranging from 0 to 120. The y-axis represents the frequency, with a scale that varies slightly between histograms. As  $n$  increases, the distribution of non-zero elements shifts to the right, indicating that more elements in the vector  $x$  are non-zero for larger values of  $n$ .

agagcaaatga	aaattcggggc	acgagtggtt	atgaagatag	gtactgtggg	tgttagaaag	60
attcacgggca	aaacaggggaa	gcattctaggc	tgcttgtgga	agtcagacca	aaatagcagg	120
aaggtattgc	agcaag	atg gat ttg gga aag gac caa tct cat ttg aag	169			
		Met Asp Leu Gly Lys Asp Gln Ser His Leu Lys				
		1 5 10				
cac cat cag aca cct gac cct cat caa gaa gag aac cat tct cca gaa	217					
His His Gln Thr Pro Asp Pro His Gln Glu Glu Asn His Ser Pro Glu						
	15 20 25					
gtc att gga acc tgg agt ttg aga aac aga gaa cta ctt aga aaa aga	265					
Val Ile Gly Thr Trp Ser Leu Arg Asn Arg Glu Leu Leu Arg Lys Arg						
	30 35 40					
aaa gct gaa gtg cat gaa aag gaa aca tca caa tgg cta ttt gga gaa	313					
Lys Ala Glu Val His Glu Lys Glu Thr Ser Gln Trp Leu Phe Gly Glu						
	45 50 55					
cag aaa aaa cgc aag cag cag aga aca gga aaa gga aat cga aga ggc	361					
Gln Lys Lys Arg Lys Gln Gln Arg Thr Gly Lys Gly Asn Arg Arg Gly						
	60 65 70 75					
aga aag aga caa caa aac aca gaa ttg aag gtg gag cct cag cca cag	409					
Arg Lys Arg Gln Gln Asn Thr Glu Leu Lys Val Glu Pro Gln Pro Gln						
	80 85 90					
ata gaa aag gaa ata gtg gag aaa gca ctg gca cct ata gag aaa aaa	457					
Ile Glu Lys Glu Ile Val Glu Lys Ala Leu Ala Pro Ile Glu Lys Lys						
	95 100 105					
act gag cca cct ggg agc ata acc aaa gta ttt cct tca gta gcc tcc	505					
Thr Glu Pro Pro Gly Ser Ile Thr Lys Val Phe Pro Ser Val Ala Ser						
	110 115 120					
ccg caa aaa gtt gtg cct gag gaa cac ttt tct gaa ata tgt caa gaa	553					
Pro Gln Lys Val Val Pro Glu Glu His Phe Ser Glu Ile Cys Gln Glu						
	125 130 135					
agt aac ata tat cag gag aat ttt tct gag tac caa gaa ata gca gta	601					
Ser Asn Ile Tyr Gln Glu Asn Phe Ser Glu Tyr Gln Glu Ile Ala Val						
	140 145 150 155					
caa aac cat tct tct gaa aca tgc caa cat gtg tct gaa cct gaa gac	649					
Gln Asn His Ser Ser Glu Thr Cys Gln His Val Ser Glu Pro Glu Asp						
	160 165 170					
ctc tct cct aaa atg tac caa gaa ata tct gta ctt caa gac aat tct	697					
Leu Ser Pro Lys Met Tyr Gln Glu Ile Ser Val Leu Gln Asp Asn Ser						
	175 180 185					

tcc aaa ata tgc caa gac atg aag gaa cct gaa gac aac tct cct aac	745
Ser Lys Ile Cys Gln Asp Met Lys Glu Pro Glu Asp Asn Ser Pro Asn	
190 195 200	
aca tgc caa gta ata tct gta att caa gac cat cct ttc aaa atg tac	793
Thr Cys Gln Val Ile Ser Val Ile Gln Asp His Pro Phe Lys Met Tyr	
205 210 215	
caa gat atg gct aaa cga gaa gat ctg gct cct aaa atg tgc caa gaa	841
Gln Asp Met Ala Lys Arg Glu Asp Leu Ala Pro Lys Met Cys Gln Glu	
220 225 230 235	
gct gct gta ccc aaa atc ctt cct tgt cca aca tct gaa gac aca gct	889
Ala Ala Val Pro Lys Ile Leu Pro Cys Pro Thr Ser Glu Asp Thr Ala	
240 245 250	
gat ctg gca gga tgc tct ctt caa gca tat cca aaa cca gat gtg cct	937
Asp Leu Ala Gly Cys Ser Leu Gln Ala Tyr Pro Lys Pro Asp Val Pro	
255 260 265	
aaa ggc tat att ctt gac aca gac caa aat cca gca gaa cca gag gaa	985
Lys Gly Tyr Ile Leu Asp Thr Asp Gln Asn Pro Ala Glu Pro Glu Glu	
270 275 280	
tac aat gaa aca gat caa gga ata gct gag aca gaa ggc ctt ttt cct	1033
Tyr Asn Glu Thr Asp Gln Gly Ile Ala Glu Thr Glu Gly Leu Phe Pro	
285 290 295	
aaa ata caa gaa ata gct gag cct aaa gac ctt tct aca aaa aca cac	1081
Lys Ile Gln Glu Ile Ala Glu Pro Lys Asp Leu Ser Thr Lys Thr His	
300 305 310 315	
caa gaa tca gct gaa cct aaa tac ctt cct cat aaa aca tgt aac gaa	1129
Gln Glu Ser Ala Glu Pro Lys Tyr Leu Pro His Lys Thr Cys Asn Glu	
320 325 330	
att att gtg cct aaa gcc ccc tct cat aaa aca atc caa gaa aca cct	1177
Ile Ile Val Pro Lys Ala Pro Ser His Lys Thr Ile Gln Glu Thr Pro	
335 340 345	
cat tct gaa gac tat tca att gaa ata aac caa gaa act cct ggg tct	1225
His Ser Glu Asp Tyr Ser Ile Glu Ile Asn Gln Glu Thr Pro Gly Ser	
350 355 360	
gaa aaa tat tca cct gaa acg tat caa gaa ata cct ggg ctt gaa gaa	1273
Glu Lys Tyr Ser Pro Glu Thr Tyr Gln Glu Ile Pro Gly Leu Glu Glu	
365 370 375	
tat tca cct gaa ata tac caa gaa aca tcc cag ctt gaa gaa tat tca	1321
Tyr Ser Pro Glu Ile Tyr Gln Glu Thr Ser Gln Leu Glu Glu Tyr Ser	
380 385 390 395	
cct gaa ata tac caa gaa aca ccg ggg cct gaa gac ctc tct act gag	1369
Pro Glu Ile Tyr Gln Glu Thr Pro Gly Pro Glu Asp Leu Ser Thr Glu	
400 405 410	
aca tat aaa aat aag gat gtg cct aaa gaa tgc ttt cca gaa cca cac	1417

Thr	Tyr	Lys	Asn	Lys	Asp	Val	Pro	Lys	Glu	Cys	Phe	Pro	Glu	Pro	His	
			415					420					425			
caa	gaa	aca	ggg	ggg	ccc	caa	ggc	cag	gat	cct	aaa	gca	cac	cag	gaa	1465
Gln	Glu	Thr	Gly	Gly	Pro	Gln	Gly	Gln	Asp	Pro	Lys	Ala	His	Gln	Glu	
		430					435					440				
gat	gct	aaa	gat	gct	tat	act	ttt	cct	caa	gaa	atg	aaa	gaa	aaa	ccc	1513
Asp	Ala	Lys	Asp	Ala	Tyr	Thr	Phe	Pro	Gln	Glu	Met	Lys	Glu	Lys	Pro	
	445					450					455					
aaa	gaa	gag	cca	gga	ata	cca	gca	att	ctg	aat	gag	agt	cat	cca	gaa	1561
Lys	Glu	Glu	Pro	Gly	Ile	Pro	Ala	Ile	Leu	Asn	Glu	Ser	His	Pro	Glu	
460				465					470					475		
aat	gat	gtc	tat	agt	tat	gtt	ttg	ttt	taa	c	aatgctcaac	cataaagttg				1612
Asn	Asp	Val	Tyr	Ser	Tyr	Val	Leu	Phe	*							
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				Met	Ala	Ala	Ser	Leu								
				1				5								
cgg	ctc	ctc	gga	gct	gcc	tcc	ggg	ctc	cgg	tac	tgg	agc	cgg	cgg	ctg	162
Arg	Leu	Leu	Gly	Ala	Ala	Ser	Gly	Leu	Arg	Tyr	Trp	Ser	Arg	Arg	Leu	
			10					15						20		
cgg	ccg	gca	gcc	ggc	agc	ttt	gca	gcg	gtg	tgt	tct	agg	tca	gtg	gct	210
Arg	Pro	Ala	Ala	Gly	Ser	Phe	Ala	Ala	Val	Cys	Ser	Arg	Ser	Val	Ala	
			25					30					35			
tca	aag	act	cca	gtt	gga	ttc	att	gga	ctg	ggc	aac	atg	ggg	aat	cca	258
Ser	Lys	Thr	Pro	Val	Gly	Phe	Ile	Gly	Leu	Gly	Asn	Met	Gly	Asn	Pro	
		40					45				50					
atg	gca	aaa	aat	ctc	atg	aaa	cat	ggc	tat	cca	ctt	att	att	tat	gat	306
Met	Ala	Lys	Asn	Leu	Met	Lys	His	Gly	Tyr	Pro	Leu	Ile	Ile	Tyr	Asp	
		55				60					65					
gtg	ttc	cct	gat	gcc	tgc	aaa	gag	ttt	caa	gat	gca	ggg	gaa	cag	gta	354

Val	Phe	Pro	Asp	Ala	Cys	Lys	Glu	Phe	Gln	Asp	Ala	Gly	Glu	Gln	Val	
70					75					80					85	
gta tct tcc cca gca gat gtt gct gaa aaa gct gac aga att att aca																402
Val	Ser	Ser	Pro	Ala	Asp	Val	Ala	Glu	Lys	Ala	Asp	Arg	Ile	Ile	Thr	
				90					95					100		
atg ctg ccc acc agt atc aat gca ata gaa gct tat tcc gga gca aat																450
Met	Leu	Pro	Thr	Ser	Ile	Asn	Ala	Ile	Glu	Ala	Tyr	Ser	Gly	Ala	Asn	
			105					110					115			
ggg att cta aaa aaa gtg aag aag ggc tca tta tta ata gat tcc agc																498
Gly	Ile	Leu	Lys	Lys	Val	Lys	Lys	Gly	Ser	Leu	Leu	Ile	Asp	Ser	Ser	
		120					125					130				
act att gat cct gca gtt tca aaa gaa ttg gcc aaa gaa gtt gag aaa																546
Thr	Ile	Asp	Pro	Ala	Val	Ser	Lys	Glu	Leu	Ala	Lys	Glu	Val	Glu	Lys	
		135				140					145					
atg gga gca gtt ttc atg gat gcc cct gtt tct ggt ggt gta gga gct																594
Met	Gly	Ala	Val	Phe	Met	Asp	Ala	Pro	Val	Ser	Gly	Gly	Val	Gly	Ala	
150					155					160					165	
gca cga tct ggg aac ctc acg ttt atg gtg gga gga gtt gaa gat gaa																642
Ala	Arg	Ser	Gly	Asn	Leu	Thr	Phe	Met	Val	Gly	Gly	Val	Glu	Asp	Glu	
				170					175					180		
ttt gct gct gcc caa gag ttg ctg ggg tgc atg ggc tcc aac gtg gtg																690
Phe	Ala	Ala	Ala	Gln	Glu	Leu	Leu	Gly	Cys	Met	Gly	Ser	Asn	Val	Val	
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tac tgt gga gct gtt ggg act ggg cag gcg gca aag atc tgc aac aac																738
Tyr	Cys	Gly	Ala	Val	Gly	Thr	Gly	Gln	Ala	Ala	Lys	Ile	Cys	Asn	Asn	
		200					205					210				
atg ctg tta gct att agt atg att gga act gct gaa gct atg aat ctt																786
Met	Leu	Leu	Ala	Ile	Ser	Met	Ile	Gly	Thr	Ala	Glu	Ala	Met	Asn	Leu	
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gga atc agg tta ggg ctt gac cca aaa cta ctg gct aaa atc cta aat																834
Gly	Ile	Arg	Leu	Gly	Leu	Asp	Pro	Lys	Leu	Leu	Ala	Lys	Ile	Leu	Asn	
230					235				240					245		
atg agc tca gga cgg tgt tgg tca agt gac act tat aat cct gta cct																882
Met	Ser	Ser	Gly	Arg	Cys	Trp	Ser	Ser	Asp	Thr	Tyr	Asn	Pro	Val	Pro	
				250					255					260		
gga gtg atg gat ggc gtt ccc tcg gct aat aac tat cag ggt gga ttt																930
Gly	Val	Met	Asp	Gly	Val	Pro	Ser	Ala	Asn	Asn	Tyr	Gln	Gly	Gly	Phe	
			265					270					275			
gga aca aca ctc atg gct aag gat ctg gga ttg gca caa gac tct gct																978
Gly	Thr	Thr	Leu	Met	Ala	Lys	Asp	Leu	Gly	Leu	Ala	Gln	Asp	Ser	Ala	
		280					285					290				
acc agc aca aag agc cca atc ctt ctt ggc agt ctg gcc cat cag atc																1026
Thr	Ser	Thr	Lys	Ser	Pro	Ile	Leu	Leu	Gly	Ser	Leu	Ala	His	Gln	Ile	

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tac agg atg atg tgt gca aag ggc tac tca aag	aaa gac ttc tca tcc	1074	
Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys	Lys Asp Phe Ser Ser		
310	315 320 325		
gtg ttc cag ttc cta cga gag gag gag acc ttc	tga gtgt gccctttggc	1124	
Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe	*		
330	335		
cacggacact gttgggaacc aaactctgtc ttggagcctc	cttttagctc actccacaag	1184	
taaattggatt taatcaaagg tcacctatct gcttttgatt	gtctagggtca cagtaatccc	1244	
taggattttt caccgcttat tctttttgtc tttttaacaa	acatattatc cgaatttttt	1304	
ttctgcaagc cactgatagt ctctgctaac tagcttaatt	gaccttttta caaagtttga	1364	
tccccaagca tccccaacta aatcattgaa tacttcaatc	aggatattat ctgctttact	1424	
ttacaaataa aaccaaactc tttgtcaaca ggatgaaacc	catcttaaag gaaagaaaag	1484	
gaattggtgt gaagagagaa gttagagaag ggaaatgcag	tgaattacta tctgtgtcca	1544	
tcaggaagtt tgtcctgtta accaaatggt tactgcacta	ccagggttac tggtttattt	1604	
tccagggagc tgataaagca ggagaactgt tgctgcatgt	tttctatttg gactccgtca	1664	
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	Met
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Lys Asn Ile Lys Ala Leu Val Ala Phe His Ser	Thr Ala Leu Asp Lys
5	10 15
	105



gaa att aca tca gca aat tat gct ggt gtc tgt aca tca tct gtg att	153
Glu Ile Thr Ser Ala Asn Tyr Ala Gly Val Cys Thr Ser Ser Val Ile	
20 25 30	
aaa gaa gaa aac att gat caa cca gga tac tgt tat ctc tca cct gat	201
Lys Glu Glu Asn Ile Asp Gln Pro Gly Tyr Cys Tyr Leu Ser Pro Asp	
35 40 45	
gga aag aga aaa act atg ctc tgc ttg gct tgt gga caa tcc atg aga	249
Gly Lys Arg Lys Thr Met Leu Cys Leu Ala Cys Gly Gln Ser Met Arg	
50 55 60 65	
aca gag aaa gga ctg aaa caa ttg ctt cca ggg gtt cca ttc ctc tgt	297
Thr Glu Lys Gly Leu Lys Gln Leu Leu Pro Gly Val Pro Phe Leu Cys	
70 75 80	
att tca ggc acc aag act cag aag ccc ttc tta caa ggg ccc ttc aag	345
Ile Ser Gly Thr Lys Thr Gln Lys Pro Phe Leu Gln Gly Pro Phe Lys	
85 90 95	
gtc atc agt gtg gct gag gtt gat ttg tgc tgt gac aag gct gaa aaa	393
Val Ile Ser Val Ala Glu Val Asp Leu Ser Cys Asp Lys Ala Glu Lys	
100 105 110	
act cta agt tac tac caa gca cgt cta ttg tct tta cgg atg aag acc	441
Thr Leu Ser Tyr Tyr Gln Ala Arg Leu Leu Ser Leu Arg Met Lys Thr	
115 120 125	
tgc acg caa gct gca tct cac agt ggc atg gca gcc aca cac cag aag	489
Cys Thr Gln Ala Ala Ser His Ser Gly Met Ala Ala Thr His Gln Lys	
130 135 140 145	
gca gtg aaa ata att gca tac aaa aat ggg gat ggg tat cgt aat ggg	537
Ala Val Lys Ile Ile Ala Tyr Lys Asn Gly Asp Gly Tyr Arg Asn Gly	
150 155 160	
aag tta att gtg gct gga aca ttc ccc atg ctt ctt aca gaa tgc acg	585
Lys Leu Ile Val Ala Gly Thr Phe Pro Met Leu Leu Thr Glu Cys Thr	
165 170 175	
gaa caa ctt ggg ctt gcc aga gca gcc tcc aaa gta tat acc aaa gat	633
Glu Gln Leu Gly Leu Ala Arg Ala Ala Ser Lys Val Tyr Thr Lys Asp	
180 185 190	
gga acc cca atc ttt acc ttg cgt gat ttg gtt tta tgg gct cta gat	681
Gly Thr Pro Ile Phe Thr Leu Arg Asp Leu Val Leu Trp Ala Leu Asp	
195 200 205	
gaa tcc ttt ctc cag aga gac tct gag aaa caa aag caa gat gca gct	729
Glu Ser Phe Leu Gln Arg Asp Ser Glu Lys Gln Lys Gln Asp Ala Ala	
210 215 220 225	
cct gtt gga aaa gaa cag ata att gtt gaa agt atg gaa gaa aat cca	777
Pro Val Gly Lys Glu Gln Ile Ile Val Glu Ser Met Glu Glu Asn Pro	
230 235 240	
aga atg aaa gtg aaa aac aga tta ttt gca aaa tct gtg aca tcc gat	825

Arg	Met	Lys	Val	Lys	Asn	Arg	Leu	Phe	Ala	Lys	Ser	Val	Thr	Ser	Asp	
			245					250					255			
agt	ttg	gat	ggg	ata	gac	aag	tct	ttg	ctt	acc	ctc	atc	ctc	aga	aat	873
Ser	Leu	Asp	Gly	Ile	Asp	Lys	Ser	Leu	Leu	Thr	Leu	Ile	Leu	Arg	Asn	
		260					265					270				
cct	att	gcc	atc	tgg	gtg	tct	tgt	ggg	gaa	cca	ttt	cta	cct	cca	aat	921
Pro	Ile	Ala	Ile	Trp	Val	Ser	Cys	Gly	Glu	Pro	Phe	Leu	Pro	Pro	Asn	
	275					280					285					
gct	ttg	cag	aaa	gca	gaa	aaa	tta	gag	aaa	cag	aac	tgg	cta	aaa	aag	969
Ala	Leu	Gln	Lys	Ala	Glu	Lys	Leu	Glu	Lys	Gln	Asn	Trp	Leu	Lys	Lys	
290					295					300					305	
gac	aga	att	ttg	gct	gat	cta	gat	acc	atg	aga	cac	aaa	atg	aga	cag	1017
Asp	Arg	Ile	Leu	Ala	Asp	Leu	Asp	Thr	Met	Arg	His	Lys	Met	Arg	Gln	
			310					315					320			
tta	aaa	ggg	cgg	cga	gta	gcg	gca	tgt	cag	cca	gcc	acc	atg	gtt	cct	1065
Leu	Lys	Gly	Arg	Arg	Val	Ala	Ala	Cys	Gln	Pro	Ala	Thr	Met	Val	Pro	
			325					330					335			
acc	aag	agc	cct	gtg	cag	ccc	gtg	gtg	gtt	gaa	gga	ggc	tgg	acc	gaa	1113
Thr	Lys	Ser	Pro	Val	Gln	Pro	Val	Val	Val	Glu	Gly	Gly	Trp	Thr	Glu	
		340					345					350				
cag	act	caa	cag	gaa	att	aaa	ctc	atg	gaa	ctt	ata	aga	cat	aca	gag	1161
Gln	Thr	Gln	Gln	Glu	Ile	Lys	Leu	Met	Glu	Leu	Ile	Arg	His	Thr	Glu	
	355					360					365					
gca	cac	ctt	tct	gaa	atc	caa	gaa	atg	gaa	tcc	aaa	ata	aat	ttt	cca	1209
Ala	His	Leu	Ser	Glu	Ile	Gln	Glu	Met	Glu	Ser	Lys	Ile	Asn	Phe	Pro	
370					375					380					385	
att	gca	acc	aaa	cgt	ata	gca	gtc	aag	ccg	agc	aac	ctg	tat	aag	cag	1257
Ile	Ala	Thr	Lys	Arg	Ile	Ala	Val	Lys	Pro	Ser	Asn	Leu	Tyr	Lys	Gln	
			390					395					400			
ccc	aac	aca	aaa	cga	gtg	tgg	att	tat	cta	aat	gga	ggc	aga	cct	gaa	1305
Pro	Asn	Thr	Lys	Arg	Val	Trp	Ile	Tyr	Leu	Asn	Gly	Gly	Arg	Pro	Glu	
			405				410						415			
gat	ggc	act	tat	gcc	tgg	ggc	aaa	act	att	tca	gag	ctg	ctg	caa	gac	1353
Asp	Gly	Thr	Tyr	Ala	Trp	Gly	Lys	Thr	Ile	Ser	Glu	Leu	Leu	Gln	Asp	
		420					425					430				
tgc	tcc	tct	cgt	ctc	aaa	atg	acc	cac	cca	gct	aga	gca	ctg	tac	acc	1401
Cys	Ser	Ser	Arg	Leu	Lys	Met	Thr	His	Pro	Ala	Arg	Ala	Leu	Tyr	Thr	
	435					440					445					
ccc	agt	gga	gag	cca	att	cag	tcc	tgg	gac	gac	ata	gag	cga	gat	atg	1449
Pro	Ser	Gly	Glu	Pro	Ile	Gln	Ser	Trp	Asp	Asp	Ile	Glu	Arg	Asp	Met	
450					455					460					465	
gtc	atc	tgt	gtg	tct	atg	gga	cat	ggg	ttc	aaa	acc	cca	aaa	gag	tta	1497
Val	Ile	Cys	Val	Ser	Met	Gly	His	Gly	Phe	Lys	Thr	Pro	Lys	Glu	Leu	

470	475	480	
aaa caa ctg atg gag atc aga gca aat tat gcc aga atc cga agg cag			1545
Lys Gln Leu Met Glu Ile Arg Ala Asn Tyr Ala Arg Ile Arg Arg Gln			
485	490	495	
cag ggc cct caa gcc aca gac att gtg gtg tca cca tcc acg aag ctg			1593
Gln Gly Pro Gln Ala Thr Asp Ile Val Val Ser Pro Ser Thr Lys Leu			
500	505	510	
ctg tct ctg gca cat ctc cac aat taa ctct atcagaacca tcggattttc			1645
Leu Ser Leu Ala His Leu His Asn *			
515	520		
tgctgtatattt ttctggaaag aaaacttttct ttaccactt ataaacagaa gactgtgaca			1705
agaaggccaa ttatttccat cgctgaagac tctaaatttg gcaaattcttc taaataacaa			1765
tcctgcatag ttattataaaa aaaattagtc gtaaaattta tccttcaaaa atctgcattt			1825
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Lys Leu Gly Ser Ser Gly Gly Trp Phe Leu Arg Val Leu Gly Pro Gly			
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ggc tgt aat aca aaa gct gcg cgt ccc tta att tcc tcg gcg gtt tat			149
Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr			
25	30	35	
gtg aag aac cag ctc agt ggg act cta cag att aaa cca ggg gtt ttc			197
Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe			
40	45	50	

aat gaa tac aga acc ata tgg ttc aaa tcc tac agg acg atc ttt tcc	245
Asn Glu Tyr Arg Thr Ile Trp Phe Lys Ser Tyr Arg Thr Ile Phe Ser	
55 60 65	
tgt ttg aac aga ata aag agt ttc agg tac cct tgg gcg aga ctg tac	293
Cys Leu Asn Arg Ile Lys Ser Phe Arg Tyr Pro Trp Ala Arg Leu Tyr	
70 75 80 85	
agt act tcc caa acc act gtc gac agc ggt gag gta aaa acc ttc ttg	341
Ser Thr Ser Gln Thr Thr Val Asp Ser Gly Glu Val Lys Thr Phe Leu	
90 95 100	
gcc ctg gct cac aaa tgg tgg gat gaa caa gga gta tat gca cct ctt	389
Ala Leu Ala His Lys Trp Trp Asp Glu Gln Gly Val Tyr Ala Pro Leu	
105 110 115	
cat tcc atg aat gac ctg agg gtg cca ttt att agg gac aat ctt ctg	437
His Ser Met Asn Asp Leu Arg Val Pro Phe Ile Arg Asp Asn Leu Leu	
120 125 130	
aaa aca att cct aat cac cag cca gga aaa cct ttg ttg ggg atg aag	485
Lys Thr Ile Pro Asn His Gln Pro Gly Lys Pro Leu Leu Gly Met Lys	
135 140 145	
att ctt gac gtt ggc tgt ggt ggt ggg ctg tta act gaa cct cta ggg	533
Ile Leu Asp Val Gly Cys Gly Gly Gly Leu Leu Thr Glu Pro Leu Gly	
150 155 160 165	
cgg ctt ggg gct tca gtt att gga atc gac cct gtg gat gag aac att	581
Arg Leu Gly Ala Ser Val Ile Gly Ile Asp Pro Val Asp Glu Asn Ile	
170 175 180	
aaa aca gca caa tgc cat aaa tca ttt gat cca gtc cgg gat aag aga	629
Lys Thr Ala Gln Cys His Lys Ser Phe Asp Pro Val Arg Asp Lys Arg	
185 190 195	
ata gag tac aga gtg tgt tcc ctg gaa gag att gtg gaa gag act gca	677
Ile Glu Tyr Arg Val Cys Ser Leu Glu Glu Ile Val Glu Glu Thr Ala	
200 205 210	
gaa aca ttt gat gct gtt gta gct tct gaa gtt gta gaa cat gtg att	725
Glu Thr Phe Asp Ala Val Val Ala Ser Glu Val Val Glu His Val Ile	
215 220 225	
gat cta gaa aca ttt tta cag tgc tgc tgt caa gtg tta aaa ccc ggt	773
Asp Leu Glu Thr Phe Leu Gln Cys Cys Cys Gln Val Leu Lys Pro Gly	
230 235 240 245	
ggg tct tta ttc att act aca atc aac aaa aca caa ctt tcc tat gcc	821
Gly Ser Leu Phe Ile Thr Thr Ile Asn Lys Thr Gln Leu Ser Tyr Ala	
250 255 260	
ttg gga att gtt ttt tca gag caa att gca ggt att gta cca aaa ggt	869
Leu Gly Ile Val Phe Ser Glu Gln Ile Ala Gly Ile Val Pro Lys Gly	
265 270 275	
act cat aca tgg gag aag ttt gtt tca cct gaa aca cta gag agc att	917

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Leu	Glu	Ser	Asn	Gly	Leu	Ser	Val	Gln	Thr	Val	Val	Gly	Met	Leu	Tyr	
	295				300					305						
aac	ccc	ttc	tca	ggt	tac	tgg	cat	tgg	agt	gaa	aat	acc	agc	ctt	aac	1013
Asn	Pro	Phe	Ser	Gly	Tyr	Trp	His	Trp	Ser	Glu	Asn	Thr	Ser	Leu	Asn	
310				315					320					325		
tat	gca	gct	cat	gct	gtg	aaa	tcc	agg	gtc	cag	gaa	cac	cca	gcc	tct	1061
Tyr	Ala	Ala	His	Ala	Val	Lys	Ser	Arg	Val	Gln	Glu	His	Pro	Ala	Ser	
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gct	gag	ttt	gtt	tta	aag	gga	gaa	aca	gaa	gag	ctc	caa	gct	aat	gcc	1109
Ala	Glu	Phe	Val	Leu	Lys	Gly	Glu	Thr	Glu	Glu	Leu	Gln	Ala	Asn	Ala	
		345				350						355				
tgc	acc	aat	cca	gct	gtg	cat	gaa	aag	ctg	aag	aaa	tga	attg	tttctg		1158
Cys	Thr	Asn	Pro	Ala	Val	His	Glu	Lys	Leu	Lys	Lys	*				
	360				365						370					
aga	actatag	taatatggct	tg	gat	atctg	atg	ttttcaa	atacaagaaa	tgtacaattt							1218
atc	ctttgag	agagaatcat	gaagaaaaga	agg	tcaataa	aaagg	gctaa	aac	cttggac							1278
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catata	cttc	ccatg	ataaa	ctta	agtgg	c	agta	agaaa	aga	agct	atg	atg	ggt			176
											Met	Met	Gly			
											1					
ctg	gct	cag	ctt	tat	aag	aaa	tac	tgt	ctt	cat	ggt	gaa	gca	gga	aag	224
Leu	Ala	Gln	Leu	Tyr	Lys	Lys	Tyr	Cys	Leu	His	Gly	Glu	Ala	Gly	Lys	
	5				10					15						
gaa	gct	gca	gag	aaa	gtc	agc	tgg	ata	aag	gac	aaa	ctt	ctg	cat	att	272

Glu	Ala	Ala	Glu	Lys	Val	Ser	Trp	Ile	Lys	Asp	Lys	Leu	Leu	His	Ile		
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Tyr	Tyr	Gln	Asn	Ser	Ile	Asp	Asp	Lys	Leu	Leu	Val	Glu	Lys	Ile	Phe		
			40					45						50			
gct	cag	tat	ctt	gtc	ccc	cac	aac	ctg	gaa	aca	gaa	gag	aga	atg	aaa	368	
Ala	Gln	Tyr	Leu	Val	Pro	His	Asn	Leu	Glu	Thr	Glu	Glu	Arg	Met	Lys		
			55					60					65				
tgc	tta	tat	tac	tta	tat	gct	agt	ttg	gat	cca	aat	gct	gta	aaa	gct	416	
Cys	Leu	Tyr	Tyr	Leu	Tyr	Ala	Ser	Leu	Asp	Pro	Asn	Ala	Val	Lys	Ala		
		70				75						80					
ctc	aac	gaa	atg	tgg	aag	tgt	cag	aac	atg	ctt	cgg	agc	cat	gta	cgc	464	
Leu	Asn	Glu	Met	Trp	Lys	Cys	Gln	Asn	Met	Leu	Arg	Ser	His	Val	Arg		
	85					90					95						
gaa	cta	ttg	gat	ttg	cac	aag	cag	cct	aca	tca	gag	gct	aac	tgt	tct	512	
Glu	Leu	Leu	Asp	Leu	His	Lys	Gln	Pro	Thr	Ser	Glu	Ala	Asn	Cys	Ser		
100					105				110					115			
gcc	atg	ttt	gga	aaa	ctg	atg	acc	ata	gca	aag	aat	ttg	cct	gac	ccc	560	
Ala	Met	Phe	Gly	Lys	Leu	Met	Thr	Ile	Ala	Lys	Asn	Leu	Pro	Asp	Pro		
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ggg	aaa	gca	caa	gat	ttt	gtg	aag	aaa	ttt	aac	cag	gtt	ctc	ggc	gat	608	
Gly	Lys	Ala	Gln	Asp	Phe	Val	Lys	Lys	Phe	Asn	Gln	Val	Leu	Gly	Asp		
			135					140					145				
gat	gag	aaa	ctt	cgg	tct	cag	ttg	gag	tta	tta	att	agc	cca	acc	tgt	656	
Asp	Glu	Lys	Leu	Arg	Ser	Gln	Leu	Glu	Leu	Leu	Ile	Ser	Pro	Thr	Cys		
		150				155						160					
tct	tgc	aaa	caa	gca	gat	att	tgt	gtg	aga	gaa	ata	gcc	cgg	aaa	ctt	704	
Ser	Cys	Lys	Gln	Ala	Asp	Ile	Cys	Val	Arg	Glu	Ile	Ala	Arg	Lys	Leu		
	165					170					175						
gca	aat	cct	aag	caa	cca	aca	aat	cct	ttt	cta	gag	atg	gtc	aaa	ttt	752	
Ala	Asn	Pro	Lys	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met	Val	Lys	Phe		
180					185					190					195		
ctg	ttg	gaa	aga	atc	gca	cct	gtg	cac	att	gat	tca	gaa	gcc	ata	agt	800	
Leu	Leu	Glu	Arg	Ile	Ala	Pro	Val	His	Ile	Asp	Ser	Glu	Ala	Ile	Ser		
			200					205						210			
gcg	cta	gtg	aaa	ttg	atg	aat	aag	tca	ata	gag	ggg	aca	gca	gat	gat	848	
Ala	Leu	Val	Lys	Leu	Met	Asn	Lys	Ser	Ile	Glu	Gly	Thr	Ala	Asp	Asp		
			215					220					225				
gaa	gag	gag	ggg	gta	agt	cca	gat	aca	gct	atc	cgt	tca	gga	ctt	gaa	896	
Glu	Glu	Glu	Gly	Val	Ser	Pro	Asp	Thr	Ala	Ile	Arg	Ser	Gly	Leu	Glu		
		230					235					240					
ctt	ctt	aag	gtt	ctg	tct	ttt	aca	cat	cct	acc	tcg	ttc	cac	tct	gca	944	
Leu	Leu	Lys	Val	Leu	Ser	Phe	Thr	His	Pro	Thr	Ser	Phe	His	Ser	Ala		



gaa cct tgt tac cat gaa att att acc cca gaa cag ttt cag ctc tgt	1664
Glu Pro Cys Tyr His Glu Ile Ile Thr Pro Glu Gln Phe Gln Leu Cys	
485 490 495	
gca ctt gtt att aat gat gag tgt tac caa gta agg cag ata ttt gct	1712
Ala Leu Val Ile Asn Asp Glu Cys Tyr Gln Val Arg Gln Ile Phe Ala	
500 505 510 515	
cag aag ctg cat aag gca ctt gtg aag tta ctg ctc cca ttg gag tat	1760
Gln Lys Leu His Lys Ala Leu Val Lys Leu Leu Leu Pro Leu Glu Tyr	
520 525 530	
atg gcg atc ttt gcc ttg tgt gcc aaa gat cct gtg aag gag aga aga	1808
Met Ala Ile Phe Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg	
535 540 545	
gca cac gca cga caa tgt tta ctg aaa aat atc agt ata cgc agg gaa	1856
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ccc	acc	aag	aag	ctg	gcc	aac	aaa	cca	gat	aaa	aac	agt	tct	tcc	gag	295	
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cag	ttg	ttt	tct	agc	gca	cgc	tta	cag	aat	gag	aaa	aaa	aca	att	ctt	343	
Gln	Leu	Phe	Ser	Ser	Ala	Arg	Leu	Gln	Asn	Glu	Lys	Lys	Thr	Ile	Leu		
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gaa	aga	aag	aaa	gac	tgt	aga	cag	gtg	ata	caa	agg	gaa	gat	tct	acc	391	
Glu	Arg	Lys	Lys	Asp	Cys	Arg	Gln	Val	Ile	Gln	Arg	Glu	Asp	Ser	Thr		
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tct	gag	tct	gag	gat	gac	tct	cgg	gat	gag	agc	cag	gag	agt	tca	gat	439	
Ser	Glu	Ser	Glu	Asp	Asp	Ser	Arg	Asp	Glu	Ser	Gln	Glu	Ser	Ser	Asp		
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gct	ttg	ctg	aaa	agg	acc	atg	aac	atc	aag	gag	aac	aaa	gcc	atg	ctt	487	
Ala	Leu	Leu	Lys	Arg	Thr	Met	Asn	Ile	Lys	Glu	Asn	Lys	Ala	Met	Leu		
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gcc	cag	tta	ttg	gcg	gaa	ttg	aac	tcg	atg	cca	gat	ttc	ttc	cca	gta	535	
Ala	Gln	Leu	Leu	Ala	Glu	Leu	Asn	Ser	Met	Pro	Asp	Phe	Phe	Pro	Val		
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Arg	Thr	Pro	Thr	Ser	Ala	Ser	Arg	Lys	Lys	Thr	Val	Arg	Arg	Ala	Phe		
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tcg	gag	gga	cag	atc	acg	cgg	cgt	atg	aac	cca	acc	cgg	agt	gcg	cgg	631	
Ser	Glu	Gly	Gln	Ile	Thr	Arg	Arg	Met	Asn	Pro	Thr	Arg	Ser	Ala	Arg		
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cct	cct	gag	aag	ttt	gct	cta	gag	aac	ttc	act	gtc	tca	gcc	gct	aaa	679	
Pro	Pro	Glu	Lys	Phe	Ala	Leu	Glu	Asn	Phe	Thr	Val	Ser	Ala	Ala	Lys		
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Phe	Ala	Glu	Glu	Phe	Tyr	Ser	Phe	Arg	Arg	Arg	Lys	Thr	Ile	Gly	Gly		
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Lys	Cys	Arg	Glu	Tyr	Arg	Arg	Arg	His	Arg	Ile	Ser	Ser	Phe	Arg	Pro		
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gtg	gag	gat	atc	acc	gaa	gag	gac	tta	gaa	aat	gtt	gcc	ata	act	gtt	823	
Val	Glu	Asp	Ile	Thr	Glu	Glu	Asp	Leu	Glu	Asn	Val	Ala	Ile	Thr	Val		
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cga	gat	aaa	atc	tat	gat	aaa	gtt	ctg	ggc	aac	acg	tgc	cat	cag	tgt	871	
Arg	Asp	Lys	Ile	Tyr	Asp	Lys	Val	Leu	Gly	Asn	Thr	Cys	His	Gln	Cys		



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Arg Gln Lys Thr Ile Asp Thr Lys Thr	Val Cys Arg Asn Gln Gly Cys		
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tgt ggt gtg cga gga cag ttc tgt gga	cca tgc ctg cgg aac cgc tat		967
Cys Gly Val Arg Gly Gln Phe Cys Gly	Pro Cys Leu Arg Asn Arg Tyr		
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Gly Glu Asp Val Arg Ser Ala Leu Leu	Asp Pro Asp Trp Val Cys Pro		
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Pro Cys Arg Gly Ile Cys Asn Cys Ser	Tyr Cys Arg Lys Arg Asp Gly		
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cgc tgt gcc aca gga atc ctc att cat	ctg gcc aag ttt tat ggt tat		1111
Arg Cys Ala Thr Gly Ile Leu Ile His	Leu Ala Lys Phe Tyr Gly Tyr		
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Asp Asn Val Lys Glu Tyr Leu Glu Ser	Leu Gln Lys Glu Leu Val Glu		
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<222> (402)..(2084)

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gggcttgctg gcccgaagtg agttgtcagg gtttcagagg acaccagtca tggcaacccc 180
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tgtagatgaa aaatgaggta acggcactcc cctgccccac cctcctccca gaagtgccca 300
gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct 360
taaccaacac aggccccagc acccgagag cagacactgc g      atg aca acg gac 413
                                Met Thr Thr Asp
                                1

gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg 461
Asp Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu
  5              10              15              20

gaa act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca 509
Glu Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro
      25              30              35

gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc 557

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cct gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg	605
Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met	
55 60 65	
gtg ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc	653
Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro	
70 75 80	
gag gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc	701
Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro	
85 90 95 100	
gag gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag	749
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu	
105 110 115	
gca aag aca ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca	797
Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr	
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Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro	
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His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser	
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Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser	
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Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser	
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Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser	
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Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Leu His Pro Val Ile	
215 220 225	
acc ccg tca cgg gcc tca gag agc agc gcc tct tcc gac ggc ccc cat	1133
Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His	
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cca gtc atc acc ccc tca tgg tcc ccg gga tct gac gtc act ctc ctc	1181
Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu	
245 250 255 260	
gct gaa gcc ctg gtg act gtc aca aac atc gag gtt att aat tgc agc	1229
Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser	

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Ile	Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp								
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Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	Thr	Glu								
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325								330								335							
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Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	Thr	Leu	Ser	Gly	Ala								
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Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	Glu	Thr	Ser	Ala	Leu	Ser								
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Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	Ser	Gly	Ala	Ala	Pro	Val	Ser								
390								395								400							
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Ser	Ala	Ser	Ser	Tyr	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr								
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Pro	Ser	Glu	Thr	Pro	Thr	Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro								
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Thr	Ser	Arg	Asp	Pro	Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser								
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Ser	Arg	Gly	Thr	Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys								
470								475								480							
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Thr	Thr	Met	Lys	Pro	Pro	Thr	Ala	Thr	Pro	Thr	Thr	Ala	Arg	Thr	Arg								
485								490								495							
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Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu Leu
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cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg gca      1997
Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala
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gaa agg ctg atg cag cag ctc cac ccg gaa ctc cac gcc cac gcg cct      2045
Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro
      535                      540                      545

cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacatcag      2094
His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly *
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cgacagactg cagctgcgtt actgtgctga gaggtaccca gaagggtccc atgaagggca      2214

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tgtatgtatg gggaggggct tcacctgttc ccagaggtgt ccttggactc accttggcac      2334

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gggcttgctg gcccgaagtg agttgtcagg gtttcagagg acaccagtca tggcaacccc      180

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gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct      360

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Glu	Thr	Gln	Thr	Leu	Ser	Ala	Glu	Thr	Ser	Ser	Arg	Ala	Ser	Thr	Pro	
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gcc	ggc	ccc	att	cca	gaa	gca	gag	acc	agg	gga	gcc	aag	aga	att	tcc	557
Ala	Gly	Pro	Ile	Pro	Glu	Ala	Glu	Thr	Arg	Gly	Ala	Lys	Arg	Ile	Ser	
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Pro	Ala	Arg	Glu	Thr	Arg	Ser	Phe	Thr	Lys	Thr	Ser	Pro	Asn	Phe	Met	
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Val	Leu	Ile	Ala	Thr	Ser	Val	Glu	Thr	Ser	Ala	Ala	Ser	Gly	Ser	Pro	
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Ser	Ile	Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	
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Asp	Thr	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	
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Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	Thr	
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tct gtt gag aca cca agt tac gtc aaa gtc tca gga gca gct ccg gtc Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val 295 300 305			1325
tcc ata gag gct ggg tca gca gtg ggc aaa aca act tcc ttt gct ggg Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly 310 315 320			1373
agc tct gct tcc tcc tac agc ccc tcg gaa gcc gcc ctc aag aac ttc Ser Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe 325 330 335 340			1421
acc cct tca gag aca ccg acc atg gac atc gca acc aag ggg ccc ttc Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe 345 350 355			1469
ccc acc agc agg gac cct ctt cct tct gtc cct ccg act aca acc aac Pro Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn 360 365 370			1517
agc agc cga ggg acg aac agc acc tta gcc aag atc aca acc tca gcg Ser Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala 375 380 385			1565
aag acc acg atg aag ccc cca aca gcc acg ccc acg act gcc cgg acg Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr 390 395 400			1613
agg ccg acc aca gac gtg agt gca ggt gaa aat gga ggt ttc ctc ctc Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu 405 410 415 420			1661
ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val 425 430 435			1709
gca gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala 440 445 450			1757
cct cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacat Pro His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly * 455 460 465			1806

cagctgcagc cagggcatgtc ccgtatgcc aagaggggtg ctgcccctag cctgggcccc 1866  
caccgacaga ctgcagctgc gttactgtgc tgagagggtac ccagaagggt cccatgaagg 1926  
gcagcatgtc caagccccta accccagatg tggcaacagg accctcgctc acatccaccg 1986  
gagtgtatgt atggggaggg gttcacctg ttcccagagg tgtccttgga ctcaccttgg 2046  
cacatgttct gtgtttcagt aaagagagac ctgatcacc aaaaaaaaa aa 2098

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<211> 636  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (394) .. (618)

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cccactttac aagtgcagca tccggagagg aggtctcat cagtgcaggc tcatccacac 120  
cagccgtgtt ttggggactt aaggaggtca ttcgcgctca gaggtgtcc cgggcacat 180  
gcccgtctg ccgggggtctt tctcctgcc agcctcattt gcctgtgcat gcacttggtt 240  
atccaacaag agctagaaca ttctgggaga agcccacgtt ggctccttgc cgggctggtc 300  
agactccgtg gttgtcctga gacaccacc ctctgtgcc ctgagggtgg ccaggaag 360  
tttgtgtgac cttccacacg gatccctgg gac atg cag gtg tgg ctc ttg aca 414  
Met Gln Val Trp Leu Leu Thr  
1 5  
ctg gaa agg ctg agg gtt ctg ccc aaa cct agg agt gaa ttc gac ttc 462  
Leu Glu Arg Leu Arg Val Leu Pro Lys Pro Arg Ser Glu Phe Asp Phe  
10 15 20  
ttt ccc atc tca cac aca cac ccg aga cgt cac ccg aat cca cgt att 510  
Phe Pro Ile Ser His Thr His Pro Arg Arg His Pro Asn Pro Arg Ile  
25 30 35  
tcc cac gtt cgg ctg cca ctg cct ccc agg tgg gct ttg cag gac cca 558  
Ser His Val Arg Leu Pro Leu Pro Pro Arg Trp Ala Leu Gln Asp Pro  
40 45 50 55  
cca tcg cat ccc ctc tca ctc cac aga aaa ctc gtg ggg ccg tgt tcc 606  
Pro Ser His Pro Leu Ser Leu His Arg Lys Leu Val Gly Pro Cys Ser  
60 65 70  
ccc tgc cac tga ccacgtttc cttgcaga 636



Pro Cys His \*  
75

<210> 13  
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<212> DNA  
<213> Homo sapiens

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<222> (314)..(1279)

<400> 13

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gggacaaact aggggatgca tggccctctc taggggtcat ccaatacccc agctctgacc      120
agttgttccc ctgctagccc agttggcctc tgattttagg agaagccaga agtccagatt      180
tttctgtgag ctctccttag ttgtccacat tggaagcaaa cttttaaatg ctgtgtatgc      240
gtggcccaag caaaacacat ctggaggcca gattgaatcc acaggctgaa agcagtcaac      300
caggcctgat gtc      atg acc ctg tat cct ctc cac tgg cag gaa gag atg      349
                   Met Thr Leu Tyr Pro Leu His Trp Gln Glu Glu Met
                   1              5              10

tca gga gaa agt gtg gtg agc tca gcg gtg cca gcg gct gct acc cgc      397
Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala Ala Ala Thr Arg
                   15              20              25

acc act tcc ttc aag ggc acg agc ccc agc tcc aaa tac gtg aag ctg      445
Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys Leu
                   30              35              40

aat gtg ggt gga gcc ctc tac tat acc acc atg cag acg ctg acc aag      493
Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr Lys
                   45              50              55              60

cag gac acc atg ctg aag gcc atg ttc agc ggg cgc atg gaa gtg ctc      541
Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val Leu
                   65              70              75

acc gac agt gaa ggc tgg atc ctc att gac cgc tgt ggg aag cac ttt      589
Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His Phe
                   80              85              90

ggt acg ata ctc aac tac ctt cga gac ggg gcg gtg cct tta ccc gag      637
Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro Glu
                   95              100              105

agc cgc cgg gag atc gag gag ctg cta gca gaa gcc aag tac tac cta      685
Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu
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110	115	120	
gtc caa ggc ctg gtg gaa gag tgc cag gcg gcc cta caa aac aaa gat			733
Val Gln Gly Leu Val Glu Glu Cys Gln Ala Leu Gln Asn Lys Asp			
125	130	135	140
act tat gag cct ttc tgc aag gtc cct gtg atc acc tca tcc aag gaa			781
Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr Ser Ser Lys Glu			
	145	150	155
gaa caa aaa ctt ata gcg act tca aat aag cca gcc gtg aag ttg ctc			829
Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala Val Lys Leu Leu			
	160	165	170
tac aac aga agt aac aac aaa tac tca tat acc agc aat tct gac gac			877
Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp Asp			
	175	180	185
aat atg ttg aaa aac att gaa ctg ttt gat aag ctg tct ctg cgc ttt			925
Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg Phe			
	190	195	200
aac gga agg gtc ctg ttc ata aag gat gtt att ggg gat gaa atc tgc			973
Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile Cys			
	205	210	215
tgc tgg tcc ttt tat ggt cag ggc cgg aag att gct gaa gtc tgt tgt			1021
Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys Cys			
	225	230	235
acc tcc atc gtc tat gcc act gag aag aaa cag acc aag gtg gag ttt			1069
Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr Lys Val Glu Phe			
	240	245	250
ccc gaa gcc cgg att tat gag gag acc ctg aac att ttg ctg tat gag			1117
Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile Leu Leu Tyr Glu			
	255	260	265
gcc cag gat ggc cgg gga cct gac aat gcg ctc ctg gag gcc aca ggc			1165
Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu Glu Ala Thr Gly			
	270	275	280
ggg gcg gcg ggg cgc tcc cac cac ctg gac gag gac gag gag cgg gag			1213
Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp Glu Glu Arg Glu			
	285	290	295
cgg atc gag cgc gtg cgg agg atc cac atc aag cgc cct gat gac cgg			1261
Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg Pro Asp Asp Arg			
	305	310	315
gcc cac ctc cac cag tga gcaggc aagagaccga gccgccctcc tctcaccgcc			1315
Ala His Leu His Gln *			
	320		
cccactccct gccgtgctac acccagatcc tgtgcaggct gccgggcccc ttctgcttcc			1375
cttgagcct ggagatactt ttgtaacaag ccagatgatt attttggtat tgcttgacaa			1435



<213> Homo sapiens

<220>

<221> CDS

<222> (287)..(1924)

<400> 14

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cctctagagc gtccgctcgc gatctagaac ccaaggccag agctgtggac accttatccc      120
actcactctc atcctcttcc tctgataaag cccctaccag tgctgataaa gtctttctcg      180
tgagagccta gaggccttaa aaaaaaaagt gcttgaaaga gaagggggaca aaggaacacc      240
agtattaaga ggattttcca gtgtttctgg cagttgggtcc agaagg  atg cct cca      295
                                     Met Pro Pro
                                     1

ttc ctg ctt ctc acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc      343
Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro
      5                      10                      15

gtg gcc cta gat cct tgt tct gct tac atc agc ctg aat gag ccc tgg      391
Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp
      20                      25                      30                      35

agg aac act gac cac cag ttg gat gag tct caa ggt cct cct cta tgt      439
Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys
                        40                      45                      50

gac aac cat gtg aat ggg gag tgg tac cac ttc acg ggc atg gcg gga      487
Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly
                        55                      60                      65

gat gcc atg cct acc ttc tgc ata cca gaa aac cac tgt gga acc cac      535
Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His
                        70                      75                      80

gca cct gtc tgg ctc aat ggc agc cac ccc cta gaa ggc gac ggc att      583
Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile
      85                      90                      95

gtg caa cgc cag gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg      631
Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp
      100                      105                      110                      115

aac acc acg gtg gaa gtc aag gct tgc cct gga ggc tac tat gtg tat      679
Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr
                        120                      125                      130

cgt ctg acc aag ccc agc gtc tgc ttc cac gtc tac tgt ggt cat ttt      727
Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe
                        135                      140                      145

tat gac atc tgc gac gag gac tgc cat ggc agc tgc tca gat acc agc      775
Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser
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150	155	160	
gag tgc aca tgc gct cca gga act gtg cta ggc cct gac agg cag aca Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp Arg Gln Thr 165 170 175			823
tgc ttt gat gaa aat gaa tgt gag caa aac aac ggt ggc tgc agt gag Cys Phe Asp Glu Asn Glu Cys Glu Gln Asn Asn Gly Gly Cys Ser Glu 180 185 190 195			871
atc tgt gtg aac ctc aaa aac tcc tac cgc tgt gag tgt ggg gtt ggc Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val Gly 200 205 210			919
cgt gtg cta aga agt gat ggc aag act tgt gaa gac gtt gaa gga tgc Arg Val Leu Arg Ser Asp Gly Lys Thr Cys Glu Asp Val Glu Gly Cys 215 220 225			967
cac aat aac aat ggt ggc tgc agc cac tct tgc ctt gga tct gag aaa His Asn Asn Asn Gly Gly Cys Ser His Ser Cys Leu Gly Ser Glu Lys 230 235 240			1015
ggc tac cag tgt gaa tgt ccc cgg ggc ctg gtg ctg tct gag gat aac Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu Ser Glu Asp Asn 245 250 255			1063
cac act tgc caa gtc cct gtg ttg tgc aaa tca aat gcc att gaa gtg His Thr Cys Gln Val Pro Val Leu Cys Lys Ser Asn Ala Ile Glu Val 260 265 270 275			1111
aac atc ccc agg gag ctg gtt ggt ggc ctg gag ctc ttc ctg acc aac Asn Ile Pro Arg Glu Leu Val Gly Gly Leu Glu Leu Phe Leu Thr Asn 280 285 290			1159
acc tcc tgc cga gga gtg tcc aac ggc acc cat gtc aac atc ctc ttc Thr Ser Cys Arg Gly Val Ser Asn Gly Thr His Val Asn Ile Leu Phe 295 300 305			1207
tct ctc aag aca tgt ggt aca gtg gtc gat gtg gtg aat gac aag att Ser Leu Lys Thr Cys Gly Thr Val Val Asp Val Val Asn Asp Lys Ile 310 315 320			1255
gtg gcc agc aac ctc gtg aca ggt cta ccc aag cag acc ccg ggg agc Val Ala Ser Asn Leu Val Thr Gly Leu Pro Lys Gln Thr Pro Gly Ser 325 330 335			1303
agc ggg gac ttc atc atc cga acc agc aag ctg ctg atc ccg gtg acc Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys Leu Leu Ile Pro Val Thr 340 345 350 355			1351
tgc gag ttt cca cgc ctg tac acc att tct gaa gga tac gtt ccc aac Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser Glu Gly Tyr Val Pro Asn 360 365 370			1399
ctt cga aac tcc cca ctg gaa atc atg agc cga aat cat ggg atc ttc Leu Arg Asn Ser Pro Leu Glu Ile Met Ser Arg Asn His Gly Ile Phe 375 380 385			1447

cca ttc act ctg gag atc ttc aag gac aat gag ttt gaa gag cct tac	1495
Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn Glu Phe Glu Glu Pro Tyr	
390 395 400	
cgg gaa gct ctg ccc acc ctc aag ctt cgt gac tcc ctc tac ttt ggc	1543
Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly	
405 410 415	
att gag ccc gtg gtg cac gtg agc ggc ttg gaa agc ttg gtg gag agc	1591
Ile Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser	
420 425 430 435	
tgc ttt gcc acc ccc acc tcc aag atc gac gag gtc ctg aaa tac tac	1639
Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr Tyr	
440 445 450	
ctc atc cgg gat ggc tgt gtt tca gat gac tcg gta aag cag tac aca	1687
Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln Tyr Thr	
455 460 465	
tcc cgg gat cac cta gca aag cac ttc cag gtc cct gtc ttc aag ttt	1735
Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val Phe Lys Phe	
470 475 480	
gtg ggc aaa gac cac aag gaa gtg ttt ctg cac tgc cgg gtt ctt gtc	1783
Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu Val	
485 490 495	
tgt gga gtg ttg gac gag cgt tcc cgc tgt gcc cag ggt tgc cac cgg	1831
Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala Gln Gly Cys His Arg	
500 505 510 515	
cga atg cgt cgt ggg gca gga gga gag gac tca gcc ggt cta cag ggc	1879
Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu Gln Gly	
520 525 530	
cag acg cta aca ggc ggc ccg atc cgc atc gac tgg gag gac tag ttc	1927
Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile Asp Trp Glu Asp *	
535 540 545	
gtagccatac ctcgagtccc tgcattggac ggctctgctc tttggagctt ctccccccac	1987
cgccctctaa gaacatctgc caacagctgg gttcagactt cacactgtga gttcagactc	2047
ccagcaccaa ctactctga ttctggtcca ttcagtgggc acaggtcaca gcactgctga	2107
acaatgtggc ctgggtgggg tttcatcttt ctagggttga aaactaaact gtccaccag	2167
aaagacactc accccatttc cctcatttct ttctacact taaatacctc gtgtatggtg	2227
caatcagacc acaaaatcag aagctgggta taatatttca agttacaaac cctagaaaaa	2287
ttaaacagtt actgaaatta tgacttaaata acccaatgac tccttaaata tgtaaattat	2347
agttatacct tgaaatttca attcaaatgc agactaatta tagggaattt ggaagtgtat	2407

caataaaaca gtatataatt ttaaaaaaaaa aaaaaaa

2444

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<212> DNA  
<213> Homo sapiens

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<222> (118)..(828)

<400> 15

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gggttgaggc tgcctgaccc cagcctaatt gggtaggtag gccttgggaa gtggagc 117  
atg ggg gca aag gat cca agc att gag cct tca tcc tct att ccc cat 165  
Met Gly Ala Lys Asp Pro Ser Ile Glu Pro Ser Ser Ser Ile Pro His  
1 5 10 15

cca gtg ggg tgc cga ggc tca ggc agc atg acg acg gag acc ttt gtg 213  
Pro Val Gly Cys Arg Gly Ser Gly Ser Met Thr Thr Glu Thr Phe Val  
20 25 30

aag gat atc aag cct ggg ctc aag aat ctg aac ctt atc ttc att gtg 261  
Lys Asp Ile Lys Pro Gly Leu Lys Asn Leu Asn Leu Ile Phe Ile Val  
35 40 45

ctg gag aca ggc cga gtg acc aag aca aag gac ggg cat gag gtt cgg 309  
Leu Glu Thr Gly Arg Val Thr Lys Thr Lys Asp Gly His Glu Val Arg  
50 55 60

acc tgc aaa gtg gcg gac aaa aca ggc agc atc aat atc tct gtc tgg 357  
Thr Cys Lys Val Ala Asp Lys Thr Gly Ser Ile Asn Ile Ser Val Trp  
65 70 75 80

gac gat gtt ggc aat ctg atc cag cct ggg gac att atc cgg ctc acc 405  
Asp Asp Val Gly Asn Leu Ile Gln Pro Gly Asp Ile Ile Arg Leu Thr  
85 90 95

aaa ggg tac gct tca gtt ttc aaa ggt tgt ctg aca cta tat act ggc 453  
Lys Gly Tyr Ala Ser Val Phe Lys Gly Cys Leu Thr Leu Tyr Thr Gly  
100 105 110

cgt ggg ggt gat ctg cag aag att gga gaa ttc tgt atg gtt tat tct 501  
Arg Gly Gly Asp Leu Gln Lys Ile Gly Glu Phe Cys Met Val Tyr Ser  
115 120 125

gag gtt cct aac ttc agt gag cca aac cca gag tac agc acc cag cag 549  
Glu Val Pro Asn Phe Ser Glu Pro Asn Pro Glu Tyr Ser Thr Gln Gln  
130 135 140

gca ccc aac aag gcg gtg cag aac gac agc aac cct tca gct tcc cag 597  
Ala Pro Asn Lys Ala Val Gln Asn Asp Ser Asn Pro Ser Ala Ser Gln  
145 150 155 160

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cct acc act gga ccc tct gct gcc tct cca gcc tct gag aac cag aat      645
Pro Thr Thr Gly Pro Ser Ala Ala Ser Pro Ala Ser Glu Asn Gln Asn
      165                      170                      175

ggg aat gga ctg agt gcc cca cca ggt ccc ggt ggt ggc cca cat ccc      693
Gly Asn Gly Leu Ser Ala Pro Pro Gly Pro Gly Gly Gly Pro His Pro
      180                      185                      190

cct cat act ccc tcc cac cca ccc agc acc cga atc act cga agc cag      741
Pro His Thr Pro Ser His Pro Pro Ser Thr Arg Ile Thr Arg Ser Gln
      195                      200                      205

ccc aac cac aca cct gca ggc ccg cct ggc cct ttc agc aac cct gtt      789
Pro Asn His Thr Pro Ala Gly Pro Pro Gly Pro Phe Ser Asn Pro Val
      210                      215                      220

agt aac ggc aaa gaa acc cgg agg agc agc aag aga tag catgacattc      838
Ser Asn Gly Lys Glu Thr Arg Arg Ser Ser Lys Arg *
      225                      230                      235

ttttcttctg ccaccaacca catcccaagt gtcccctgga gagcaagata gccttccact      898

gattggctgg ttagcagta ttttagccac tgaacttcag tggaggggtgg tgagcagtgt      958

ccttatccac cctaattctca tactccctca ttgtccagct gaactacctg tcccctggga      1018

gtcaggaccc tctgcctgct ctctttcctc tttagaaatg gcagttactg gctgggcgca      1078

gtggctcacg cttgtaatcc cagcactttg ggaagccgag gtgggcggat cacctgaggt      1138

cgggagttca agaccagcct gaccaacatg gagaaacccc gtgtctacta aaaatacaga      1198

attagccagg catggtggcg tatgcctgta atcccagcta ctaggagggc tgaggcagga      1258

gaatctcttg aaaccgggag gcggaggttg aggtgagccg aaattgcacc attgcactcc      1318

agcctgggca ataagagcga aactccatct caaaaaaaaaa agaaagaaag aaagaaagaa      1378

atggcagtta ccatctgttt cttctgtgtg agacatggga gtctaactga agtctctcct      1438

tcctaataaa tgttaccact ctaaaaaaaaa aaaa                                1472

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<210> 16  
 <211> 2098  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (301)..(897)

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cccatatccc atttccagct gcaaattact gcagaatctg aacccaggaa agaaacccat	180
ttgcgcgaccc cctctttccct ctccagacag gtggagagcg ggtgaggggtc tgcctcggt	240
ttccccctgc acctttccca ccttcccgcc cgtccctggg ggtcctccgt caccgcggcc	300
atg gcc cag aag ccg aag gtg gac ccc cac gtc ggg cgg ctg gga tac	348
Met Ala Gln Lys Pro Lys Val Asp Pro His Val Gly Arg Leu Gly Tyr	
1 5 10 15	
ctg cag gcg ctg gtc acg gaa ttc cag gag acc caa agc caa gac gcc	396
Leu Gln Ala Leu Val Thr Glu Phe Gln Glu Thr Gln Ser Gln Asp Ala	
20 25 30	
aag gag caa gtc ctc gcc aac ctc gcc aac ttc gct tat gac ccc agc	444
Lys Glu Gln Val Leu Ala Asn Leu Ala Asn Phe Ala Tyr Asp Pro Ser	
35 40 45	
aac tac gag tat ctg cgg cag ctg cag gtc ctg gat tta ttt ctc gat	492
Asn Tyr Glu Tyr Leu Arg Gln Leu Gln Val Leu Asp Leu Phe Leu Asp	
50 55 60	
tcg ctg tcg gag gag aat gag acc ctg gtg gag ttt gct att gga ggc	540
Ser Leu Ser Glu Glu Asn Glu Thr Leu Val Glu Phe Ala Ile Gly Gly	
65 70 75 80	
ctg tgc aac ctg tgc cca gac agg gcc aac aag gag cac atc ctg cac	588
Leu Cys Asn Leu Cys Pro Asp Arg Ala Asn Lys Glu His Ile Leu His	
85 90 95	
gca gga ggt gtc cca ctc atc atc aac tgc cta tcc agc ccc aat gag	636
Ala Gly Gly Val Pro Leu Ile Ile Asn Cys Leu Ser Ser Pro Asn Glu	
100 105 110	
gag acg gtg ctg tct gcc atc acc acg ctc atg cac ctg agc ccg ccg	684
Glu Thr Val Leu Ser Ala Ile Thr Thr Leu Met His Leu Ser Pro Pro	
115 120 125	
ggc cgc agc ttt ctc cca gag ctg acc gcc acg ccc gtg gtg cag tgc	732
Gly Arg Ser Phe Leu Pro Glu Leu Thr Ala Thr Pro Val Val Gln Cys	
130 135 140	
atg ctt cgc ttc tcc ctc tcg gcc agc gcc agg ctc cgg aac ctg gca	780
Met Leu Arg Phe Ser Leu Ser Ala Ser Ala Arg Leu Arg Asn Leu Ala	
145 150 155 160	
cag atc ttc ctg gag gac ttc tgc tcc ccc cgc cag gtg gcc gag gcc	828
Gln Ile Phe Leu Glu Asp Phe Cys Ser Pro Arg Gln Val Ala Glu Ala	
165 170 175	
cgc agc cgg cag gcg cac tct gcc ctg ggt atc cca ctg ccg agg agc	876
Arg Ser Arg Gln Ala His Ser Ala Leu Gly Ile Pro Leu Pro Arg Ser	
180 185 190	

gtg gcc cca cgg cag cgc tga tc catggagact gcgagaccgt ggcaccccta	929
Val Ala Pro Arg Gln Arg *	
195	
ctgctgggga ccacagtcct gatgtggacg cagggaacgg ggagcacata ctgccccatt	989
ggtgcctttt cagccatctg aaaggcgggt tctttcagca ggacaggcat ttacactgat	1049
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<213> Homo sapiens

<220>
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<222> (119) .. (580)

<400> 17

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atg aat gtg ggc aca gcg cac agc gag gtg aac ccc aac acg cgg gtg	166
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1 5 10 15	
atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc	214
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu	
20 25 30	
ctc cac atc gtg ctg ctg agc atc ccg ttt gtg agt gtc cct gtc gtc	262
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val	
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Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu	
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cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg	358
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala	
65 70 75 80	
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Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr	
85 90 95	
gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc	454
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu	
100 105 110	
acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc	502
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr	
115 120 125	
gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga	550
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly	
130 135 140	
gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttcccctgc	601
Val Arg Ile Phe Gly Ile Asn Lys Tyr *	
145 150	
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<212> DNA
<213> Homo sapiens

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tgggcgggag cccttgtctg ggtctcgcg ggggctgcca gatgcgtagg ccacactgac 180
tagttccttc ttgtcgcttt tcccagcaa atg gcg gat gac gcc ggt gca gcg 233
Met Ala Asp Asp Ala Gly Ala Ala
1 5

ggg ggg ccc ggg ggc cct ggt ggc cct ggg atg ggg aac cgc ggt ggc 281
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
10 15 20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt 329
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
25 30 35 40

gga cgg ggc cgg ggc cga ggc cgc gga gct cgc gga ggc aag gcc gag 377
Gly Arg Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu
45 50 55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac 425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
60 65 70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att 473

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Met	Lys	Ile	Lys	Ser	Leu	Glu	Glu	Ile	Tyr	Leu	Phe	Ser	Leu	Pro	Ile		
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Lys	Glu	Ser	Glu	Ile	Ile	Asp	Phe	Phe	Leu	Gly	Ala	Ser	Leu	Lys	Asp		
	90					95				100							
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Glu	Val	Leu	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	Gly	Gln		
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cgc	acc	agg	ttc	aag	gca	ttt	gtt	gct	atc	ggg	gac	tac	aat	ggc	cac	617	
Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Ala	Ile	Gly	Asp	Tyr	Asn	Gly	His		
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Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala	Ile	Arg		
			140					145					150				
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Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Ile	Val	Pro	Val	Arg	Arg	Gly		
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Tyr	Trp	Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val		
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aca	gcg	tgg	ggc	cat	cat	cct	ggc	caa	gct	ctc	cat	cgt	ccc	cgt	gcg	809	
Thr	Ala	Trp	Gly	His	His	Pro	Gly	Gln	Ala	Leu	His	Arg	Pro	Arg	Ala		
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cag	agg	cta	ctg	ggg	gaa	caa	gat	cgg	caa	gcc	cca	cac	tgt	cac	ctt	857	
Gln	Arg	Leu	Leu	Gly	Glu	Gln	Asp	Arg	Gln	Ala	Pro	His	Cys	His	Leu		
				205				210						215			
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Ala	Arg	Asp	Ser	Val	Gly	Leu	Ala	Asp	Leu	Val	Pro	Pro	Val	Ala	Ser		
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gcg	cac	ggg	gac	gat	gga	gag	ctt	ggc	cag	gat	gat	ggc	ccc	acg	gat	953	
Ala	His	Gly	Asp	Asp	Gly	Glu	Leu	Gly	Gln	Asp	Asp	Gly	Pro	Thr	Asp		
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ggc	ggt	ggc	cac	ctc	ctt	gga	gca	ctt	aac	acc	cag	acc	gac	gtg	gcc	1001	
Gly	Gly	Gly	His	Leu	Leu	Gly	Ala	Leu	Asn	Thr	Gln	Thr	Asp	Val	Ala		
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Ile	Val	Val	Pro	Asp	Ser	Asn	Lys	Cys	Leu	Glu	Pro	Gly	Ala	Leu	Ala		
265					270					275					280		
ggc	acg	ggt	ctg	ctt	ctg	cac	tgg	cat	aat	ctt	caa	aac	ctc	atc	ctt	1097	
Gly	Thr	Gly	Leu	Leu	Leu	His	Trp	His	Asn	Leu	Gln	Asn	Leu	Ile	Leu		
				285				290						295			
gag	aga	ggg	cac	cac	aca	gtg	aac	gaa	agt	caa	atg	agt	gct	gct	gat	1145	
Glu	Arg	Gly	His	His	Thr	Val	Asn	Glu	Ser	Gln	Met	Ser	Ala	Ala	Asp		

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Ser Leu Ile Gly Arg Glu Lys Arg *			
315	320		
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			Met
			1
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt			164
Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe			
5 10 15			
gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg			212
Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp			
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ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct			260
Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala			
35 40 45			
gtg att gga acc agg ctg cat gct gct gtg gca att gct tgt gtt gta			308
Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val			
50 55 60 65			
atg gcc ttt tac gtc ctg ttt ata aaa tga a ttccaaagca cccaagtcac			359
Met Ala Phe Tyr Val Leu Phe Ile Lys *			
70 75			
caactgccaa ccaaggggac ggggatgaag aacctgttgg agacctgaac ccagtgtagg			419



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agagttcagc tgaaatcatc ggtccccagg atgacaccac agcatctgcc cctgctatat 479
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Met Gly Lys Val
1

aag gtc gga gtc aac gga ttt ggt cgt att ggg cgc ctg gtc acc agg 162
Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr Arg
5 10 15 20

gct gct ttt aac tct ggt aaa gtg gat att gtt gcc atc aat gac ccc 210
Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp Pro
25 30 35

ttc att gac ctc aac tac atg gtt tac atg ttc caa tat gat tcc acc 258
Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser Thr
40 45 50

cat ggc aaa ttc cat ggc acc gtc aag gct gag aac ggg aag ctt gtc 306
His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val
55 60 65

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa 354
Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys
70 75 80

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aaa agg gtc atc atc tct gcc ccc tct gct gat gcc ccc atg ttc gtc Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe Val 120 125 130	498
atg ggt gtg aac cat gag aag tat gac aac agc ctc aag atc atc agc Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile Ser 135 140 145	546
aat gcc tcc tgc acc acc aac tgc tta gca ccc ctg gcc aag gtc atc Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile 150 155 160	594
cat gac aac ttt ggt atc gtg gaa gga ctc atg acc aca gtc cat gcc His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala 165 170 175 180	642
atc act gcc acc cag aag act gtg gga tgg ccc ctt ccg gga aac tgt Ile Thr Ala Thr Gln Lys Thr Val Gly Trp Pro Leu Pro Gly Asn Cys 185 190 195	690
ggc gtg atg gcc gcg ggg gcg tct gcc aga aac atc atc cct gcc tct Gly Val Met Ala Ala Gly Ala Ser Ala Arg Asn Ile Ile Pro Ala Ser 200 205 210	738
act ggc gct gcc aag gct gtg ggc aag gtc atc cct gag ctg aac ggg Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly 215 220 225	786
aag ctc act ggc atg gcc ttc cgt gtc ccc act gcc aac gtg tca gtg Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val 230 235 240	834
gtg gac ctg acc tgc cgt cta gaa aaa cct gcc aaa tat gat gac atc Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile 245 250 255 260	882
aag aag gtg gtg aag cag gcg tcg gag ggc ccc ctc aag ggc atc ctg Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu 265 270 275	930
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cac tcc tcc acc ttt gac gct ggg gct ggc att gcc ctc aac gac cac His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp His 295 300 305	1026
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Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn	
310 315 320	
agg gtg gtg gac ctc atg gcc cac atg gcc tcc aag gag taa gacccct	1123
Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu *	
325 330 335	
ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg ctggggagtc	1183
cctgccacac tcagtcccc accacactga atctcccctc ctcacagttg ccatgtagac	1243
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	Met Pro
	1
ctc ttc act ctg gcc tcg ctg agc ggc tgc ccg agg agg agc tct agg	585
Leu Phe Thr Leu Ala Ser Leu Ser Gly Cys Pro Arg Arg Ser Ser Arg	
5 10 15	
ccg acg ccc acc gca ggc ctt aca gtc ttc tct gga cgc tcc ctt gca	633
Pro Thr Pro Thr Ala Gly Leu Thr Val Phe Ser Gly Arg Ser Leu Ala	
20 25 30	
gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg	681

Asp	Ala	Pro	Trp	Pro	Gly	Gly	Glu	Pro	Pro	Val	Thr	Phe	Leu	Arg	Thr	
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Glu	Glu	Gly	Pro	Asp	Ala	Thr	Phe	Pro	Arg	Thr	Ile	Pro	Leu	Ile	Gln	
			55						60					65		
cag ttg cta aac gcc acg gag ctc acg cag gac ccg gcc gcc tac tcc 777																
Gln	Leu	Leu	Asn	Ala	Thr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Ala	Tyr	Ser	
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cag ctg gtg gcc gtg ctg gtc tac acc gcc gag cgg gcc aag ttc gcc 825																
Gln	Leu	Val	Ala	Val	Leu	Val	Tyr	Thr	Ala	Glu	Arg	Ala	Lys	Phe	Ala	
		85					90					95				
acc ggg gta gag cgg cag gac tgg atg gag ctg ttc att gac acc ttt 873																
Thr	Gly	Val	Glu	Arg	Gln	Asp	Trp	Met	Glu	Leu	Phe	Ile	Asp	Thr	Phe	
	100					105					110					
aag ctg gtg cac agg gac atc gtg ggg gac ccc gag acc gcg ctg gcc 921																
Lys	Leu	Val	His	Arg	Asp	Ile	Val	Gly	Asp	Pro	Glu	Thr	Ala	Leu	Ala	
	115				120				125					130		
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Leu	Cys	*														
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Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro Ile Asp Val Leu	
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His Gln Pro Gly Ser Ile Arg Leu Ala Thr Thr Pro Val Arg Val Asp  
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Tyr	Leu	Ile	Glu	Pro	Glu	Lys	Ile	Gln	Glu	Met	Phe	Pro	Leu	Leu	Asn	
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Ser	Asp	Gly	Thr	Trp	Asp	Val	Glu	Thr	Pro	Gln	Gly	Ser	Met	Arg	Ala	
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Met	Ile	Gly	Leu	Glu	His	Pro	Leu	Ile	Pro	Val	Gln	His	Gln	Tyr	Val	
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Ile His Ala Gly Gly Val Gly Lys Tyr Leu Ser Asp Trp Ile Leu His	
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Gly Val Thr Asp Leu Ser Pro Phe Gly Lys Phe Asn Ile Lys Gly Gln	
415 420 425	



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Ser	Gly	Ser	Tyr	Ser	Tyr	Ser	Ile	Gln	Lys	Ser	Leu	Ala	Phe	Ala	Tyr	
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Leu	Gly	Lys	Asn	Tyr	Pro	Ala	Val	Ile	Ile	Gln	Glu	Pro	Leu	Val	Leu	
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Thr	Glu	Pro	Thr	Arg	Asn	Arg	Leu	Gln	Lys	Lys	Gly	Gly	Lys	Asp	Lys	
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Thr	*															
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Glu His Ile Ala His Phe Leu Gly Thr Gly Gly Ala Ala Thr Thr Met						
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Gly Asn Ser Cys Ile Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val						
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Pro Pro Tyr Ser Met Ile Thr Leu His Glu Met Ala Glu Thr Asp Glu						
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Trp Tyr Asn Ala Arg Ser Lys Pro His Ile His Pro Cys Trp Lys Glu	
410 415 420	
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Lys Ile Ile Leu Pro Arg His Arg Arg Leu Ala Leu Leu Lys Gln Val	
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Ser Ile Arg Glu Asn Cys Cys Ser Leu Cys Cys Asp Glu Val Ala Asp	
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Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser
                   95                   100                   105

aag aca aat tcc tgt ccc ttg tgc cgc cat gag ctg ccc act gat gac   385
Lys Thr Asn Ser Cys Pro Leu Cys Arg His Glu Leu Pro Thr Asp Asp
                   110                   115                   120

gac act tat gag gag cac aga cga gat aag gct cga aaa cag cag cag   433
Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln
                   125                   130                   135                   140

caa cac cga ctg gag aac ctc cat gga gcc atg tac acg tga ggaggtt   482
Gln His Arg Leu Glu Asn Leu His Gly Ala Met Tyr Thr *
                   145                   150

ggggctgagt gctggccctc tgcgtcttcc ttattaacct tgaatcctca ttaaaggttt   542

ctttaccac aaaaaaaaaa aa   564

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<210> 27  
 <211> 609  
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 <213> Homo sapiens

<220>  
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 <222> (18)..(581)

<400> 27

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	Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu	
	1 5 10	
ccg tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc	98	
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu		
15 20 25		
gca agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta	146	
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val		
30 35 40		
gta gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt	194	
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val		
45 50 55		
gag aac ctc ccc agg aca gtc atc aga ggc tct cag gct gct ctc acc	242	
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Ala Leu Thr		
60 65 70 75		
gtg ccc tgg gcc cag tac tca agc ttc ttt ctg ttc atg gac tgc tgg	290	
Val Pro Trp Ala Gln Tyr Ser Ser Phe Phe Leu Phe Met Asp Cys Trp		
80 85 90		
ggg atg gaa gaa gag tgg cag ttg gga gca ggg gag ggt ggt tat cag	338	
Gly Met Glu Glu Glu Trp Gln Leu Gly Ala Gly Glu Gly Gly Tyr Gln		
95 100 105		
ctt atg aag atc aga cca agg cta gaa cac tac tct act ttt ctc aga	386	
Leu Met Lys Ile Arg Pro Arg Leu Glu His Tyr Ser Thr Phe Leu Arg		
110 115 120		
caa att cct gtc cct tgt gcc gct atg agc tgc cca ctg atg acg aca	434	
Gln Ile Pro Val Pro Cys Ala Ala Met Ser Cys Pro Leu Met Thr Thr		
125 130 135		
ctt atg agg agc aca gac gag ata agg ctc gaa aac agc agc agc aac	482	
Leu Met Arg Ser Thr Asp Glu Ile Arg Leu Glu Asn Ser Ser Ser Asn		
140 145 150 155		
acc gac tgg aga acc tcc atg gag cca tgt aca cgt gag gag gtt ggg	530	
Thr Asp Trp Arg Thr Ser Met Glu Pro Cys Thr Arg Glu Glu Val Gly		
160 165 170		
gct gag tgc tgg ccc tct gcg tct tcc tta tta acc ttg aat cct cat	578	
Ala Glu Cys Trp Pro Ser Ala Ser Ser Leu Leu Thr Leu Asn Pro His		

175

180

185

taa aggtttcttt acccacaaaa aaaaaaaaa

609

\*

&lt;210&gt; 28

&lt;211&gt; 1291

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)..(1057)

&lt;400&gt; 28

tgctggaatt ccccggcgcc gcgcc	atg tgg gct gcg gcg ggc ggg ctg tgg	52
	Met Trp Ala Ala Ala Gly Gly Leu Trp	
	1 5	

cgc tcc cgc gcg ggt ctc cgg gcc ctg ttc cgt agc cgc gat gct gcg	100
Arg Ser Arg Ala Gly Leu Arg Ala Leu Phe Arg Ser Arg Asp Ala Ala	
10 15 20 25	

cta ttt cca ggc tgc gag cgg gga ctt cac tgc tct gct gtc tcc tgc	148
Leu Phe Pro Gly Cys Glu Arg Gly Leu His Cys Ser Ala Val Ser Cys	
30 35 40	

aag aac tgg ctc aag aaa ttt gcc tcg aaa acc aaa aaa aag gtt tgg	196
Lys Asn Trp Leu Lys Lys Phe Ala Ser Lys Thr Lys Lys Lys Val Trp	
45 50 55	

tat gaa agt cct tcc ttg ggt tct cac tcg act tac aaa cca tcc aag	244
Tyr Glu Ser Pro Ser Leu Gly Ser His Ser Thr Tyr Lys Pro Ser Lys	
60 65 70	

ttg gaa ttc ctc atg agg agc acc tca aag aaa acc agg aag gaa gac	292
Leu Glu Phe Leu Met Arg Ser Thr Ser Lys Lys Thr Arg Lys Glu Asp	
75 80 85	

cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca	340
His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr	
90 95 100 105	

gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac	388
Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn	
110 115 120	

gtg gag ctc tcc aag gtt tcc ctg act cca gac ttc tca gcc tgc cga	436
Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg	
125 130 135	

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag	484
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Ala Tyr Trp Lys Thr Thr Leu Ser Ala Glu Gln Asn Ala His Met Glu	
140 145 150	
gct gtc ctg cag aga agt gcc gcg cac atg agg cac ctt ttg atg tcc	532
Ala Val Leu Gln Arg Ser Ala Ala His Met Arg His Leu Leu Met Ser	
155 160 165	
cag cag acc ctg agg aat gtg cca ccg ata gtg ttt gtt caa gac aag	580
Gln Gln Thr Leu Arg Asn Val Pro Pro Ile Val Phe Val Gln Asp Lys	
170 175 180 185	
gga aat gca gct cta gct gag ctt gat cag tta ctg gca gtc gca gac	628
Gly Asn Ala Ala Leu Ala Glu Leu Asp Gln Leu Leu Ala Val Ala Asp	
190 195 200	
ttt gga ccc cgg gat gaa aga gac aac ttt gta caa aat gat ttc agg	676
Phe Gly Pro Arg Asp Glu Arg Asp Asn Phe Val Gln Asn Asp Phe Arg	
205 210 215	
gac cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc	724
Asp Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser	
220 225 230	
tcc agt ctg tgt ggg atc gat cat gag gcg ctc cac aag cag att atg	772
Ser Ser Leu Cys Gly Ile Asp His Glu Ala Leu His Lys Gln Ile Met	
235 240 245	
gag tac aaa agg agg aaa gat aaa ggg ctc ggg ggc ctg gtg tgg cag	820
Glu Tyr Lys Arg Arg Lys Asp Lys Gly Leu Gly Gly Leu Val Trp Gln	
250 255 260 265	
ggg cag gtg gct gag ctg aca acg cag atg aaa aag gga agg aag agg	868
Gly Gln Val Ala Glu Leu Thr Thr Gln Met Lys Lys Gly Arg Lys Arg	
270 275 280	
gcc aag ccc cgc ctg gag cag gac agc tcc ctc aag agt tac ctg tca	916
Ala Lys Pro Arg Leu Glu Gln Asp Ser Ser Leu Lys Ser Tyr Leu Ser	
285 290 295	
ggc gag gag gtt gaa gat gac ctg gac ctg gtt ggt gcc ccg gag tac	964
Gly Glu Glu Val Glu Asp Asp Leu Asp Leu Val Gly Ala Pro Glu Tyr	
300 305 310	
gaa tgc tat gcc ccg gac aca gag gag ttg gag gca gag aga gga ggt	1012
Glu Cys Tyr Ala Pro Asp Thr Glu Glu Leu Glu Ala Glu Arg Gly Gly	
315 320 325	
ggc aga aca gag gat ggc cac agc tgc gga gca agc agg gag tag atg	1060
Gly Arg Thr Glu Asp Gly His Ser Cys Gly Ala Ser Arg Glu *	
330 335 340	
gagaggctct gcccatccca catttgcagg gaaaagcatt ggcacgcaac gcagcatgtg 1120	
gcttcattga ggcagttgat ggagttaaac catctgctct tctgctactt caacattttc 1180	
tagcttttcc gtgtatctaa acacaatttg ctacacaagt cactgttttt ttttccatgc 1240	

actgtgtgta atttaaaaat taaatggcca tcttatcaca aaaaaaaaaa a

1291

<210> 29  
<211> 766  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (103)..(759)

<400> 29

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ggcggttgca ggcttcagcc tgcgctggtt ggtgaaacag ag atg tca gaa aag 114  
Met Ser Glu Lys  
1

gag aac aac ttc ccg cca ctg ccc aag ttc atc cct gtg aag ccc tgc 162  
Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro Val Lys Pro Cys  
5 10 15 20

ttc tac cag aac ttc tcc gac gag atc cca gtg gag cac cag gtc ctg 210  
Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu His Gln Val Leu  
25 30 35

gtg aag agg atc tac ccg ctg tgg atg ttt tac tgc gcc acc ctc ggc 258  
Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly  
40 45 50

gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg 306  
Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly  
55 60 65

acc aac ttc ggc ctg gcc ttc gtg tgg ctg ctc ctg ttc acg cct tgc 354  
Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Phe Thr Pro Cys  
70 75 80

ggc tac gtg tgc tgg ttc ccg cct gtc tac aag gcc ttc cga gcc gac 402  
Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp  
85 90 95 100

agc tcc ttt aat ttc atg gcg ttt ttc ttc atc ttc gga gcc cag ttt 450  
Ser Ser Phe Asn Phe Met Ala Phe Phe Phe Ile Phe Gly Ala Gln Phe  
105 110 115

gtc ctg acc gtc atc cag gcg att ggc ttc tcc ggc tgg ggc gcg tgc 498  
Val Leu Thr Val Ile Gln Ala Ile Gly Phe Ser Gly Trp Gly Ala Cys  
120 125 130

ggc tgg ctg tcg gca att gga ttc ttc cag tac agc ccg ggc gct gcc 546  
Gly Trp Leu Ser Ala Ile Gly Phe Phe Gln Tyr Ser Pro Gly Ala Ala  
135 140 145

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gtg gtc atg ctg ctt cca gcc atc atg ttc tcc gtg tcg gct gcc atg      594
Val Val Met Leu Leu Pro Ala Ile Met Phe Ser Val Ser Ala Ala Met
    150                      155                      160

atg gcc atc gcg atc atg aag gtg cac agg atc tac cga ggg ggc tgg      642
Met Ala Ile Ala Ile Met Lys Val His Arg Ile Tyr Arg Gly Gly Trp
    165                      170                      175                      180

cgg aag ctt cca gaa ggc cag acg gag tgg cac acg ggc ctt ggc gga      690
Arg Lys Leu Pro Glu Gly Gln Thr Glu Trp His Thr Gly Leu Gly Gly
                185                      190                      195

acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc      738
Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro
                200                      205                      210

agt acc ccc ttg tgc ccg taa ccggcgg      766
Ser Thr Pro Leu Cys Pro *
    215

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<210> 30
<211> 3922
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (139)..(3633)

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gacggcagggg gtcctcagac cggcgctcgc tcgccggcgc catccctata gagaagaacg      120

gaggtacggc ctgtggtc  atg gcg ctg ttc cca gcc ttt gcg ggg ctt agt      171
                   Met Ala Leu Phe Pro Ala Phe Ala Gly Leu Ser
                   1                   5                   10

gag gct ccc gat ggc ggg agc tcc agg aaa gag tta gac tgg ctg agc      219
Glu Ala Pro Asp Gly Gly Ser Ser Arg Lys Glu Leu Asp Trp Leu Ser
                15                      20                      25

aac cca agc ttt tgt gtt gga tcc ata acg tcc ctg agc caa caa act      267
Asn Pro Ser Phe Cys Val Gly Ser Ile Thr Ser Leu Ser Gln Gln Thr
                30                      35                      40

gaa gca gct cca gcc cat gtt tct gaa ggg tta ccg ctg aca agg agt      315
Glu Ala Ala Pro Ala His Val Ser Glu Gly Leu Pro Leu Thr Arg Ser
                45                      50                      55

cat ctg aaa tca gag tct tca gat gaa agt gac act aac aaa aag ctc      363
His Leu Lys Ser Glu Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu
    60                      65                      70                      75

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cca gac agc gag agt gcg gct ctc aag gcc aag gtg gag gag ttt aac	1083
Pro Asp Ser Glu Ser Ala Ala Leu Lys Ala Lys Val Glu Glu Phe Asn	
300 305 310 315	
agg agg gtg cgg gag aat cct cgg gat acg cag ctg tgg atg gca ttt	1131
Arg Arg Val Arg Glu Asn Pro Arg Asp Thr Gln Leu Trp Met Ala Phe	
320 325 330	
gtt gct ttt cag gac gag gtc atg aaa agt cct ggc ctg tat gcc atc	1179
Val Ala Phe Gln Asp Glu Val Met Lys Ser Pro Gly Leu Tyr Ala Ile	
335 340 345	
gag gaa gga gag cag gaa aag cga aag agg tcc ctg aag ctc att ctg	1227
Glu Glu Gly Glu Gln Glu Lys Arg Lys Arg Ser Leu Lys Leu Ile Leu	
350 355 360	
gag aag aag ctg gcc att ctg gag cgg gcc att gag agc aac cag agc	1275
Glu Lys Lys Leu Ala Ile Leu Glu Arg Ala Ile Glu Ser Asn Gln Ser	
365 370 375	
agt gtg gat ctg aaa ctg gcc aag ctg aag ctc tgc aca gag ttc tgg	1323
Ser Val Asp Leu Lys Leu Ala Lys Leu Lys Leu Cys Thr Glu Phe Trp	
380 385 390 395	
gag ccc tcc act ctg gtc aaa gag tgg cag aaa ctg ata ttt ttg cat	1371
Glu Pro Ser Thr Leu Val Lys Glu Trp Gln Lys Leu Ile Phe Leu His	
400 405 410	
ccc aat aat aca gcc ctt tgg cag aaa tac ctt tta ttt tgc cag agc	1419
Pro Asn Asn Thr Ala Leu Trp Gln Lys Tyr Leu Leu Phe Cys Gln Ser	
415 420 425	
cag ttt agt acc ttt tcg ata tca aaa att cac agt ctt tat gga aaa	1467
Gln Phe Ser Thr Phe Ser Ile Ser Lys Ile His Ser Leu Tyr Gly Lys	
430 435 440	
tgc ttg agc act ttg tct gct gtt aag gac ggc agc atc tta tct cac	1515
Cys Leu Ser Thr Leu Ser Ala Val Lys Asp Gly Ser Ile Leu Ser His	
445 450 455	
cct gcg ttg cct ggc acg gaa gag gcc atg ttt gca ctc ttt ctt cag	1563
Pro Ala Leu Pro Gly Thr Glu Glu Ala Met Phe Ala Leu Phe Leu Gln	
460 465 470 475	
cag tgc cac ttt ctg cgg cag gct ggc cac tct gag aag gcc atc tca	1611
Gln Cys His Phe Leu Arg Gln Ala Gly His Ser Glu Lys Ala Ile Ser	
480 485 490	
ttg ttc cag gcc atg gtg gac ttc acc ttc ttc aaa ccc gac agc gta	1659
Leu Phe Gln Ala Met Val Asp Phe Thr Phe Phe Lys Pro Asp Ser Val	
495 500 505	
aaa gat ctg cct acc aaa gga cag gtg gaa ttc ttt gaa ccc ttt tgg	1707
Lys Asp Leu Pro Thr Lys Gly Gln Val Glu Phe Phe Glu Pro Phe Trp	
510 515 520	
gac agt gga gag ccc cgg gct ggg gag aag gga gcc cga ggc tgg aag	1755

Asp	Ser	Gly	Glu	Pro	Arg	Ala	Gly	Glu	Lys	Gly	Ala	Arg	Gly	Trp	Lys		
525						530					535						
gcg	tgg	atg	cac	cag	cag	gaa	cga	ggt	ggc	tgg	gtg	gtc	atc	aac	cca	1803	
Ala	Trp	Met	His	Gln	Gln	Glu	Arg	Gly	Gly	Trp	Val	Val	Ile	Asn	Pro		
540					545					550					555		
gat	gag	gat	gac	gat	gaa	cca	gaa	gag	gat	gac	cag	gaa	ata	aaa	gat	1851	
Asp	Glu	Asp	Asp	Asp	Glu	Pro	Glu	Glu	Asp	Asp	Gln	Glu	Ile	Lys	Asp		
				560					565					570			
aag	act	ctg	ccc	agg	tgg	cag	atc	tgg	ctt	gct	gct	gag	cgt	tcc	cgt	1899	
Lys	Thr	Leu	Pro	Arg	Trp	Gln	Ile	Trp	Leu	Ala	Ala	Glu	Arg	Ser	Arg		
			575					580					585				
gac	cag	agg	cac	tgg	cgg	ccc	tgg	cgc	cct	gat	aag	acc	aag	aag	caa	1947	
Asp	Gln	Arg	His	Trp	Arg	Pro	Trp	Arg	Pro	Asp	Lys	Thr	Lys	Lys	Gln		
			590				595					600					
acc	gag	gaa	gac	tgt	gag	gat	ccc	gag	aga	cag	ggg	gtg	ttt	gat	gat	1995	
Thr	Glu	Glu	Asp	Cys	Glu	Asp	Pro	Glu	Arg	Gln	Gly	Val	Phe	Asp	Asp		
			605				610					615					
att	ggg	caa	tct	ttg	atc	aga	ctt	tcc	agc	cat	gat	ctt	cag	ttc	cag	2043	
Ile	Gly	Gln	Ser	Leu	Ile	Arg	Leu	Ser	Ser	His	Asp	Leu	Gln	Phe	Gln		
					625					630					635		
ctg	gtg	gag	gcc	ttc	ctg	cag	ttc	ttg	ggt	gtg	cct	tct	ggc	ttt	act	2091	
Leu	Val	Glu	Ala	Phe	Leu	Gln	Phe	Leu	Gly	Val	Pro	Ser	Gly	Phe	Thr		
				640					645					650			
cct	cca	gcc	tcc	tgt	ctt	tat	ctg	gcc	atg	gat	gag	aac	agc	atc	ttt	2139	
Pro	Pro	Ala	Ser	Cys	Leu	Tyr	Leu	Ala	Met	Asp	Glu	Asn	Ser	Ile	Phe		
			655					660					665				
gat	aat	gga	ctt	tat	gat	gaa	aag	ccc	ttg	act	ttt	ttc	aac	cct	ttg	2187	
Asp	Asn	Gly	Leu	Tyr	Asp	Glu	Lys	Pro	Leu	Thr	Phe	Phe	Asn	Pro	Leu		
			670				675					680					
ttt	tct	ggg	gct	agc	tgt	gtt	ggc	cgc	atg	gat	agg	ttg	ggc	tat	cct	2235	
Phe	Ser	Gly	Ala	Ser	Cys	Val	Gly	Arg	Met	Asp	Arg	Leu	Gly	Tyr	Pro		
			685			690					695						
cgc	tgg	acc	agg	ggt	cag	aac	cga	gag	ggc	gag	gag	ttc	atc	cgc	aat	2283	
Arg	Trp	Thr	Arg	Gly	Gln	Asn	Arg	Glu	Gly	Glu	Glu	Phe	Ile	Arg	Asn		
					705				710						715		
gtc	ttc	cac	ctt	gtc	atg	cct	tta	ttt	tca	ggc	aaa	gag	aag	tcc	cag	2331	
Val	Phe	His	Leu	Val	Met	Pro	Leu	Phe	Ser	Gly	Lys	Glu	Lys	Ser	Gln		
				720					725					730			
ctc	tgc	ttc	tcc	tgg	tta	cag	tat	gag	att	gca	aag	gtc	att	tgg	tgc	2379	
Leu	Cys	Phe	Ser	Trp	Leu	Gln	Tyr	Glu	Ile	Ala	Lys	Val	Ile	Trp	Cys		
				735				740					745				
ctg	cac	act	aaa	aac	aag	aag	aga	tta	aag	tct	caa	ggg	aag	aac	tgc	2427	
Leu	His	Thr	Lys	Asn	Lys	Lys	Arg	Leu	Lys	Ser	Gln	Gly	Lys	Asn	Cys		

750	755	760	
aaa aaa cta gcc aag aat ctc ctt aag gag cca gaa aac tgc aac aac			2475
Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn			
765	770	775	
ttt tgc ctg tgg aag cag tat gca cat ctg gag tgg ttg ctt ggc aac			2523
Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn			
780	785	790	795
acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga			2571
Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly			
	800	805	810
agc aga gaa ctg aaa gac tct gac ctc tgt gag ctc agt ctg ctc tat			2619
Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr			
	815	820	825
gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca			2667
Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr			
	830	835	840
gct cga gct gtt cac ata tta acc aag ctg act gag agc agc ccc tat			2715
Ala Arg Ala Val His Ile Leu Thr Lys Leu Thr Glu Ser Ser Pro Tyr			
	845	850	855
ggg ccc tac act gga cag gtg ttg gct gtt cac att ttg aaa gcg cga			2763
Gly Pro Tyr Thr Gly Gln Val Leu Ala Val His Ile Leu Lys Ala Arg			
	860	865	870
aag gct tat gag cac gca ctg cag gac tgt ttg ggt gac agc tgt gtc			2811
Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val			
	880	885	890
tcc aat cca gct ccc acc gat tcc tgt agc cgc cta att agc ctg gct			2859
Ser Asn Pro Ala Pro Thr Asp Ser Cys Ser Arg Leu Ile Ser Leu Ala			
	895	900	905
aaa tgc ttc atg ctc ttc cag tat ttg acc ata ggg att gat gct gct			2907
Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala			
	910	915	920
gtg cag ata tac gaa cag gtg ttt gca aaa ctg aac agt tct gtt ttc			2955
Val Gln Ile Tyr Glu Gln Val Phe Ala Lys Leu Asn Ser Ser Val Phe			
	925	930	935
cca gaa ggc tct ggc gag ggg gac agt gcc agc tcc cag agt tgg acc			3003
Pro Glu Gly Ser Gly Glu Gly Asp Ser Ala Ser Ser Gln Ser Trp Thr			
	940	945	950
agt gtt ctc gaa gcc atc aca ctg atg cac acg agc ctg ctg aga ttc			3051
Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe			
	960	965	970
cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc			3099
His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu			
	975	980	985

tca cag gct tta aag ttg tat cca ggc aac cag gtt ctt tgg agg tcc	3147
Ser Gln Ala Leu Lys Leu Tyr Pro Gly Asn Gln Val Leu Trp Arg Ser	
990 995 1000	
tat gta cag att cag aat aag tcc cac agt gcc agc aaa acc agg aga	3195
Tyr Val Gln Ile Gln Asn Lys Ser His Ser Ala Ser Lys Thr Arg Arg	
1005 1010 1015	
ttt ttt gac aca atc acc agg tct gcc aaa ccc ttg gag cct tgg ttg	3243
Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu	
1020 1025 1030 1035	
ttt gca att gaa gct gag aaa ctg agg aag aga ctg gtg gaa act gtc	3291
Phe Ala Ile Glu Ala Glu Lys Leu Arg Lys Arg Leu Val Glu Thr Val	
1040 1045 1050	
cag agg tta gac ggt aga gag atc cac gcc aca att cct gag acc ggc	3339
Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly	
1055 1060 1065	
tta atg cat cgg atc caa gcc ctg ttt gaa aat gcc atg cgc agc gac	3387
Leu Met His Arg Ile Gln Ala Leu Phe Glu Asn Ala Met Arg Ser Asp	
1070 1075 1080	
agt ggc agc cag tgc ccc ttg ctg tgg agg atg tat ttg aac ttt ctg	3435
Ser Gly Ser Gln Cys Pro Leu Leu Trp Arg Met Tyr Leu Asn Phe Leu	
1085 1090 1095	
gtt tcc tta gga aat aaa gaa aga agc aaa ggt gta ttc tac aaa gca	3483
Val Ser Leu Gly Asn Lys Glu Arg Ser Lys Gly Val Phe Tyr Lys Ala	
1100 1105 1110 1115	
ctt cag aat tgc cct tgg gca aag gtg ttg tac ctg gac gcc gtg gag	3531
Leu Gln Asn Cys Pro Trp Ala Lys Val Leu Tyr Leu Asp Ala Val Glu	
1120 1125 1130	
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Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys	
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gag ctc cgg gtg cgc ctg ccg ctg gag gag ctg gag ctg ctg ctg gag	3627
Glu Leu Arg Val Arg Leu Pro Leu Glu Glu Leu Glu Leu Leu Glu	
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gat tag agagcagtgg gaaaacgggc tgtgcctgcg aggccaagtt gccaccctg	3683
Asp *	
1165	
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tctttctcga tagtaataat gtgggctgcc agcctctcac atcttgacaca ctttttgggt	3803
gtgtaaataga cacaaaagtt atttacatat tatatatgtg aatatgtgta tatatgtaca	3863
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Ala Ala Ala Ala Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu
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ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg   145
Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu
                   30                   35                   40

tct att tgt gta cgg ctt tgt gaa caa gga att aac cca gaa gct tta   193
Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu
                   45                   50                   55                   60

tca tcg gtt att aag gag ctt cgc aag gct act gaa gca ctg aag gct   241
Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala
                   65                   70                   75

gct gaa aat atg aca agc tga ct ttctggagaa attctgatga gatatgtcaa   294
Ala Glu Asn Met Thr Ser *
                   80

gctctgcaag agggttagaa gattgcattg tagttgagaa tgtacaatga aattactgca   354

tgcagcagtg tagaaaaatt ttacttttta aaagaattat aaaaccatag ctttataaat   414

cagtggaaag tggcttacag agagaactat cagatgtggt tacatcacat cttattcact   474

ttttttaaca gctctaatgc tttggcattg ctatgttcat atttatgtat tccttattta   534

tagctctgat agctttaatt ttctaagcag tctgtctatc agatgtgcac atctgctgtg   594

ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttggtgac   654

atttccatta taaacttta ttttgaattg tttatgcatt ataactgtgg atttatattg   714

tattgggctg aaagttgaca ggatttcagc caccacttgt gaatttttat ttagattcat   774

tatgtatatc agaatcttgt tttttgaaat aagagcatgg aaaacatttc ttgtaatcta   834

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tccaagc atg tct tcc ccg ttg caa aga gct gtg gga gat acc aag agg 289  
Met Ser Ser Pro Leu Gln Arg Ala Val Gly Asp Thr Lys Arg  
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gcc ttt tct gca tct tct agt tcc tct gcc agt cta ccc ttt gat gac 337  
Ala Phe Ser Ala Ser Ser Ser Ser Ser Ala Ser Leu Pro Phe Asp Asp  
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Arg Asp Ser Asn His Thr Ser Glu Gly Asn Gly Asp Ser Leu Leu Ala  
35 40 45  
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Asp Glu Asp Thr Asp Phe Glu Asp Ser Leu Asn Arg Asn Val Lys Lys  
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Arg Ala Ala Lys Arg Pro Pro Lys Thr Thr Pro Val Ala Lys His Pro  
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Lys Lys Gly Ser Arg Val Val His Arg His Ser Arg Lys Lys Ser Glu  
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cca cca gcc aat gat ctt ttc aat gct gtg aaa gcc gcc aaa agt gac 577  
Pro Pro Ala Asn Asp Leu Phe Asn Ala Val Lys Ala Ala Lys Ser Asp  
95 100 105 110



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Thr	Leu	His	Asp	Lys	His	Arg	Glu	Val	Arg	Val	Lys	Cys	Val	Lys	Ala	
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Leu	Lys	Gly	Leu	Tyr	Gly	Asn	Arg	Asp	Leu	Thr	Ala	Arg	Leu	Glu	Leu	
			370					375					380			
ttc	acc	agc	cgc	ttc	aag	gac	cgg	atg	gtt	tcc	atg	atc	atg	gac	aga	1441
Phe	Thr	Ser	Arg	Phe	Lys	Asp	Arg	Met	Val	Ser	Met	Ile	Met	Asp	Arg	
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gag	tac	agt	gtg	gca	gtg	gag	gcc	gtc	aga	tta	ctg	ata	ctt	ata	ctt	1489
Glu	Tyr	Ser	Val	Ala	Val	Glu	Ala	Val	Arg	Leu	Leu	Ile	Leu	Ile	Leu	
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Lys	Asn	Met	Glu	Gly	Leu	Leu	Thr	Asp	Ala	Asp	Cys	Glu	Ser	Val	Tyr	
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Pro	Val	Val	Tyr	Pro	Ser	Asn	Arg	Gly	Leu	Ala	Ser	Ala	Ala	Gly	Glu	
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Phe	Leu	Tyr	Trp	Lys	Leu	Phe	Tyr	Pro	Glu	Cys	Glu	Ile	Arg	Thr	Met	
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Gly	Gly	Arg	Glu	Gln	Arg	Gln	Ser	Pro	Gly	Ala	Gln	Arg	Thr	Phe	Phe	
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cag	ctt	ctg	ctg	tcc	ttc	ttt	gtg	gag	agc	gag	ctc	cat	gac	cac	gct	1729
Gln	Leu	Leu	Leu	Ser	Phe	Phe	Val	Glu	Ser	Glu	Leu	His	Asp	His	Ala	
	480					485					490					
gct	tac	tta	gta	gac	agt	ctg	tgg	gac	tgt	gca	ggg	gct	cgg	ctg	aag	1777
Ala	Tyr	Leu	Val	Asp	Ser	Leu	Trp	Asp	Cys	Ala	Gly	Ala	Arg	Leu	Lys	
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gac	tgg	gag	ggg	ctg	aca	agc	ctg	ctg	ctg	gag	aag	gac	cag	aac	ctg	1825
Asp	Trp	Glu	Gly	Leu	Thr	Ser	Leu	Leu	Leu	Glu	Lys	Asp	Gln	Asn	Leu	
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Gly	Asp	Val	Gln	Glu	Ser	Thr	Leu	Ile	Glu	Ile	Leu	Val	Ser	Ser	Ala	
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cgg	caa	gct	tca	gag	ggg	cac	cgg	cct	gtg	ggc	cgg	gtc	act	ggg	agg	1921
Arg	Gln	Ala	Ser	Glu	Gly	His	Pro	Pro	Val	Gly	Arg	Val	Thr	Gly	Arg	
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Lys	Gly	Leu	Thr	Ser	Lys	Glu	Arg	Lys	Thr	Gln	Ala	Asp	Asp	Arg	Val	

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Lys Leu Thr Glu His Leu Ile Pro Leu Leu Pro Gln Leu Leu Ala Lys			
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Phe Ser Ala Asp Ala Glu Lys Val Thr Pro Leu Leu Gln Leu Leu Ser			
	595	600	605
tgc ttt gac ctc cac atc tac tgc act ggg cgc ttg gag aag cac ctg			2113
Cys Phe Asp Leu His Ile Tyr Cys Thr Gly Arg Leu Glu Lys His Leu			
	610	615	620
gag ctg ttc ctg cag caa ctc cag gag gtg gtg gtg aag cat gca gag			2161
Glu Leu Phe Leu Gln Gln Leu Gln Glu Val Val Val Lys His Ala Glu			
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cca gcg gtg ctt gag gct ggg gcg cat gcc ctc tac ctg ctc tgt aat			2209
Pro Ala Val Leu Glu Ala Gly Ala His Ala Leu Tyr Leu Leu Cys Asn			
	640	645	650
ccc gaa ttc act ttc ttc agc cgg gcg gac ttt gcc cgc agc cag cta			2257
Pro Glu Phe Thr Phe Phe Ser Arg Ala Asp Phe Ala Arg Ser Gln Leu			
	655	660	670
gta gat ttg ctg act gac cgc ttc cag cag gag ctt gaa gag ctg tta			2305
Val Asp Leu Leu Thr Asp Arg Phe Gln Gln Glu Leu Glu Glu Leu Leu			
	675	680	685
cag tcg tcc ttc cta gat gag gat gag gta tat aat ctg gca gcc act			2353
Gln Ser Ser Phe Leu Asp Glu Asp Glu Val Tyr Asn Leu Ala Ala Thr			
	690	695	700
ctg aaa cgc ctc tct gcc ttc tac aac act cat gac ctg act cgc tgg			2401
Leu Lys Arg Leu Ser Ala Phe Tyr Asn Thr His Asp Leu Thr Arg Trp			
	705	710	715
gag ctc tat gag cca tgt tgc caa ctc ctg cag aag gct gtg gac aca			2449
Glu Leu Tyr Glu Pro Cys Cys Gln Leu Leu Gln Lys Ala Val Asp Thr			
	720	725	730
gga gag gtt cct cac cag gtt atc ctg cca gcc ttg act ctt gtc tat			2497
Gly Glu Val Pro His Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr			
	735	740	745
ttt tcc att ctc tgg aca cta acc cac att tct aaa tca gat gct tcc			2545
Phe Ser Ile Leu Trp Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser			
	755	760	765
cag aag cag ctg tcg agt ttg agg gac aga atg gtg gcc ttc tgt gaa			2593
Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu			
	770	775	780
ctc tgc cag agt tgc ctc tca gat gtg gat act gag atc cag gag cag			2641
Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln			
	785	790	795



gac aag cag ctt tta ctg tcc tat cta gaa aag tgc ctg cag cat gtc Asp Lys Gln Leu Leu Leu Ser Tyr Leu Glu Lys Cys Leu Gln His Val 1025 1030 1035	3361
tcc cag gca cct ggc cat ccc tgg ggc cca gtc acc acc tac tgc cac Ser Gln Ala Pro Gly His Pro Trp Gly Pro Val Thr Thr Tyr Cys His 1040 1045 1050	3409
tcc ctc agc cct gtg gag aac aca gca gag acc agc cct cag gtc ctc Ser Leu Ser Pro Val Glu Asn Thr Ala Glu Thr Ser Pro Gln Val Leu 1055 1060 1065 1070	3457
ccc agc tcc aag agg agg cgc gtt gaa ggg cct gcc aag cct aac aga Pro Ser Ser Lys Arg Arg Arg Val Glu Gly Pro Ala Lys Pro Asn Arg 1075 1080 1085	3505
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ccg ccc acg ccc acc ctc acc tcc aca gct gtg aag agc agg cag ccc Pro Pro Thr Pro Thr Leu Thr Ser Thr Ala Val Lys Ser Arg Gln Pro 1105 1110 1115	3601
ctg tgg ggg ttg aaa gag atg gag gaa gaa gat ggc tca gag ttg gat Leu Trp Gly Leu Lys Glu Met Glu Glu Glu Asp Gly Ser Glu Leu Asp 1120 1125 1130	3649
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gaa gag tta gaa atc cag gat gag tca aat gaa gaa cgg cag gat aca Glu Glu Leu Glu Ile Gln Asp Glu Ser Asn Glu Glu Arg Gln Asp Thr 1185 1190 1195	3841
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aaaaggagca aaatgaagca ttccccaggg cttcagccct gggctctgag gggaaagagt	4058
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Ser Leu Gln Gln Arg Leu Gln Cys Met Met Arg Ala Gly Thr Thr Leu	
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Val Glu Cys Lys Ser Gly Tyr Gly Leu Asp Leu Glu Thr Glu Leu Lys	
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Met Leu Arg Val Ile Glu Arg Ala Arg Arg Glu Leu Asp Ile Gly Ile	
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Ser Ala Thr Tyr Cys Gly Ala His Ser Val Pro Lys Gly Lys Thr Ala	
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Thr Glu Ala Ala Asp Asp Ile Ile Asn Asn His Leu Pro Lys Leu Lys	
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Glu Leu Gly Arg Asn Gly Glu Ile His Val Asp Asn Ile Asp Val Phe	
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Cys Glu Lys Gly Val Phe Asp Leu Asp Ser Thr Arg Arg Ile Leu Gln	
235 240 245	
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Arg Gly Lys Asp Ile Gly Leu Gln Ile Asn Phe His Gly Asp Glu Leu	
250 255 260	
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His Pro Met Lys Ala Ala Glu Leu Gly Ala Glu Leu Gly Ala Gln Ala	
265 270 275 280	
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Ile Ser His Leu Glu Glu Val Ser Asp Glu Gly Ile Val Ala Met Ala	
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Thr Ala Arg Cys Ser Ala Ile Leu Leu Pro Thr Thr Ala Tyr Met Leu	
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Leu	Arg	Ala	Phe	Val	Phe	Glu	Ser	Gln	Glu	Asp	Met	Glu	Val	Phe	Leu	
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Lys	Glu	Val	Arg	Asp	Asn	Lys	Lys	Leu	Arg	Val	Asn	Ala	Val	Ile	Ala	
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Pro	Lys	Ser	Ser	Tyr	Ala	Asp	Lys	Ala	Pro	Ser	Arg	Ser	Leu	Asn	Glu	
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Pro	Asp	Pro	Val	Met	Ser	Tyr	Leu	Cys	Cys	Gln	Tyr	His	Ile	His	Glu	
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Gln	Glu	Thr	Arg	Leu	Lys	Gln	Ile	Tyr	Thr	Ala	Glu	Glu	Lys	Tyr	Val	
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Val	Lys	Thr	Ser	Phe	Tyr	Ser	Asn	Lys	Val	Ile	Ser	Ser	Asn	Thr	Ser	
	415					420					425					
cta	aaa	gta	gcg	cag	ttt	ctc	act	gtc	act	gtg	gac	cta	gag	cag	aga	1584
Leu	Lys	Val	Ala	Gln	Phe	Leu	Thr	Val	Thr	Val	Asp	Leu	Glu	Gln	Arg	
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Val	Asp	Ser	Gly	Leu	Ile	Ala	Leu	Arg	Glu	Thr	Ser	Lys	His			

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Lys Thr Lys Lys Arg Gln Leu Glu Gln Lys Ile Ser Ser Lys Leu Gly			
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Ser Leu Lys Leu Met Glu Gln Asp Thr Cys Asn Leu Glu Glu Glu Glu			
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cga aaa gca agt acc aaa atc aaa gaa ata aat gtt caa aaa gcg aaa			1872
Arg Lys Ala Ser Thr Lys Ile Lys Glu Ile Asn Val Gln Lys Ala Lys			
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Leu Val Thr Glu Leu Thr Asn Leu Ile Lys Ile Cys Thr Ser Leu His			
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Ile Gln Lys Val Asp Leu Ile Leu Gln Asn Thr Thr Val Ile Ser Glu			
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Leu Gln Lys Cys Lys Glu Leu Met Lys Arg Ala Arg Gln Val Cys Asn			
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Thr Ile Pro Asn Gly His Asn Ser Ser Leu Pro Met Val Phe Gln Asp			
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 Met Pro His Leu  
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 Gly Leu Pro Arg Phe His Ser Val Ser Thr Gln Ser Glu Pro His Gly  
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Pro	Met	Val	Leu	Pro	Ile	Cys	Ser	Arg	Ser	Gly	Asp	Val	Ile	Glu	Tyr		
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175 180 185	
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Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met	
190 195 200	
tca gtg aat cct acc tgt ttg gtc ctt att att ctt ctg ttt att agc	1214
Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser	
205 210 215 220	
att atc ttg act ttt aag ggt tac ttg att agc tgt gtt tgg aac tgc	1262
Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys	
225 230 235	
tac cga tac atc aat ggt agg aac tcc tct gat gtc ctg gtt tat gtt	1310
Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu Val Tyr Val	
240 245 250	
acc agc aat gac act acg gtg ctg cta ccc ccg tat gat gat gcc act	1358
Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr	
255 260 265	
gtg aat ggt gct gcc aag gag cca ccg cca cct tac gtg tct gcc taa	1406
Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val Ser Ala *	
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 Met  
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ctc cct gga gcc tgg ctg ctc tgg acc tcc ctc ctg ctc ctg gcc agg	105
Leu Pro Gly Ala Trp Leu Leu Trp Thr Ser Leu Leu Leu Ala Arg	
5 10 15	

cct gcc cag ccc tgt ccc atg ggt tgt gac tgc ttc gtc cag gag gtg Pro Ala Gln Pro Cys Pro Met Gly Cys Asp Cys Phe Val Gln Glu Val 20 25 30	153
ttc tgc tca gat gag gag ctt gcc acc gtc ccg ctg gac atc ccg cca Phe Cys Ser Asp Glu Glu Leu Ala Thr Val Pro Leu Asp Ile Pro Pro 35 40 45	201
tat acg aaa aac atc atc ttt gtg gag acc tcg ttc acc aca ttg gaa Tyr Thr Lys Asn Ile Ile Phe Val Glu Thr Ser Phe Thr Thr Leu Glu 50 55 60 65	249
acc aga gct ttt ggc agt aac ccc aac ttg acc aag gtg gtc ttc ctc Thr Arg Ala Phe Gly Ser Asn Pro Asn Leu Thr Lys Val Val Phe Leu 70 75 80	297
aac act cag ctc tgc cag ttt agg ccg gat gcc ttt ggg ggg ctg ccc Asn Thr Gln Leu Cys Gln Phe Arg Pro Asp Ala Phe Gly Gly Leu Pro 85 90 95	345
agg ctg gag gac ctg gag gtc aca ggc agt agc ttc ttg aac ctc agc Arg Leu Glu Asp Leu Glu Val Thr Gly Ser Ser Phe Leu Asn Leu Ser 100 105 110	393
acc aac atc ttc tcc aac ctg acc tcg ctg ggc aag ctc acc ctc aac Thr Asn Ile Phe Ser Asn Leu Thr Ser Leu Gly Lys Leu Thr Leu Asn 115 120 125	441
ttc aac atg ctg gag gct ctg ccc gag ggt ctt ttc cag cac ctg gct Phe Asn Met Leu Glu Ala Leu Pro Glu Gly Leu Phe Gln His Leu Ala 130 135 140 145	489
gcc ctg gag tcc ctc cac ctg cag ggg aac cag ctc cag gcc ctg ccc Ala Leu Glu Ser Leu His Leu Gln Gly Asn Gln Leu Gln Ala Leu Pro 150 155 160	537
agg agg ctc ttc cag cct ctg acc cat ctg aag aca ctc aac ctg gcc Arg Arg Leu Phe Gln Pro Leu Thr His Leu Lys Thr Leu Asn Leu Ala 165 170 175	585
cag aac ctc ctg gcc cag ctc ccg gag gag ctg ttc cac cca ctc acc Gln Asn Leu Leu Ala Gln Leu Pro Glu Glu Leu Phe His Pro Leu Thr 180 185 190	633
agc ctg cag acc ctg aag ctg agc aac aac gcg ctc tct ggt ctc ccc Ser Leu Gln Thr Leu Lys Leu Ser Asn Asn Ala Leu Ser Gly Leu Pro 195 200 205	681
cag ggt gtg ttt ggc aaa ctg ggc agc ctg cag gag ctc ttc ctg gac Gln Gly Val Phe Gly Lys Leu Gly Ser Leu Gln Glu Leu Phe Leu Asp 210 215 220 225	729
agc aac aac atc tcg gag ctg ccc cct cag gtg ttc tcc cag ctc ttc Ser Asn Asn Ile Ser Glu Leu Pro Pro Gln Val Phe Ser Gln Leu Phe 230 235 240	777
tgc cta gag agg ctg tgg ctg caa cgc aac gcc atc acg cac ctg ccg	825

Cys	Leu	Glu	Arg	Leu	Trp	Leu	Gln	Arg	Asn	Ala	Ile	Thr	His	Leu	Pro		
			245					250					255				
ctc	tcc	atc	ttt	gcc	tcc	ctg	ggc	aat	ctg	acc	ttt	ctg	agc	ttg	cag	873	
Leu	Ser	Ile	Phe	Ala	Ser	Leu	Gly	Asn	Leu	Thr	Phe	Leu	Ser	Leu	Gln		
		260					265					270					
tgg	aac	atg	ctt	cgg	gtc	ctg	cct	gcc	ggc	ctc	ttt	gcc	cac	acc	cca	921	
Trp	Asn	Met	Leu	Arg	Val	Leu	Pro	Ala	Gly	Leu	Phe	Ala	His	Thr	Pro		
	275					280					285						
tgc	ctg	gtt	ggc	ctg	tct	ctg	acc	cat	aac	cag	ctg	gag	act	gtc	gct	969	
Cys	Leu	Val	Gly	Leu	Ser	Leu	Thr	His	Asn	Gln	Leu	Glu	Thr	Val	Ala		
290					295					300					305		
gag	ggc	acc	ttt	gcc	cac	ctg	tcc	aac	ctg	cgt	tcc	ctc	atg	ctc	tca	1017	
Glu	Gly	Thr	Phe	Ala	His	Leu	Ser	Asn	Leu	Arg	Ser	Leu	Met	Leu	Ser		
			310					315					320				
tac	aat	gcc	att	acc	cac	ctc	cca	gct	ggc	atc	ttc	aga	gac	ctg	gag	1065	
Tyr	Asn	Ala	Ile	Thr	His	Leu	Pro	Ala	Gly	Ile	Phe	Arg	Asp	Leu	Glu		
		325					330					335					
gag	ttg	gtc	aaa	ctc	tac	ctg	ggc	agc	aac	aac	ctt	acg	gcg	ctg	cac	1113	
Glu	Leu	Val	Lys	Leu	Tyr	Leu	Gly	Ser	Asn	Asn	Leu	Thr	Ala	Leu	His		
	340					345					350						
cca	gcc	ctc	ttc	cag	aac	ctg	tcc	aag	ctg	gag	ctg	ctc	agc	ctc	tcc	1161	
Pro	Ala	Leu	Phe	Gln	Asn	Leu	Ser	Lys	Leu	Glu	Leu	Leu	Ser	Leu	Ser		
	355					360				365							
aag	aac	cag	ctg	acc	aca	ctt	ccg	gag	ggc	atc	ttc	gac	acc	aac	tac	1209	
Lys	Asn	Gln	Leu	Thr	Thr	Leu	Pro	Glu	Gly	Ile	Phe	Asp	Thr	Asn	Tyr		
370				375					380					385			
aac	ctg	ttc	aac	ctg	gcc	ctg	cac	ggc	aac	ccc	tgg	cag	tgc	gac	tgc	1257	
Asn	Leu	Phe	Asn	Leu	Ala	Leu	His	Gly	Asn	Pro	Trp	Gln	Cys	Asp	Cys		
			390					395					400				
cac	ctg	gcc	tac	ctc	ttc	aac	tgg	ctg	cag	cag	tac	acc	gat	cgg	ctc	1305	
His	Leu	Ala	Tyr	Leu	Phe	Asn	Trp	Leu	Gln	Gln	Tyr	Thr	Asp	Arg	Leu		
		405					410					415					
ctg	aac	atc	cag	acc	tac	tgc	gct	ggc	cct	gcc	tac	ctc	aaa	ggc	cag	1353	
Leu	Asn	Ile	Gln	Thr	Tyr	Cys	Ala	Gly	Pro	Ala	Tyr	Leu	Lys	Gly	Gln		
	420					425					430						
gtg	gtg	ccc	gcc	ttg	aat	gag	aag	cag	ctg	gtg	tgt	ccc	gtc	acc	cgg	1401	
Val	Val	Pro	Ala	Leu	Asn	Glu	Lys	Gln	Leu	Val	Cys	Pro	Val	Thr	Arg		
	435				440					445							
gac	cac	ttg	ggc	ttc	cag	gtc	acg	tgg	ccg	gac	gaa	agc	aag	gca	ggg	1449	
Asp	His	Leu	Gly	Phe	Gln	Val	Thr	Trp	Pro	Asp	Glu	Ser	Lys	Ala	Gly		
450				455				460					465				
ggc	agc	tgg	gat	ctg	gct	gtg	cag	gaa	agg	gca	gcc	cgg	agc	cag	tgc	1497	
Gly	Ser	Trp	Asp	Leu	Ala	Val	Gln	Glu	Arg	Ala	Ala	Arg	Ser	Gln	Cys		



470	475	480	
acc tac agc aac ccc gag ggc acc	gtg gtg ctc gcc tgt gac cag gcc	1545	
Thr Tyr Ser Asn Pro Glu Gly Thr	Val Val Leu Ala Cys Asp Gln Ala		
485	490	495	
cag tgt cgc tgg ctg aac gtc cag	ctc tct cct cgg cag ggc tcc ctg	1593	
Gln Cys Arg Trp Leu Asn Val Gln	Leu Ser Pro Arg Gln Gly Ser Leu		
500	505	510	
gga ctg cag tac aat gct agt cag	gag tgg gac ctg agg tcg agc tgc	1641	
Gly Leu Gln Tyr Asn Ala Ser Gln	Glu Trp Asp Leu Arg Ser Ser Cys		
515	520	525	
ggt tct ctg cgg ctc acc gtg tct	atc gag gct cgg gca gca ggg ccc	1689	
Gly Ser Leu Arg Leu Thr Val Ser	Ile Glu Ala Arg Ala Ala Gly Pro		
530	535	540	545
tag tagc agcgcataca ggagctgggg	aagggggcct ctggggcctg accagggcag	1746	
*			
aggtagggggc ggagggggagc tgagtctccg	aagccttggc ttttcacatg caagggacag	1806	
ggttacatcc ccaaggtgag ggggtggagt	ctgggtctgct ccactaacca ggggtctctc	1866	
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gcctccccat tatgtaacac ccaaccgctc	tcacctacac cctgaggtct attcactgca	2046	
tcccagtgat acaaagtgga ggccactgcc	ttctgacatc tggctcaaaa gcccagtgtc	2106	
tgtttccatt tatttccctg gaatttcatt	taaaattggt atagagaaaa aaaggatgtg	2166	
acagaagcag agatgaccag aaagcacagg	ggcagggttc tgactggcgt gtgggagacc	2226	
ctgtggccgg caccacctc cacacgagga	ctaagctctg atttttttat cttgccccaa	2286	
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ttttatttga cctgtatat catgacttat	ttttaatctg actatggcat aacattacaa	2406	
gacgaggcaa aaatatTTaa ccccaaata	tatttctttg ccctaccttg aacttgcctt	2466	
gcagagtctc ttgtgaggag aatccacatc	ctataaagaa gcccctttcc cctttgtttt	2526	
ccttcctttc tttccagtcc aggagatcat	caactaagag ccaggcaccc cttttaagtc	2586	
gataagaaac agttttacaac ctgctctctc	tctctctgaa gtctgctgag agcttccctt	2646	
gcacaataaa acttggcctc cagatcctt	tatcttaacc tgaacattcc tttccattga	2706	
tcccaggtct tcagctaagc tcaaccaatt	gtcaaccaga aaatgtttaa atttacctac	2766	
agcctggaag caccacccc cgctgcttcg	agttgtcctg cctttctgaa ctcaaccaat	2826	

gtattttctta aatgtatttg attgatgcct cattcctccc taaaatgtat aaaaccaagc 2886  
 tgtacctoga ccaccttggg cacatgttcc caggccctcc tgaggtctgt gtcacggggcc 2946  
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 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly  
 1 5 10  
 cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg 157  
 Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met  
 15 20 25 30  
 ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac 205  
 Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His  
 35 40 45  
 atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc 253  
 Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe  
 50 55 60  
 aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg 301  
 Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala  
 65 70 75  
 tac tcc gtg aag tct agg gac agg aag atg gtt ggc gac gtg acc ggg 349  
 Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly  
 80 85 90  
 gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg 397  
 Ala Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu  
 95 100 105 110  
 att ttg ggc atc ttc atg acc att ctg ctc atc atc atc cca gtg ttg 445  
 Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Ile Pro Val Leu  
 115 120 125  
 gtc gtc cag gcc cag cga tag at caggaggcat cattgaggcc aggagctctg 498  
 Val Val Gln Ala Gln Arg \*  
 130

cccgtgagct gtatccacgt actctatctt ccattcttcg cctgccccca gaggccagag 558  
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ttagccttta caa 631

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cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgccct 180  
ggatcccagc gccccgatcc cgggcggccc acccccacgc ccgcctccgc caactttcac 240  
gctgcctcgg cggcccgggc cggtcgcagc cca atg gtg gag gcc ata gtg gag 294  
Met Val Glu Ala Ile Val Glu  
1 5  
ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt 342  
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly  
10 15 20  
gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga 390  
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly  
25 30 35  
cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa 438  
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu  
40 45 50 55  
ata aag aaa gag atg aag aaa gac cct ctg acc aac aaa gct cca gaa 486  
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu  
60 65 70  
aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa 534  
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu  
75 80 85  
acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc 582  
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys  
90 95 100  
cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg 630

Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu	
105 110 115	
aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg	678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp	
120 125 130 135	
tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc	726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe	
140 145 150	
atc aag gag ctg tca ggg gag tcg gat gag ctt ggc att tcc cag gat	774
Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp	
155 160 165	
gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt	822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
170 175 180	
gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca	870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
185 190 195	
gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt	918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
200 205 210 215	
gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att	966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
220 225 230	
gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag	1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
235 240 245	
tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac	1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
250 255 260	
agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag	1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg	1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
300 305 310	
aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	

330	335	340	
tcc gct cct gtc atc aaa caa ggg gca ggc acc act gag aga aaa cat Ser Ala Pro Val Ile Lys Gln Gly Ala Gly Thr Thr Glu Arg Lys His 345 350 355			1350
gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg 360 365 370 375			1398
aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag Thr Glu Glu Lys Glu Arg Pro Glu Arg Glu Pro Lys Leu Asp Leu Gln 380 385 390			1446
aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys 395 400 405			1494
acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu 410 415 420			1542
aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile 425 430 435			1590
gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser 440 445 450 455			1638
gac cgc agc aat gac att gac tta gaa ggt ttt gac tcc gtg gta tca Asp Arg Ser Asn Asp Ile Asp Leu Glu Gly Phe Asp Ser Val Val Ser 460 465 470			1686
tct act gag aaa ctc agt cat ccg acc aca agc aga cca aaa gct aca Ser Thr Glu Lys Leu Ser His Pro Thr Thr Ser Arg Pro Lys Ala Thr 475 480 485			1734
ggg agg cgg cct ccg tcc cag tcc ctc aca tct tca tcc ctt tca agc Gly Arg Arg Pro Pro Ser Gln Ser Leu Thr Ser Ser Leu Ser Ser 490 495 500			1782
cct gat atc ttc gac tcc cca agt ccc gaa gag gat aag gag gaa cac Pro Asp Ile Phe Asp Ser Pro Ser Pro Glu Glu Asp Lys Glu Glu His 505 510 515			1830
att tca ctt gcg cac aga gga gtg gac gcg tca aag aaa act tcc aag Ile Ser Leu Ala His Arg Gly Val Asp Ala Ser Lys Lys Thr Ser Lys 520 525 530 535			1878
act gtt acc ata tcc caa gtg tct gac aac aaa gca tcc ctg ccg ccc Thr Val Thr Ile Ser Gln Val Ser Asp Asn Lys Ala Ser Leu Pro Pro 540 545 550			1926
aag ccg ggg acc atg gca gca ggt ggc ggt ggg cca gcc cct ctg tcc Lys Pro Gly Thr Met Ala Ala Gly Gly Gly Gly Pro Ala Pro Leu Ser 555 560 565			1974

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ggatcccagc gccccgatcc cggcgccccca acccccacgc ccgcctccgc caactttcac      240
gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
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Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
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Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
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Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
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Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
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Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
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Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
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Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu
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Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
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Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg	
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cagagacaca gcaagatgcc caggagtgct cgcttcctgg gctagagaca agcaccagcc 240
tgcagtggag aacgcaggac cccgctgccc agaaggagca gccacggcct gcggaggact 300
ggcccagcaa ggtcccaggt cttccctctc ctacgcgctt aagagagagg ccagtgcggt 360
gtgaggagtc gcgaggaaga ggcggaaggc gccggaaggc acc  atg ttc cgc aag 415
                Met Phe Arg Lys

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aaa aag aag aaa cgc cct gag atc tca gcg cca cag aac ttc cag cac	463
Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro Gln Asn Phe Gln His	
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Arg Val His Thr Ser Phe Asp Pro Lys Glu Gly Lys Phe Val Gly Leu	
25 30 35	
ccc cca caa tgg cag aac atc ctg gag aca ctg cgg cgc ccc aag ccc	559
Pro Pro Gln Trp Gln Asn Ile Leu Asp Thr Leu Arg Arg Pro Lys Pro	
40 45 50	
gtg gtg gag cct tcg cga atc aca cgg gtg cag ctc cag ccc atg aag	607
Val Val Asp Pro Ser Arg Ile Thr Arg Val Gln Leu Gln Pro Met Lys	
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Thr Val Val Arg Gly Ser Ala Met Pro Val Asp Gly Tyr Ile Ser Gly	
70 75 80	
ctg ctc aac gag atc cag aag ttg tca gtc atc agc tcc aac acc ctg	703
Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr Leu	
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Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu	
105 110 115	
ctg ggg gat gag cac tgg gcc acc gag cca gag atg tac ctc cag agc	799
Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser	
120 125 130	
ccc cag tct gag cgc act gag ccc cac ggc ctc tac ctc agc tgc aac	847
Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn	
135 140 145	
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Gly Gly Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln	
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Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu	
165 170 175 180	
ggc ccc gcc gag ttt cag ggt gcc tcg cag cgc tgt ctg cag ctg ggt	991
Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu Gly	
185 190 195	
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Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly Thr	
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Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala Arg	
215 220 225	

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230 235 240	
ggc agc cct agc cct aag acc cgg gag agc agc ctg aag cgc agg cta	1183
Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg Leu	
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Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser Ser	
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Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe Arg	
280 285 290	
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Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln Ser	
295 300 305	
ttg ccc tcg gac cag ccg gtg ggg acc ttc agc cct ctg acc act tcg	1375
Leu Pro Ser Asp Gln Pro Val Gly Thr Phe Ser Pro Leu Thr Thr Ser	
310 315 320	
gat acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc	1423
Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly	
325 330 335 340	
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Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His	
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gcc cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt	1519
Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val	
360 365 370	
gcc aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag	1567
Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu	
375 380 385	
cag ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg	1615
Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg	
390 395 400	
ctg ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc	1663
Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile	
405 410 415 420	
gtc tgc ttg gcc cgg gag aag cac tcg ggc cgc cag gtg gcc gtc aag	1711
Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val Lys	
425 430 435	
atg atg gac ctc agg aag cag cag cgc agg gag ctg ctc ttc aac gag	1759
Met Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
440 445 450	

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ctg cat gct cag ggt gtc atc cac cgg gac atc aag agt gac tcc atc Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile 520 525 530	1999
ctg ctg acc ctc gat ggc agg gtg aag ctc tcg gac ttc gga ttc tgt Leu Leu Thr Leu Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys 535 540 545	2047
gct cag atc agc aaa gac gtc cct aag agg aag tcc ctg gtg gga acc Ala Gln Ile Ser Lys Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr 550 555 560	2095
ccc tac tgg atg gct cct gaa gtg atc tcc agg tct ttg tat gcc act Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr 565 570 575 580	2143
gag gtg gat atc tgg tct ctg ggc atc atg gtg att gag atg gta gat Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp 585 590 595	2191
ggg gag cca ccg tac ttc agt gac tcc cca gtg caa gcc atg aag agg Gly Glu Pro Pro Tyr Phe Ser Asp Ser Pro Val Gln Ala Met Lys Arg 600 605 610	2239
ctc cgg gac agc ccc cca ccc aag ctg aaa aac tct cac aag gtc tcc Leu Arg Asp Ser Pro Pro Pro Lys Leu Lys Asn Ser His Lys Val Ser 615 620 625	2287
cca gtg ctg cga gac ttc ctg gag cgg atg ctg gtg cgg gac ccc caa Pro Val Leu Arg Asp Phe Leu Glu Arg Met Leu Val Arg Asp Pro Gln 630 635 640	2335
gag aga gcc aca gcc cag gag ctc cta gac cac ccc ttc ctg ctg cag Glu Arg Ala Thr Ala Gln Glu Leu Leu Asp His Pro Phe Leu Leu Gln 645 650 655 660	2383
aca ggg cta cct gag tgc ctg gtg ccc ctg atc cag ctc tac cga aag Thr Gly Leu Pro Glu Cys Leu Val Pro Leu Ile Gln Leu Tyr Arg Lys 665 670 675	2431
cag acc tcc acc tgc tga gccac cccaagtatg cctgccacct acgcccacag	2485

Gln Thr Ser Thr Cys \*  
680

gcagggcaca ctgggcagcc agcctgccgg caggacttgc ctgcctcctc ctctcagtat 2545  
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cggaatcccg cttcctccct cacgtctgat gtcctgaagg tgcagtccca cctgtacagc 2965  
ccctccccgc ccagaactgt gaatggcctg ctccaggcca tggctggggg cagggagtga 3025  
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acagaatgga gaga 3099

<210> 42  
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ggtgacaggc gttgagacca ccgaagggaa ccc atg gct agg atc agt ttt tcc 174  
Met Ala Arg Ile Ser Phe Ser  
1 5  
tac ctc tgc cca gcc tcc tgg tac ttc act gtg ccc aca gtg agt cca 222  
Tyr Leu Cys Pro Ala Ser Trp Tyr Phe Thr Val Pro Thr Val Ser Pro  
10 15 20  
ttt ctc cgt cag cgg gtg gca ttc ctg gga ctc ttc ttc ata tcc tgt 270  
Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys  
25 30 35  
ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318  
Leu Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser  
40 45 50 55

tta cca cga gat agg caa tac gaa agg tat ttg gct cga gta ggg gag	366
Leu Pro Arg Asp Arg Gln Tyr Glu Arg Tyr Leu Ala Arg Val Gly Glu	
60 65 70	
ctt gaa gct act gac act gaa gac cca aat ctg aat tat gga ctt gtt	414
Leu Glu Ala Thr Asp Thr Glu Asp Pro Asn Leu Asn Tyr Gly Leu Val	
75 80 85	
gtt gac tgt ggc agc agt ggt tcc cgg att ttt gtt tat ttc tgg cca	462
Val Asp Cys Gly Ser Ser Gly Ser Arg Ile Phe Val Tyr Phe Trp Pro	
90 95 100	
aga cat aat ggg aac ccc cat gac ttg ctg gac atc aaa cag atg aga	510
Arg His Asn Gly Asn Pro His Asp Leu Leu Asp Ile Lys Gln Met Arg	
105 110 115	
gac cgc aac agc caa cca gtg gtt aaa aaa atc aag cca gga atc tct	558
Asp Arg Asn Ser Gln Pro Val Val Lys Lys Ile Lys Pro Gly Ile Ser	
120 125 130 135	
gca atg gca gac act cca gaa cat gcc agt gat tac ctt cgt cct ctg	606
Ala Met Ala Asp Thr Pro Glu His Ala Ser Asp Tyr Leu Arg Pro Leu	
140 145 150	
ctg agc ttt gct gct gct cat gtg cct gtg aag aag cac aag gag acc	654
Leu Ser Phe Ala Ala Ala His Val Pro Val Lys Lys His Lys Glu Thr	
155 160 165	
cct ctt tac atc ctc tgc aca gca ggc atg agg ctt ctc cct gag agg	702
Pro Leu Tyr Ile Leu Cys Thr Ala Gly Met Arg Leu Leu Pro Glu Arg	
170 175 180	
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Lys Gln Leu Ala Ile Leu Ala Asp Leu Val Lys Asp Leu Pro Leu Glu	
185 190 195	
ttt gac ttc ctc ttt tca cag tct caa gca gaa gtg atc tct ggg aag	798
Phe Asp Phe Leu Phe Ser Gln Ser Gln Ala Glu Val Ile Ser Gly Lys	
200 205 210 215	
cag gaa ggg gtt tat gca tgg att gga atc aac ttt gtt ttg gga aga	846
Gln Glu Gly Val Tyr Ala Trp Ile Gly Ile Asn Phe Val Leu Gly Arg	
220 225 230	
ttc gac cac gag gat gaa tca gat gct gag gct acc cag gaa ttg gca	894
Phe Asp His Glu Asp Glu Ser Asp Ala Glu Ala Thr Gln Glu Leu Ala	
235 240 245	
gca gga cgg aga agg aca gta ggg ata ctg gat atg gga gga gcc tct	942
Ala Gly Arg Arg Arg Thr Val Gly Ile Leu Asp Met Gly Gly Ala Ser	
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ctc caa att gct tat gaa gtt cct acc tca acc tct gtc ctt cct gca	990
Leu Gln Ile Ala Tyr Glu Val Pro Thr Ser Thr Ser Val Leu Pro Ala	
265 270 275	

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Lys Gln Glu Glu Ala Ala Lys Ile Leu Leu Ala Glu Phe Asn Leu Gly	
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Cys Asp Val Gln His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr	
300 305 310	
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Phe Leu Gly Phe Gly Gly Asn Phe Ala Arg Gln Arg Tyr Glu Asp Leu	
315 320 325	
gtt ctg aat gaa act ctt aac aaa aac aga ttg ctt ggt cag aag aca	1182
Val Leu Asn Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr	
330 335 340	
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Gly Leu Ser Pro Asp Asn Pro Phe Leu Asp Pro Cys Leu Pro Val Gly	
345 350 355	
ctc aca gat gtg gtg gag agg aac agc caa gtc tta cat gtc cga gga	1278
Leu Thr Asp Val Val Glu Arg Asn Ser Gln Val Leu His Val Arg Gly	
360 365 370 375	
aga gga gac tgg gtg tct tgt ggg gca atg ctg agc ccc ctg ctg gct	1326
Arg Gly Asp Trp Val Ser Cys Gly Ala Met Leu Ser Pro Leu Leu Ala	
380 385 390	
cgc tcc aac acc agc cag gcc tca ctc aat ggc ata tat caa tcg cct	1374
Arg Ser Asn Thr Ser Gln Ala Ser Leu Asn Gly Ile Tyr Gln Ser Pro	
395 400 405	
att gac ttc aac aac agc gag ttc tac ggc ttc tct gag ttt ttt tat	1422
Ile Asp Phe Asn Asn Ser Glu Phe Tyr Gly Phe Ser Glu Phe Phe Tyr	
410 415 420	
tgt aca gag gat gtg ttg cgc att ggt ggc cgc tac cat ggg cca aca	1470
Cys Thr Glu Asp Val Leu Arg Ile Gly Gly Arg Tyr His Gly Pro Thr	
425 430 435	
ttt gcc aag gct gct cag gat tac tgt ggc atg gct tgg tcg gta cta	1518
Phe Ala Lys Ala Ala Gln Asp Tyr Cys Gly Met Ala Trp Ser Val Leu	
440 445 450 455	
act cag aga ttc aag aat ggc ctc ttt tca tca cat gca gat gag cat	1566
Thr Gln Arg Phe Lys Asn Gly Leu Phe Ser Ser His Ala Asp Glu His	
460 465 470	
cga ctc aaa tat cag tgt ttt aaa tcg gct tgg atg tac caa gtc tta	1614
Arg Leu Lys Tyr Gln Cys Phe Lys Ser Ala Trp Met Tyr Gln Val Leu	
475 480 485	
cat gaa gga ttc cac ttt ccc tat gac tac cca aac ctg cgg aca gcc	1662
His Glu Gly Phe His Phe Pro Tyr Asp Tyr Pro Asn Leu Arg Thr Ala	
490 495 500	
cag ctg gtg tat gac cga gag gtt cag tgg acg ctg gga gcc att cta	1710



Gln	Leu	Val	Tyr	Asp	Arg	Glu	Val	Gln	Trp	Thr	Leu	Gly	Ala	Ile	Leu		
505						510					515						
tat	aaa	aca	cga	ttc	tta	cca	ctc	agg	gat	ctt	cgg	cag	gaa	ggt	gtc	1758	
Tyr	Lys	Thr	Arg	Phe	Leu	Pro	Leu	Arg	Asp	Leu	Arg	Gln	Glu	Gly	Val		
520					525					530					535		
cga	caa	gcc	cat	ggt	agc	tgg	ttc	cgt	ctc	tcc	ttt	gta	tac	aac	cac	1806	
Arg	Gln	Ala	His	Gly	Ser	Trp	Phe	Arg	Leu	Ser	Phe	Val	Tyr	Asn	His		
				540					545						550		
tat	ctc	ttc	ttt	gcc	tgt	atc	ctg	gtg	gtg	cta	ctg	gcc	atc	ttc	cta	1854	
Tyr	Leu	Phe	Phe	Ala	Cys	Ile	Leu	Val	Val	Leu	Leu	Ala	Ile	Phe	Leu		
				555					560						565		
tac	ctt	ctg	cgg	cta	cgc	cga	att	cac	cac	cga	caa	aca	cga	gcc	tca	1902	
Tyr	Leu	Leu	Arg	Leu	Arg	Arg	Ile	His	His	Arg	Gln	Thr	Arg	Ala	Ser		
				570				575							580		
gct	cca	ttg	gac	ttg	ctg	tgg	ctt	gaa	gag	gtg	gtg	ccc	atg	atg	gga	1950	
Ala	Pro	Leu	Asp	Leu	Leu	Trp	Leu	Glu	Glu	Val	Val	Pro	Met	Met	Gly		
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gta	cag	gtg	ggg	ccg	tga											1968	
Val	Gln	Val	Gly	Pro	*												
600					605												

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aacatggcag	ccaaagtgtt	tgagtccacg	gtaagtttgg	cttggcctta	gctgttgcag											300	
gagacctgtg	aactctgcct	tatataatgt	ggatgttggg	cacagagctg	tcatctttga											360	
ctgattccag	gacaaaaatg	acaggacatt	gtggtagggg	actcaatttc	tcatccc											417	
atg ggt aca	gaa acc aat	tat ctt tgc	ctt tct cca	cca cgt aat	gta											465	
Met Gly Thr	Glu Thr Asn	Tyr Leu Cys	Leu Ser Pro	Pro Arg Asn	Val												
1		5						10							15		

cca atc atc act ggt agc aaa gat tta cag aat gtc aat atc aca ctg	513
Pro Ile Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu	
20 25 30	
cgc atc atc ttc cag cct gtt gct agc cag ctt cct cgc atc ttc acc	561
Arg Ile Ile Phe Gln Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr	
35 40 45	
agc atc gga gag gac tat gat gag cct gtg ctg acg tac atc acg acc	609
Ser Ile Gly Glu Asp Tyr Asp Glu Pro Val Leu Thr Tyr Ile Thr Thr	
50 55 60	
gag atc ctc aag tca gtg gtg gct cgc ttt gat gct gga gaa gtt atc	657
Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly Glu Val Ile	
65 70 75 80	
act cag aga gag ctg gtc tcc agg cag gtg agc aac gac ctt acg gag	705
Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asn Asp Leu Thr Glu	
85 90 95	
caa gca gcc aca ttt ggg ctc atc ctg gac gac gtg tcc ttg aca tat	753
Gln Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr	
100 105 110	
ctg acc ttt gga aag gag ttc aca gaa gca gtg gaa gcc aaa cag gtg	801
Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val	
115 120 125	
gct cag cag gaa gca gag agg gcc aga ttt gtg aag gaa aag gct gag	849
Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Lys Glu Lys Ala Glu	
130 135 140	
cag cag aaa aag gct gag cag cag aaa aag gtt gag cag cag aaa aag	897
Gln Gln Lys Lys Ala Glu Gln Gln Lys Lys Val Glu Gln Gln Lys Lys	
145 150 155 160	
gca gcc gtg atc tct gct gag ggc gac tcc aag gca acc gag ctg att	945
Ala Ala Val Ile Ser Ala Glu Gly Asp Ser Lys Ala Thr Glu Leu Ile	
165 170 175	
gcc aac tca ctg gcc acc gcg ggg gac ggc ctg atg gag ctg tgc aag	993
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Met Glu Leu Cys Lys	
180 185 190	
ttg gaa gcc gcg gag gct ctc gga aca tga c ctacctgccg gcggggcagt	1044
Leu Glu Ala Ala Glu Ala Leu Gly Thr *	
195 200	
ccgctcctcc ggctgccccca tgaggggccca cctgcctgc acctccgcag gctgactggg	1104
ccacagcccc aatgattctt aacactgcct taccgcccta cccagaaat cactgaaatt	1164
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aaaaa	1229

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<220>  
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<400> 44

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ggagctgccca atcaaaagtg gcattac      atg aaa aat ata aaa gca ctt gtg      111
                                   Met Lys Asn Ile Lys Ala Leu Val
                                   1                               5

gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat      159
Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr
   10                               15                               20

gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa      207
Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln
   25                               30                               35                               40

cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc      255
Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu
                               45                               50                               55

tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa      303
Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln
                               60                               65                               70

ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag      351
Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln
   75                               80                               85

aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt      399
Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val
   90                               95                               100

gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca      447
Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala
  105                               110                               115                               120

cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac      495
Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His
   125                               130                               135

agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac      543
Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr
   140                               145                               150

aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca      591
Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr

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155	160	165	
ttc ccc atg ctt ctt aca gaa tgc acg gaa caa ctt ggg ctt gcc aga			639
Phe Pro Met Leu Leu Thr	Glu Cys Thr	Gln Leu Gly Leu Ala Arg	
170	175	180	
gca gcc tcc aaa gta tat acc aaa gat gga acc cca atc ttt acc ttg			687
Ala Ala Ser Lys Val Tyr Thr Lys Asp Gly Thr Pro Ile Phe Thr Leu			
185	190	195	200
cgt gat ttg gtt tta tgg gct cta gat gaa tcc ttt ctc cag aga gac			735
Arg Asp Leu Val Leu Trp Ala Leu Asp	Glu Ser Phe Leu Gln Arg Asp		
205	210	215	
tct gag aaa caa aag caa gat gca gct cct gtt gga aaa gaa cag ata			783
Ser Glu Lys Gln Lys Gln Asp Ala Ala Pro Val Gly Lys Glu Gln Ile			
220	225	230	
att gtt gaa agt atg gaa gaa aat cca aga atg aaa gtg aaa aac aga			831
Ile Val Glu Ser Met Glu Glu Asn Pro Arg Met Lys Val Lys Asn Arg			
235	240	245	
tta ttt gca aaa tct gtg aca tcc gat agt ttg gat ggt ata gac aag			879
Leu Phe Ala Lys Ser Val Thr Ser Asp Ser Leu Asp Gly Ile Asp Lys			
250	255	260	
tct ttg ctt acc ctc atc ctc aga aat cct att gcc atc tgg gtg tct			927
Ser Leu Leu Thr Leu Ile Leu Arg Asn Pro Ile Ala Ile Trp Val Ser			
265	270	275	280
tgt ggt gaa cca ttt cta cct cca aat gct ttg cag aaa gca gaa aaa			975
Cys Gly Glu Pro Phe Leu Pro Pro Asn Ala Leu Gln Lys Ala Glu Lys			
285	290	295	
tta gag aaa cag aac tgg cta aaa aag gac aga att ttg gct gat cta			1023
Leu Glu Lys Gln Asn Trp Leu Lys Lys Asp Arg Ile Leu Ala Asp Leu			
300	305	310	
gat acc atg aga cac aaa atg aga cag tta aaa ggg cgg cga gta gcg			1071
Asp Thr Met Arg His Lys Met Arg Gln Leu Lys Gly Arg Arg Val Ala			
315	320	325	
gca tgt cag cca gcc acc atg gtt cct acc aag agc cct gtg cag ccc			1119
Ala Cys Gln Pro Ala Thr Met Val Pro Thr Lys Ser Pro Val Gln Pro			
330	335	340	
gtg gtg gtt gaa gga ggc tgg acc gaa cag act caa cag gaa att aaa			1167
Val Val Val Glu Gly Gly Trp Thr Glu Gln Thr Gln Gln Glu Ile Lys			
345	350	355	360
ctc atg gaa ctt ata aga cat aca gag gca cac ctt tct gaa atc caa			1215
Leu Met Glu Leu Ile Arg His Thr Glu Ala His Leu Ser Glu Ile Gln			
365	370	375	
gaa atg gaa tcc aaa ata aat ttt cca att gca acc aaa cgt ata gca			1263
Glu Met Glu Ser Lys Ile Asn Phe Pro Ile Ala Thr Lys Arg Ile Ala			
380	385	390	

gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg	1311
Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp	
395 400 405	
att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc	1359
Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly	
410 415 420	
aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg	1407
Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met	
425 430 435 440	
acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag	1455
Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln	
445 450 455	
tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga	1503
Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly	
460 465 470	
cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga	1551
His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg	
475 480 485	
gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac	1599
Ala Asn Tyr Ala Arg Ile Arg Arg Gln Gln Gly Pro Gln Ala Thr Asp	
490 495 500	
att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac	1647
Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His	
505 510 515 520	
aat taa ctctatcag aaccatcgga ttttctgctg tatttttctg gaaagaaaac	1703
Asn *	
tttctttacc cacttataaa cagaagactg tgacaagaag gccattatt tccatcgctg	1763
aagactctaa atttggaata tcttctaaat aacaatcctg catagtattat taaaaaaaaat	1823
tagtcgtaaa atttatcctt caaaaatctg catttttaaata aaaccctgac agtgattttct	1883
caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt	1943
tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt	2003
gggacagata gtacaactga aataaaaagt ggaggcctct gcaaaaaata aaaaataaaa	2063
aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctatTTTTT aagaatgaac	2123
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agctgtaaca tgtaaatcag aactacctgg catcttctctg aacaagactt tcaatagggg      180
ccagt      atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag      227
           Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
           1             5             10

ata ctg aag tac tct ttc cca gtg gga cta aga acc agc aga aca gat      275
Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
   15             20             25             30

ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca      323
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
           35             40             45

agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag      371
Arg Pro Trp Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
           50             55             60

tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca      419
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
           65             70             75

ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
           80             85             90

aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct      515
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
           95             100            105            110

cca cca ctg gtc atg ctg atg aca aaa act tat att ccc ata tta gct      563
Pro Pro Leu Val Met Leu Met Thr Lys Thr Tyr Ile Pro Ile Leu Ala
           115            120            125

ttt act cag atg gct tat gga gcc agt ttc cta tct ttc ttg ggt ggg      611
Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
           130            135            140

atc aga tgg ggt ttt gct cta cca gaa ggt agt cca gcc aaa cca gac      659

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Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp	
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tac ctt aat tta gct agc agt gca gct cct ctt ttc ttt tca tgg ttt	707
Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe	
160 165 170	
gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata	755
Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile	
175 180 185 190	
atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat	803
Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His	
195 200 205	
tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc	851
Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala	
210 215 220	
act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa	899
Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu	
225 230 235	
aaa gga cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag	950
Lys Gly His Lys Arg Pro Gly Gln Val *	
240 245	
tgaggagcac ctctgccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg	1010
ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca	1070
cgtgtgaagt gacagccttg tgtgtgatct tttctgtctt cccaagtgtt gcatttttcca	1130
cattaaagtt tacttttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan	1190
aacatgtgtn tgccagctac acctttctcn atttctgttt ggctttttttt cccacacacca	1250
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gc	1432

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cctctctcag tccaaaagcg gcttttgggt cggcgagag agaccgggg gtctagcttt      180
tcctcgaaaa gcgcgcgcct gcccttggcc ccgagaacag acaaagagca ccgcagggcc      240
gatcacgtg ggggcgctga ggccggcc      atg gtc atg gaa gtg ggc acc ctg      292
                               Met Val Met Glu Val Gly Thr Leu
                               1                               5

gac gct gga ggc ctg cgg gcg ctg ctg ggg gag cga gcg gcg caa tgc      340
Asp Ala Gly Gly Leu Arg Ala Leu Leu Gly Glu Arg Ala Ala Gln Cys
      10                               15                               20

ctg ctg ctg gac tgc cgc tcc ttc ttc gct ttc aac gcc ggc cac atc      388
Leu Leu Leu Asp Cys Arg Ser Phe Phe Ala Phe Asn Ala Gly His Ile
      25                               30                               35                               40

gcc ggc tct gtc aac gtg cgc ttc agc acc atc gtg cgg cgc cgg gcc      436
Ala Gly Ser Val Asn Val Arg Phe Ser Thr Ile Val Arg Arg Arg Ala
      45                               50                               55

aag ggc gcc atg ggc ctg gag cac atc gtg ccc aac gcc gag ctc cgc      484
Lys Gly Ala Met Gly Leu Glu His Ile Val Pro Asn Ala Glu Leu Arg
      60                               65                               70

ggc cgc ctg ctg gcc ggc gcc tac cac gcc gtg gtg ttg ctg gac gag      532
Gly Arg Leu Leu Ala Gly Ala Tyr His Ala Val Val Leu Leu Asp Glu
      75                               80                               85

cgc agc gcc gcc ctg gac ggc gcc aag cgc gac ggc acc ctg gcc ctg      580
Arg Ser Ala Ala Leu Asp Gly Ala Lys Arg Asp Gly Thr Leu Ala Leu
      90                               95                               100

gcg gcc ggc gcg ctc tgc cgc gag gcg cgc gcc gcg caa gtc ttc ttc      628
Ala Ala Gly Ala Leu Cys Arg Glu Ala Arg Ala Ala Gln Val Phe Phe
      105                               110                               115                               120

ctc aaa gga gga tac gaa gcg ttt tcg gct tcc tgc ccg gag ctg tgc      676
Leu Lys Gly Gly Tyr Glu Ala Phe Ser Ala Ser Cys Pro Glu Leu Cys
      125                               130                               135

agc aaa cag tcg acc ccc atg ggg ctc agc ctt ccc ctg agt act agc      724
Ser Lys Gln Ser Thr Pro Met Gly Leu Ser Leu Pro Leu Ser Thr Ser
      140                               145                               150

gtc cct gac agc gcg gaa tct ggg tgc agt tcc tgc agt acc cca ctc      772
Val Pro Asp Ser Ala Glu Ser Gly Cys Ser Ser Cys Ser Thr Pro Leu
      155                               160                               165

tac gat cag ggt ggc ccg gtg gaa atc ctg ccc ttt ctg tac ctg ggc      820
Tyr Asp Gln Gly Gly Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly
      170                               175                               180

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Ser Ala Tyr His Ala Ser Arg Lys Asp Met Leu Asp Ala Leu Gly Ile	
185 190 195 200	
act gcc ttg atc aac gtc tca gcc aat tgt ccc aac cat ttt gag ggt	916
Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro Asn His Phe Glu Gly	
205 210 215	
cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac	964
His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp	
220 225 230	
atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag	1012
Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys	
235 240 245	
aat gct gga gga agg gtg ttt gtc cac tgc cag gca ggc att tcc cgg	1060
Asn Ala Gly Gly Arg Val Phe Val His Cys Gln Ala Gly Ile Ser Arg	
250 255 260	
tca gcc acc atc tgc ctt gct tac ctt atg agg act aat cga gtc aag	1108
Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg Thr Asn Arg Val Lys	
265 270 275 280	
ctg gac gag gcc ttt gag ttt gtg aag cag agg cga agc atc atc tct	1156
Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg Arg Ser Ile Ile Ser	
285 290 295	
ccc aac ttc agc ttc atg ggc cag ctg ctg cag ttt gag tcc cag gtg	1204
Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln Phe Glu Ser Gln Val	
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ctg gct ccg cac tgt tgc gca gag gct ggg agc ccc gcc atg gct gtg	1252
Leu Ala Pro His Cys Ser Ala Glu Ala Gly Ser Pro Ala Met Ala Val	
315 320 325	
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Leu Asp Arg Gly Thr Ser Thr Thr Val Phe Asn Phe Pro Val Ser	
330 335 340	
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Ile Pro Val His Ser Thr Asn Ser Ala Leu Ser Tyr Leu Gln Ser Pro	
345 350 355 360	
att acg acc tct ccc agc tgc tga aaggccacgg gaggtgaggg tcttcacatc	1402
Ile Thr Thr Ser Pro Ser Cys *	
365	
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gtacatcaag tccatctgac aaaatggggc agaagagaaa ggactcagtg tgtgatccgg	1642
tttctttttg ctgcgccctg ttttttgtag aatctcttca tgcttgacat acctaccagt	1702

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 tgagtactgt actatcctgt aaatatatct taagcaggtt tgttttcagc actgatggaa 1882  
 aataccagtg ttgggttttt ttttagttgc caacagttgt atgtttgctg attatttatg 1942  
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 cattatgatg tgtttatgtt cacagaaatt tttgtaattt ctctatggta acaacttttt 180  
 atgccttaag agtgtctctg aggcaggatt ctaagagatt ctctttgact caatcccaga 240  
 tagaggataa atctcctggc aaagcccaga atg acc aca gcc ctg gaa cct 291  
 Met Thr Thr Ala Leu Glu Pro  
 1 5  
 gag gac caa aaa gga ctt ctg ata att aag gca gag gac cat tac tgg 339  
 Glu Asp Gln Lys Gly Leu Leu Ile Ile Lys Ala Glu Asp His Tyr Trp  
 10 15 20  
 gga cag gat tcc agc tca caa aag tgc agt cct cac agg agg gaa ctc 387  
 Gly Gln Asp Ser Ser Ser Gln Lys Cys Ser Pro His Arg Arg Glu Leu  
 25 30 35  
 tat aga caa cac ttc agg aag ctc tgc tat cag gat gca cct gga ccc 435  
 Tyr Arg Gln His Phe Arg Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro  
 40 45 50 55  
 cgt gaa gct ctt acc cag ctg tgg gag ctc tgc cgt cag tgg ctg agg 483  
 Arg Glu Ala Leu Thr Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg  
 60 65 70  
 cca gaa tgc cac acc aag gag cag att tta gac ctg ctg gtg cta gaa 531  
 Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu  
 75 80 85





gaa aaa ctg aag gtg caa gtt act gat acc aac cga agg ttt caa gat	535
Glu Lys Leu Lys Val Gln Val Thr Asp Thr Asn Arg Arg Phe Gln Asp	
70 75 80	
gct gga aaa gag gtg ata gtc cac aca gaa gat atc att cga tgt aga	583
Ala Gly Lys Glu Val Ile Val His Thr Glu Asp Ile Ile Arg Cys Arg	
85 90 95	
att cag cag aga aat att aca act gta gta gaa aaa ttg cag tta tgc	631
Ile Gln Gln Arg Asn Ile Thr Thr Val Val Glu Lys Leu Gln Leu Cys	
100 105 110	
ctt cct gtg cta gaa atg tac agt aag ctg aaa gaa cag atg agt gcc	679
Leu Pro Val Leu Glu Met Tyr Ser Lys Leu Lys Glu Gln Met Ser Ala	
115 120 125 130	
aaa agg tac tat tct gcc cta aaa act atg gaa caa tta gag aat gtg	727
Lys Arg Tyr Tyr Ser Ala Leu Lys Thr Met Glu Gln Leu Glu Asn Val	
135 140 145	
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Asn Leu Pro Lys Leu Arg Glu Asp Ile Lys Glu Ile Ser Met Ser Asp	
165 170 175	
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Leu Lys Asp Phe Leu Glu Ser Ile Arg Lys His Ser Asp Lys Ile Gly	
180 185 190	
gaa aca gca atg aaa cag gca cag cat cag aaa acc ttc agt gtt tct	919
Glu Thr Ala Met Lys Gln Ala Gln His Gln Lys Thr Phe Ser Val Ser	
195 200 205 210	
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Arg Asp Arg Ile Pro Glu Glu Arg Asn Glu Thr Val Leu Lys His Ser	
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245 250 255	
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Leu Gly Asp Glu Glu Thr Phe Glu Asn Tyr Tyr Arg Lys Gln Arg Lys	
275 280 285 290	
aaa caa gca aga ctg gta ttg caa ccc cag tcg aat atg cat gaa aca	1207

Lys	Gln	Ala	Arg	Leu	Val	Leu	Gln	Pro	Gln	Ser	Asn	Met	His	Glu	Thr		
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Val	Asp	Gly	Tyr	Arg	Arg	Tyr	Phe	Thr	Gln	Ile	Val	Gly	Phe	Phe	Val		
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Val	Glu	Asp	His	Ile	Leu	His	Val	Thr	Gln	Gly	Leu	Val	Thr	Arg	Ala		
			325				330					335					
tac	act	gat	gaa	ctt	tgg	aac	atg	gcc	ctc	tca	aag	ata	att	gct	gtc	1351	
Tyr	Thr	Asp	Glu	Leu	Trp	Asn	Met	Ala	Leu	Ser	Lys	Ile	Ile	Ala	Val		
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Leu	Arg	Ala	His	Ser	Ser	Tyr	Cys	Thr	Asp	Pro	Asp	Leu	Val	Leu	Glu		
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Leu	Lys	Asn	Leu	Thr	Val	Ile	Phe	Ala	Asp	Thr	Leu	Gln	Gly	Tyr	Gly		
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Phe	Pro	Val	Asn	Arg	Leu	Phe	Asp	Leu	Leu	Phe	Glu	Ile	Arg	Asp	Gln		
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Tyr	Asn	Glu	Thr	Leu	Leu	Lys	Lys	Trp	Ala	Gly	Val	Phe	Arg	Asp	Ile		
	405					410						415					
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Phe	Glu	Glu	Asp	Asn	Tyr	Ser	Pro	Ile	Pro	Val	Val	Asn	Glu	Glu	Glu		
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435				440					445					450			
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Lys	Gln	Ser	Phe	Pro	Lys	Lys	Phe	Pro	Met	Ser	Gln	Ser	Val	Pro	His		
			455					460						465			
att	tac	att	caa	gtt	aaa	gaa	ttt	att	tat	gcc	agc	ctt	aaa	ttt	tca	1735	
Ile	Tyr	Ile	Gln	Val	Lys	Glu	Phe	Ile	Tyr	Ala	Ser	Leu	Lys	Phe	Ser		
			470					475					480				
gag	tca	cta	cac	cgg	agc	tca	aca	gaa	ata	gac	gat	atg	ctt	aga	aaa	1783	
Glu	Ser	Leu	His	Arg	Ser	Ser	Thr	Glu	Ile	Asp	Asp	Met	Leu	Arg	Lys		
			485				490					495					
tca	aca	aat	ctg	ctg	ctg	acc	aga	act	ttg	agt	agc	tgt	tta	ctg	aac	1831	
Ser	Thr	Asn	Leu	Leu	Leu	Thr	Arg	Thr	Leu	Ser	Ser	Cys	Leu	Leu	Asn		
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ctt	att	aga	aaa	cct	cat	ata	ggt	ttg	aca	gag	ctg	gta	caa	atc	atc	1879	
Leu	Ile	Arg	Lys	Pro	His	Ile	Gly	Leu	Thr	Glu	Leu	Val	Gln	Ile	Ile		

515	520	525	530	
ata aac aca aca cac ctg gag caa gct tgt aaa tat ctt gag gac ttt				1927
Ile Asn Thr Thr His Leu Glu Gln Ala Cys Lys Tyr Leu Glu Asp Phe	535	540	545	
ata act aac att aca aat att tcc caa gaa act gtt cat act aca aga				1975
Ile Thr Asn Ile Thr Asn Ile Ser Gln Glu Thr Val His Thr Thr Arg	550	555	560	
ctt tat gga ctt tct act ttc aag gat gct cga cat gca gca gaa gga				2023
Leu Tyr Gly Leu Ser Thr Phe Lys Asp Ala Arg His Ala Ala Glu Gly	565	570	575	
gaa ata tat acc aaa ctg aat caa aaa att gat gaa ttt gtt cag ctt				2071
Glu Ile Tyr Thr Lys Leu Asn Gln Lys Ile Asp Glu Phe Val Gln Leu	580	585	590	
gct gat tat gac tgg aca atg tct gag cca gat gga aga gct agt ggt				2119
Ala Asp Tyr Asp Trp Thr Met Ser Glu Pro Asp Gly Arg Ala Ser Gly	595	600	605	610
tat tta atg gac ctt ata aat ttt ttg aga agc atc ttt caa gtg ttt				2167
Tyr Leu Met Asp Leu Ile Asn Phe Leu Arg Ser Ile Phe Gln Val Phe	615	620	625	
act cat ttg cct ggg aaa gtt gct cag aca gct tgc atg tca gcc tgc				2215
Thr His Leu Pro Gly Lys Val Ala Gln Thr Ala Cys Met Ser Ala Cys	630	635	640	
cag cat ctg tca aca tcc tta atg cag atg cta ctg gac agt gag tta				2263
Gln His Leu Ser Thr Ser Leu Met Gln Met Leu Leu Asp Ser Glu Leu	645	650	655	
aaa caa ata agc atg gga gct gtt cag cag ttt aac tta gat gtc ata				2311
Lys Gln Ile Ser Met Gly Ala Val Gln Gln Phe Asn Leu Asp Val Ile	660	665	670	
cag tgt gaa ttg ttt gcc agc tct gag cct gtg cca gga ttc cag ggg				2359
Gln Cys Glu Leu Phe Ala Ser Ser Glu Pro Val Pro Gly Phe Gln Gly	675	680	685	690
gat acc ctg cag cta gca ttc att gac ctc aga caa ctc ctt gac ctg				2407
Asp Thr Leu Gln Leu Ala Phe Ile Asp Leu Arg Gln Leu Leu Asp Leu	695	700	705	
ttt atg gtt tgg gat tgg tct act tac cta gct gat tat ggg cag cca				2455
Phe Met Val Trp Asp Trp Ser Thr Tyr Leu Ala Asp Tyr Gly Gln Pro	710	715	720	
gct tct aag tac ctt cgg gtg aat cca aac aca gcc ctt act ctt ttg				2503
Ala Ser Lys Tyr Leu Arg Val Asn Pro Asn Thr Ala Leu Thr Leu Leu	725	730	735	
gag aag atg aag gat act agc aaa aag aac aat ata ttt gct cag ttc				2551
Glu Lys Met Lys Asp Thr Ser Lys Lys Asn Asn Ile Phe Ala Gln Phe	740	745	750	

agg aag aat gat cga gac aaa cag aag ttg ata gag aca gtc gtg aaa	2599
Arg Lys Asn Asp Arg Asp Lys Gln Lys Leu Ile Glu Thr Val Val Lys	
755 760 765 770	
cag ctg aga agt ttg gtg aat ggt atg tcc cag cac atg tag acctcac	2648
Gln Leu Arg Ser Leu Val Asn Gly Met Ser Gln His Met *	
775 780	
atggccttgca ctcaagtgcaca ccaaattccat gattcaatgt tgatcttgag caagtattgg	2708
tcatgataca gtaatttggt tacagaatcc aaaaatacaa tagagaagat acatgagggc	2768
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS



<222> (41)..(250)

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aag	aag	gaa	gct	cct	gcc	cct	cct	aaa	gcc	gaa	gcc	aaa	gcg	aag	gct	103
Lys	Lys	Glu	Ala	Pro	Ala	Pro	Pro	Lys	Ala	Glu	Ala	Lys	Ala	Lys	Ala	
				10				15					20			

ttg	caa	ggc	caa	gaa	ggc	agt	gtt	gaa	aga	tgt	cca	cag	cca	caa	aaa	151
Leu	Gln	Gly	Gln	Glu	Gly	Ser	Val	Glu	Arg	Cys	Pro	Gln	Pro	Gln	Lys	
			25					30					35			

aaa	caa	gat	cca	cat	gtc	acc	cac	ctt	ccg	gcg	gcc	caa	gac	act	gtg	199
Lys	Gln	Asp	Pro	His	Val	Thr	His	Leu	Pro	Ala	Ala	Gln	Asp	Thr	Val	
		40					45					50				

act	ccg	gag	gca	gcc	caa	ata	tcc	ttg	gaa	gag	cac	ccc	cag	gag	aaa	247
Thr	Pro	Glu	Ala	Ala	Gln	Ile	Ser	Leu	Glu	Glu	His	Pro	Gln	Glu	Lys	
		55				60					65					

taa	gctt	gaccaccatg	ttatcatcaa	gtttccgctg	accactgagt	aggctgtgaa	304
*							
70							

gaagatagaa	aacaacagcc	tacttgtgtt	cactgtggat	gttaaagcca	acaagcacca	364
------------	------------	------------	------------	------------	------------	-----

gatcaaacag	gctgtgaaga	agtttgtgac	attgatgtgg	ccaaagtcaa	cactctgatt	424
------------	------------	------------	------------	------------	------------	-----

cagtctgatg	gagagaggaa	ggcatatggt	cgactggctc	ctgactacga	tgcttttggt	484
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gttgccacca	aaattgggat	cacctaaact	gagtcaagct	ggctaattcc	aatatatgt	544
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atatcttttc	accattaaaa	gaatcttaat	ctctcaaaaa	aaaaaaaa		591
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<220>

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<222> (150)..(2729)

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cggccccgga	gccctcggc	ggcgccacc	atg	tac	tcg	gga	gcc	ggc	ccc	gca	173
			Met	Tyr	Ser	Gly	Ala	Gly	Pro	Ala	
			1				5				

ctt gca cct cct gcg ccg ccg ccc ccc atc caa gga tat gcc ttc aag	221
Leu Ala Pro Pro Ala Pro Pro Pro Pro Ile Gln Gly Tyr Ala Phe Lys	
10 15 20	
cct cca cct aga ccc gac ttt ggg acc tcc ggg aga aca atc aaa tta	269
Pro Pro Pro Arg Pro Asp Phe Gly Thr Ser Gly Arg Thr Ile Lys Leu	
25 30 35 40	
cag gcc aat ttc ttc gaa atg gac atc ccc aaa att gac atc tat cat	317
Gln Ala Asn Phe Phe Glu Met Asp Ile Pro Lys Ile Asp Ile Tyr His	
45 50 55	
tat gaa ttg gat atc aag cca gag aag tgc ccg agg aga gtt aac agg	365
Tyr Glu Leu Asp Ile Lys Pro Glu Lys Cys Pro Arg Arg Val Asn Arg	
60 65 70	
gaa atc gtg gaa cac atg gtc cag cac ttt aaa aca cag atc ttt ggg	413
Glu Ile Val Glu His Met Val Gln His Phe Lys Thr Gln Ile Phe Gly	
75 80 85	
gat cgg aag ccc gtg ttt gac ggc agg aag aat cta tac aca gcc atg	461
Asp Arg Lys Pro Val Phe Asp Gly Arg Lys Asn Leu Tyr Thr Ala Met	
90 95 100	
ccc ctt ccg att ggg agg gac aag gtg gag ctg gag gtc acg ctg cca	509
Pro Leu Pro Ile Gly Arg Asp Lys Val Glu Leu Glu Val Thr Leu Pro	
105 110 115 120	
gga gaa ggc aag gat cgc atc ttc aag gtg tcc atc aag tgg gtg tcc	557
Gly Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Val Ser	
125 130 135	
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Cys Val Ser Leu Gln Ala Leu His Asp Ala Leu Ser Gly Arg Leu Pro	
140 145 150	
agc gtc cct ttt gag acg atc cag gcc ctg gac gtg gtc atg agg cac	653
Ser Val Pro Phe Glu Thr Ile Gln Ala Leu Asp Val Val Met Arg His	
155 160 165	
ttg cca tcc atg agg tac acc ccc gtg ggc cgc tcc ttc ttc acc gcg	701
Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Thr Ala	
170 175 180	
tcc gaa ggc tgc tct aac cct ctt ggc ggg ggc cga gaa gtg tgg ttt	749
Ser Glu Gly Cys Ser Asn Pro Leu Gly Gly Gly Arg Glu Val Trp Phe	
185 190 195 200	
ggc ttc cat cag tcc gtc ccg cct tct ctc tgg aaa atg atg ctg aat	797
Gly Phe His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn	
205 210 215	
att gat gtg tca gca aca gcg ttt tac aag gca cag cca gta atc gag	845
Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu	
220 225 230	

ttt gtt tgt gaa gtt ttg gat ttt aaa agt att gaa gaa caa caa aaa	893
Phe Val Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys	
235 240 245	
cct ctg aca gat tcc caa agg gta aag ttt acc aaa gaa att aaa ggt	941
Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly	
250 255 260	
cta aag gtg gag ata acg cac tgt ggg cag atg aag agg aag tac cgt	989
Leu Lys Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg	
265 270 275 280	
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Val Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu	
285 290 295	
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Gln Gln Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe	
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aag gac agg cac aag ttg gtt ctg cgc tac ccc cac ctc cca tgt tta	1133
Lys Asp Arg His Lys Leu Val Leu Arg Tyr Pro His Leu Pro Cys Leu	
315 320 325	
caa gtc gga cag gag cag aaa cac acc tac ctt ccc ctg gag gtc tgt	1181
Gln Val Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys	
330 335 340	
aac att gtg gca gga caa aga tgt att aaa aaa tta acg gac aat cag	1229
Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln	
345 350 355 360	
acc tca acc atg atc aga gcg act gct agg tgc gcg ccc gat cgg caa	1277
Thr Ser Thr Met Ile Arg Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln	
365 370 375	
gaa gag att agc aaa ttg atg cga agt gca agt ttc aac aca gat cca	1325
Glu Glu Ile Ser Lys Leu Met Arg Ser Ala Ser Phe Asn Thr Asp Pro	
380 385 390	
tac gtc cgt gaa ttt gga atc atg gtc aaa gat gag atg aca gac gtg	1373
Tyr Val Arg Glu Phe Gly Ile Met Val Lys Asp Glu Met Thr Asp Val	
395 400 405	
act ggg cgg gtg ctg cag ccg ccc tcc atc ctc tac ggg ggc agg aat	1421
Thr Gly Arg Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg Asn	
410 415 420	
aaa gct att gcg acc cct gtc cag ggc gtc tgg gac atg cgg aac aag	1469
Lys Ala Ile Ala Thr Pro Val Gln Gly Val Trp Asp Met Arg Asn Lys	
425 430 435 440	
cag ttc cac acg ggc atc gag atc aag gtg tgg gcc att gcg tgc ttc	1517
Gln Phe His Thr Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe	
445 450 455	
gcc ccc cag cgc cag tgc acg gaa gtc cat ctg aag tcc ttc aca gag	1565



685	690	695	
gac tac cag ccc ggg atc acc ttc atc gtg gtg cag aag agg cac cac Asp Tyr Gln Pro Gly Ile Thr Phe Ile Val Val Gln Lys Arg His His 700 705 710			2285
acc cgg ctc ttc tgc act gac aag aac gag cgg gtt ggg aaa agt gga Thr Arg Leu Phe Cys Thr Asp Lys Asn Glu Arg Val Gly Lys Ser Gly 715 720 725			2333
aac att cca gca ggc acg act gtg gac acg aaa atc acc cac ccc acc Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Lys Ile Thr His Pro Thr 730 735 740			2381
gag ttc gac ttc tac ctg tgt agt cac gct ggc atc cag ggg aca agc Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser 745 750 755 760			2429
agg cct tcg cac tat cac gtc ctc tgg gac gac aat cgt ttc tcc tct Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn Arg Phe Ser Ser 765 770 775			2477
gat gag ctg cag atc cta acc tac cag ctg tgt cac acc tac gtg cgc Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg 780 785 790			2525
tgc aca cgc tcc gtg tcc atc cca gcg cca gca tac tac gct cac ctg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu 795 800 805			2573
gtg gcc ttc cgg gcc agg tac cac ctg gtg gat aag gaa cat gac agt Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser 810 815 820			2621
gct gaa gga agc cat acc tct ggg cag agt aac ggg cga gac cac caa Ala Glu Gly Ser His Thr Ser Gly Gln Ser Asn Gly Arg Asp His Gln 825 830 835 840			2669
gca ctg gcc aag gcg gtc cag gtt cac caa gac act ctg cgc acc atg Ala Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met 845 850 855			2717
tac ttt gct tga cat gttttagtgt ttagcgattg tgtaccgagt gggattcacg Tyr Phe Ala * 860			2772
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tgctggaggc gaatgctaca cccctggaca gaggcgacgg tgtcttaaga acctgcgctc      300
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cattgacctt ggtctactgc tttgcttttc taacagag      atg gtt cac ttc att      653
                                   Met Val His Phe Ile
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Leu Gly Arg Leu Tyr Asn Phe Gln Pro Phe Leu Thr Arg Thr Glu Val
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tac aaa act ggt gtc aca cat tat ttt agc tta gag aaa gcc aag aaa      749
Tyr Lys Thr Gly Val Thr His Tyr Phe Ser Leu Glu Lys Ala Lys Lys
                                   25               30               35

gag cta ggt tat aag gct cag cca ttt gac ctc cag gaa gca gtg gaa      797
Glu Leu Gly Tyr Lys Ala Gln Pro Phe Asp Leu Gln Glu Ala Val Glu
                                   40               45               50

tgg ttt aaa gcc cat ggt cat ggc aga agt tct gga agt cgt gac tcg      845
Trp Phe Lys Ala His Gly His Gly Arg Ser Ser Gly Ser Arg Asp Ser
                                   55               60               65

gag tgt ttt gtt tgg gat ggg cta ttg gtc ttc ctc ctg att ata gca      893
Glu Cys Phe Val Trp Asp Gly Leu Leu Val Phe Leu Leu Ile Ile Ala
                                   70               75               80               85

gtt ctc atg tgg ctg cct tct tct gtg att ctg tca ctg tga aggaggg      942
Val Leu Met Trp Leu Pro Ser Ser Val Ile Leu Ser Leu *
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Ile	Lys	Tyr	Ser	Cys	Pro	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser		
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Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asn	Thr	Val	Ile	Trp	Asp	Asn	Lys	Thr		
135					140				145					150			
cct	gtt	tgt	gac	agt	gag	ttg	aaa	tat	gca	ttc	cta	ttt	ctt	tta	ccg	655	
Pro	Val	Cys	Asp	Ser	Glu	Leu	Lys	Tyr	Ala	Phe	Leu	Phe	Leu	Leu	Pro		
			155					160					165				
ata	cat	tct	aat	ttt	tct	ctg	gaa	taa	taaaa	atctattccg	aaaaaaaaaa	707					
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aaa																710	

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						Met											
						1											
gtg	ggg	aga	tcc	cgg	cgg	cgc	gga	gca	gct	aag	tgg	gca	gct	gtg	cga	224	
Val	Gly	Arg	Ser	Arg	Arg	Arg	Gly	Ala	Ala	Lys	Trp	Ala	Ala	Val	Arg		
			5				10					15					
gcc	aag	gca	ggg	ccc	acg	ctc	acc	gac	gaa	aat	gga	gat	gat	tta	gga	272	
Ala	Lys	Ala	Gly	Pro	Thr	Leu	Thr	Asp	Glu	Asn	Gly	Asp	Asp	Leu	Gly		
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Leu	Pro	Pro	Ser	Pro	Gly	Asp	Thr	Ser	Tyr	Tyr	Gln	Asp	Gln	Val	Asp		
		35				40					45						
gac	ttt	cat	gag	gca	cga	tcc	cgg	gcc	gcc	tta	gct	aag	ggc	tgg	aat	368	
Asp	Phe	His	Glu	Ala	Arg	Ser	Arg	Ala	Ala	Leu	Ala	Lys	Gly	Trp	Asn		
	50				55					60					65		
gaa	gta	cag	agt	gga	gac	gag	gag	gat	ggc	gag	gag	gag	gag	gag	gag	416	
Glu	Val	Gln	Ser	Gly	Asp	Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Glu	Glu		
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Val Leu Ala Leu Asp Met Asp Asp Glu Asp Asp Glu Asp Gly Gly Asn	
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gcg ggg gag gag gag gag gag gag aat gcc gat gat gat ggt ggg agc	512
Ala Gly Glu Glu Glu Glu Glu Glu Asn Ala Asp Asp Asp Gly Gly Ser	
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Ser Val Gln Ser Glu Ala Glu Ala Ser Val Asp Pro Ser Leu Ser Trp	
115 120 125	
ggt cag agg aaa aaa ctt tac tat gac acg gac tat ggt tcc aag tcc	608
Gly Gln Arg Lys Lys Leu Tyr Tyr Asp Thr Asp Tyr Gly Ser Lys Ser	
130 135 140 145	
cga ggc cgg cag agt caa cag gag gca gag gag gag gaa aga gag gag	656
Arg Gly Arg Gln Ser Gln Gln Glu Ala Glu Glu Glu Glu Arg Glu Glu	
150 155 160	
gag gag gag gca cag atc att cag cgg cgc cta gcc caa gcg ctg caa	704
Glu Glu Glu Ala Gln Ile Ile Gln Arg Arg Leu Ala Gln Ala Leu Gln	
165 170 175	
gag gat gat ttt ggt gtc gcc tgg gtt gag gcc ttt gca aaa cca gtg	752
Glu Asp Asp Phe Gly Val Ala Trp Val Glu Ala Phe Ala Lys Pro Val	
180 185 190	
cct cag gta gat gag gct gag aca cgg gtc gtg aag gat ttg gct aaa	800
Pro Gln Val Asp Glu Ala Glu Thr Arg Val Val Lys Asp Leu Ala Lys	
195 200 205	
gtt tca gtg aaa gag aag ctg aaa atg ttg cga aag gaa tca cca gaa	848
Val Ser Val Lys Glu Lys Leu Lys Met Leu Arg Lys Glu Ser Pro Glu	
210 215 220 225	
ctc ttg gag ctg ata gaa gac ctg aaa gtc aag ttg aca gag gtt aag	896
Leu Leu Glu Leu Ile Glu Asp Leu Lys Val Lys Leu Thr Glu Val Lys	
230 235 240	
gat gag ctg gag cca ttg tta gag ttg gtg gaa caa ggg atc att cca	944
Asp Glu Leu Glu Pro Leu Leu Glu Leu Val Glu Gln Gly Ile Ile Pro	
245 250 255	
ccc gga aaa gga agc caa tac ttg agg acc aag tac aac ctc tac ttg	992
Pro Gly Lys Gly Ser Gln Tyr Leu Arg Thr Lys Tyr Asn Leu Tyr Leu	
260 265 270	
aat tat tgc tcg aac atc agt ttt tat ttg atc ctg aaa gct agg aga	1040
Asn Tyr Cys Ser Asn Ile Ser Phe Tyr Leu Ile Leu Lys Ala Arg Arg	
275 280 285	
gtc cca gca cat gga cat cct gtc ata gaa agg ctt gtt acc tac cga	1088
Val Pro Ala His Gly His Pro Val Ile Glu Arg Leu Val Thr Tyr Arg	
290 295 300 305	

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Asn Leu Ile Asn Lys Leu Ser Val Val Asp Gln Lys Leu Ser Ser Glu	
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att cgt cat ctg ttg aca ctt aag gat gat gct gta aag aaa gaa ctg	1184
Ile Arg His Leu Leu Thr Leu Lys Asp Asp Ala Val Lys Lys Glu Leu	
325 330 335	
att cca aaa gca aaa tcc acc aag ccc aaa cca aag tct gtt tca aag	1232
Ile Pro Lys Ala Lys Ser Thr Lys Pro Lys Pro Lys Ser Val Ser Lys	
340 345 350	
act tct gct gct gcc tgt gct gtt aca gat ctt tct gat gat tct gat	1280
Thr Ser Ala Ala Ala Cys Ala Val Thr Asp Leu Ser Asp Asp Ser Asp	
355 360 365	
ttt gat gaa aaa gca aaa ctg aag tac tat aaa gaa ata gaa gac agg	1328
Phe Asp Glu Lys Ala Lys Leu Lys Tyr Tyr Lys Glu Ile Glu Asp Arg	
370 375 380 385	
caa aag cta aag aga aag aaa gaa gaa aat agc act gaa gaa cag gct	1376
Gln Lys Leu Lys Arg Lys Lys Glu Glu Asn Ser Thr Glu Glu Gln Ala	
390 395 400	
ctt gaa gat caa aat gca aag aga gct att acc tat caa att gct aaa	1424
Leu Glu Asp Gln Asn Ala Lys Arg Ala Ile Thr Tyr Gln Ile Ala Lys	
405 410 415	
aat agg gga ctt act cct agg aga aag aag att gat cgc aat ccc aga	1472
Asn Arg Gly Leu Thr Pro Arg Arg Lys Lys Ile Asp Arg Asn Pro Arg	
420 425 430	
gtg aaa cac aga gag aag ttc aga aga gcc aaa att aga aga aga ggc	1520
Val Lys His Arg Glu Lys Phe Arg Arg Ala Lys Ile Arg Arg Arg Gly	
435 440 445	
cag gtt cgt gaa gtt cgt aaa gaa gag caa cgt tat agt ggt gaa tta	1568
Gln Val Arg Glu Val Arg Lys Glu Glu Gln Arg Tyr Ser Gly Glu Leu	
450 455 460 465	
tct ggc att cgt gca gga gtt aaa aag agc att aag ctt aaa tga agt	1616
Ser Gly Ile Arg Ala Gly Val Lys Lys Ser Ile Lys Leu Lys *	
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aaggaagaaa attggtaact ttaagtggga cttatcattt gttgtgtgtg ctttcctcat	180
agtgagtcta attttcacaa ttacaccttg gtctcattga atgaagaatt taatcgtgga	240
cgaggactaa atgtgggtgc ccgagcttgg gacaaggag aggtcttg atg ttt ttc	297
Met Phe Phe	
1	
tgt gat gtt gat atc tat ttc tca gcc gaa ttc ctt aac agc tgc cgg	345
Cys Asp Val Asp Ile Tyr Phe Ser Ala Glu Phe Leu Asn Ser Cys Arg	
5 10 15	
tta aat gct gag cca ggt aag aag gtg ttt tac cct gtg gtg ttc agt	393
Leu Asn Ala Glu Pro Gly Lys Lys Val Phe Tyr Pro Val Val Phe Ser	
20 25 30 35	
ctt tac aat cct gcc att gtt tat gcc aac cag gaa gtg cca cca cct	441
Leu Tyr Asn Pro Ala Ile Val Tyr Ala Asn Gln Glu Val Pro Pro Pro	
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gtg gag cag cag ctg gtt cac aaa aag gat tct ggc ttt tgg cga gat	489
Val Glu Gln Gln Leu Val His Lys Lys Asp Ser Gly Phe Trp Arg Asp	
55 60 65	
ttt ggc ttt gga atg act tgt cag tat cgt tca gat ttc ctg acc att	537
Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Leu Thr Ile	
70 75 80	
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Gly Gly Phe Asp Met Glu Val Lys Gly Trp Gly Gly Glu Asp Val His	
85 90 95	
ctt tat cga aaa tac tta cat ggt gac ctc att gtg att cgg act ccg	633
Leu Tyr Arg Lys Tyr Leu His Gly Asp Leu Ile Val Ile Arg Thr Pro	
100 105 110 115	
gtt cct ggt ctt ttc cac ctc tgg cat gaa aag cgc tgt gct gat gag	681
Val Pro Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Ala Asp Glu	
120 125 130	
ctg acc ccc gag cag tac cgc atg tgc atc cag tct aaa gcc atg aat	729
Leu Thr Pro Glu Gln Tyr Arg Met Cys Ile Gln Ser Lys Ala Met Asn	
135 140 145	
gag gcc tct cac tcc cac ctg gga atg ctg gtc ttc agg gag gaa ata	777
Glu Ala Ser His Ser His Leu Gly Met Leu Val Phe Arg Glu Glu Ile	
150 155 160	
gag acg cat ctt cat aaa cag gca tac agg aca aac agt gaa gct gtt	825





gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat	484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr	
140 145 150	
tggtagg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat	532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
155 160 165 170	
gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa	580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
175 180 185	
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt	628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
190 195 200	
gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag	676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln	
205 210 215	
gcgcgc cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa	724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys	
220 225 230	
gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg	772
Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val	
235 240 245 250	
gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa	820
Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys	
255 260 265	
gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga	868
Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly	
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tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat	916
Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp	
285 290 295	
ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt	964
Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu	
300 305 310	
tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag	1012
Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys	
315 320 325 330	
aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa	1060
Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys	
335 340 345	
caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat	1108
Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp	
350 355 360	
gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca	1156

Glu	Asn	Pro	Leu	Asp	Asp	Asn	Ser	Glu	Glu	Glu	Met	Glu	Asp	Ala	Pro		
		365					370					375					
aaa	caa	aag	ctt	tct	aaa	aaa	cag	aag	aca	caa	gaa	aca	gta	aac	cag		1204
Lys	Gln	Lys	Leu	Ser	Lys	Lys	Gln	Lys	Thr	Gln	Glu	Thr	Val	Asn	Gln		
	380					385					390						
cac	agg	atg	tac	ctg	gca	aag	att	cat	atc	tgc	ctg	cag	ctc	act	ttc		1252
His	Arg	Met	Tyr	Leu	Ala	Lys	Ile	His	Ile	Cys	Leu	Gln	Leu	Thr	Phe		
	395				400					405					410		
aga	tgg	ctt	ggg	gaa	aaa	agt	gtg	tgt	agg	gag	aga	gaa	gag	atg	gag		1300
Arg	Trp	Leu	Gly	Glu	Lys	Ser	Val	Cys	Arg	Glu	Arg	Glu	Glu	Met	Glu		
			415						420					425			
aga	gcg	agc	aca	aat	gtg	cca	aaa	tgt	tgc	ttg	aaa	aca	gac	aga	att		1348
Arg	Ala	Ser	Thr	Asn	Val	Pro	Lys	Cys	Cys	Leu	Lys	Thr	Asp	Arg	Ile		
			430					435					440				
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Met	Met	Thr	Ile	Ser	Met	*											
			445														
atgaag	atac	taact	tatat	caagac	agtg	caaaga	aatt	ggaag	atagt	ccccag	gaaa						1461
atgtc	agtg	cacag	atgat	cattac	acca	tgtgat	gatac	caaaa	agtga	agctaaa	aagg						1521
taagt	caaag	ttgcat	atatta	tttgtaa	aatt	actga	aatatt	gatag	taagg	atgtag	cttt						1581
tcatat	atca	aataaaa	atct	tctttcc	cat	gactg	accag	gtaatt	ttaga	tgtat	ctgta						1641
catat	ttatg	tatag	ataca	cacacac	ata	tgtata	caga	tgaag	agcgt	tgaga	agagg						1701
atgct	agagg	aatgtg	ccca	cacacat	ctc	agcag	catgg	ccaaa	atcag	aaagat	gtca						1761
ctttg	atcca	gttctc	gttt	accttat	cct	gctgtg	ggcgc	tgatct	cgtc	gtggat	catt						1821
aacact	tgac	actcac	atga	gaaca	agact	cctgct	gcgt	ccctgg	agtg	tcacta	agca						1881
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Arg Arg Asp Ala Ser Glu Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu	
15 20 25	
gcc ctg aaa tgg cac ccg gat aaa aat ctg gat aat gcc gca gaa gca	148
Ala Leu Lys Trp His Pro Asp Lys Asn Leu Asp Asn Ala Ala Glu Ala	
30 35 40	
gct gaa caa ttt aaa tta atc caa gca gca tat gat gtg ttg agt gac	196
Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp	
45 50 55	
cct cag gaa aga gca tgg tat gat aat cat aga gag gcc cta ctt aaa	244
Pro Gln Glu Arg Ala Trp Tyr Asp Asn His Arg Glu Ala Leu Leu Lys	
60 65 70	
ggg ggg ttt gat ggc gaa tat caa gat gac agc tta gat ttg cta cgc	292
Gly Gly Phe Asp Gly Glu Tyr Gln Asp Asp Ser Leu Asp Leu Leu Arg	
75 80 85 90	
tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga	340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly	
95 100 105	
ttt tac acg gtg tat cgt aat gtt ttt gaa atg att gcc aag gaa gaa	388
Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu	
110 115 120	
cta gaa tct gtg tta gag gaa gag gtt gat gat ttc cca act ttt gga	436
Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly	
125 130 135	
gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat	484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr	
140 145 150	
tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat	532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
155 160 165 170	
gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa	580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
175 180 185	
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt	628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
190 195 200	
gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag	676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln	
205 210 215	
gcg cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa	724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys	



220	225	230	
gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val 235 240 245 250			772
gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys 255 260 265			820
gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly 270 275 280			868
tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp 285 290 295			916
ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu 300 305 310			964
tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys 315 320 325 330			1012
aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys 335 340 345			1060
caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp 350 355 360			1108
gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro 365 370 375			1156
aaa caa aag ctt tct aaa aaa cag aag aaa aag aaa cag aaa cca gca Lys Gln Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala 380 385 390			1204
cag aat tat gat gac aat ttc aat gta aat gga cct gga gaa gga gta Gln Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val 395 400 405 410			1252
aag gtt gat cca gaa gat act aac tta aat caa gac agt gcc aaa gaa Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys Glu 415 420 425			1300
ttg gaa gat agt ccc cag gaa aat gtc agt gtc aca gag atc att aaa Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile Ile Lys 430 435 440			1348
cca tgt gat gat cca aaa agt gaa gct aaa agt gtt cct aaa ccc aaa Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro Lys Pro Lys 445 450 455			1396

gga aag aaa acc aaa gat atg aaa aaa cct gtc aga gta cct gct gaa	1444
Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu	
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Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu	
475 480 485 490	
ttt cca tct cgg aat aaa ctt ttt gac cat cta aag gcc aca ggt cat	1540
Phe Pro Ser Arg Asn Lys Leu Phe Asp His Leu Lys Ala Thr Gly His	
495 500 505	
gca aga gca cct tca tca tcg tct tta aac agc gca aca agt agt caa	1588
Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln	
510 515 520	
agc aag aaa gag aaa cgt aaa aac aga tag a gattctgcct gtgcttttgt	1639
Ser Lys Lys Glu Lys Arg Lys Asn Arg *	
525 530	
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tgtaataact tcataatatg tgaaaaactc ggatctttta aaaagcatca tagatcattt	2059
ttccatatga cactgggtcc gatttttaaaa attattttta aataaccgat tattgattac	2119
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caagaatagt gtctcttcaa ggttttactt gatttaattt gatattttac tggtttacca	2239
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Glu Val Pro Ala Ala Cys Leu Ser Pro Cys Gly Pro Pro Asn Pro Thr	
10 15 20 25	
 gag ctg ttc agc gag tca cgg cgc ctg gct ctg gag gag ctg gtg gcg	149
Glu Leu Phe Ser Glu Ser Arg Arg Leu Ala Leu Glu Glu Leu Val Ala	
30 35 40	
 ggc ggc ccc gaa gcc ttc gcg gcc ttc ctg cga cgc gag cgc ctg gct	197
Gly Gly Pro Glu Ala Phe Ala Ala Phe Leu Arg Arg Glu Arg Leu Ala	
45 50 55	
 cgt ttc ctg aac ccc gat gag gtg cac gcc att ctg cgc gcg gcg gag	245
Arg Phe Leu Asn Pro Asp Glu Val His Ala Ile Leu Arg Ala Ala Glu	
60 65 70	
 agg ccg gga gag gag ggc gcg gcg gcg gcg gcg gcc gag gac tcg	293
Arg Pro Gly Glu Glu Gly Ala Ala Ala Ala Ala Ala Glu Asp Ser	
75 80 85	
 ttc ggc tcc tcg cac gac tgc tct tcg ggc acc tac ttc ccc gag cag	341
Phe Gly Ser Ser His Asp Cys Ser Ser Gly Thr Tyr Phe Pro Glu Gln	
90 95 100 105	
 tcg gac ctg gag cca ccg ctg ttg gag ctt ggc tgg ccc gcc ttc tac	389
Ser Asp Leu Glu Pro Pro Leu Leu Glu Leu Gly Trp Pro Ala Phe Tyr	
110 115 120	
 cag ggc gcc tac cgc ggc gcc acg cgt gtc gag acg cac ttc cag ccc	437
Gln Gly Ala Tyr Arg Gly Ala Thr Arg Val Glu Thr His Phe Gln Pro	
125 130 135	
 cgc ggc gct ggc gaa ggt ggc ccc tac ggc tgc aag gac gct ctg cgc	485
Arg Gly Ala Gly Glu Gly Gly Pro Tyr Gly Cys Lys Asp Ala Leu Arg	
140 145 150	
 cag cag ctc cgc tcg gcg cga gag gtg att gca gtg gtc atg gac gtg	533
Gln Gln Leu Arg Ser Ala Arg Glu Val Ile Ala Val Val Met Asp Val	
155 160 165	
 ttc aca gac atc gac atc ttc aga gac ctg caa gaa ata tgc agg aaa	581
Phe Thr Asp Ile Asp Ile Phe Arg Asp Leu Gln Glu Ile Cys Arg Lys	
170 175 180 185	
 cag gga gtt gct gtg tat atc ctt ctg gac cag gct ctc ctc tct caa	629
Gln Gly Val Ala Val Tyr Ile Leu Leu Asp Gln Ala Leu Leu Ser Gln	
190 195 200	

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Phe Leu Asp Met Cys Met Asp Leu Lys Val His Pro Glu Gln Glu Lys	
205 210 215	
tta atg aca gtt cgg act atc aca gga aat atc tac tat gca agg tca	725
Leu Met Thr Val Arg Thr Ile Thr Gly Asn Ile Tyr Tyr Ala Arg Ser	
220 225 230	
gga act aag att att ggg aag gtt cac gaa aag ttc acg ttg att gat	773
Gly Thr Lys Ile Ile Gly Lys Val His Glu Lys Phe Thr Leu Ile Asp	
235 240 245	
ggc atc cgc gtg gca aca ggc tcc tac agt ttt aca tgg acg gat ggc	821
Gly Ile Arg Val Ala Thr Gly Ser Tyr Ser Phe Thr Trp Thr Asp Gly	
250 255 260 265	
aaa tta aac agc agt aac ttg gta att ctg tct ggc caa gtg gtt gaa	869
Lys Leu Asn Ser Ser Asn Leu Val Ile Leu Ser Gly Gln Val Val Glu	
270 275 280	
cac ttt gat ctg gag ttc cga atc ctg tat gcc cag tcc aag ccc atc	917
His Phe Asp Leu Glu Phe Arg Ile Leu Tyr Ala Gln Ser Lys Pro Ile	
285 290 295	
agc ccc aaa ctc ctg tct cac ttc cag agc agc aac aag ttt gat cac	965
Ser Pro Lys Leu Leu Ser His Phe Gln Ser Ser Asn Lys Phe Asp His	
300 305 310	
ctc acc aac cga aaa cca cag tcc aag gag ctc acc ctg ggc aac ctg	1013
Leu Thr Asn Arg Lys Pro Gln Ser Lys Glu Leu Thr Leu Gly Asn Leu	
315 320 325	
ctg cgg atg cgg ctg gct agg ctg tca agt act ccc agg aag gcg gac	1061
Leu Arg Met Arg Leu Ala Arg Leu Ser Ser Thr Pro Arg Lys Ala Asp	
330 335 340 345	
ctg gac cca gag atg ccc gca gag ggc aag gca gag cgc aag ccc cat	1109
Leu Asp Pro Glu Met Pro Ala Glu Gly Lys Ala Glu Arg Lys Pro His	
350 355 360	
gac tgt gag tcc tct act gtt agt gag gaa gac tac ttc agc agc cac	1157
Asp Cys Glu Ser Ser Thr Val Ser Glu Glu Asp Tyr Phe Ser Ser His	
365 370 375	
agg gac gag ctc cag agc aga aag gcc att gac gct gcc act caa aca	1205
Arg Asp Glu Leu Gln Ser Arg Lys Ala Ile Asp Ala Ala Thr Gln Thr	
380 385 390	
gag cca gga gag gag atg cca ggg ctg agt gtg agt gag gtg gga aca	1253
Glu Pro Gly Glu Glu Met Pro Gly Leu Ser Val Ser Glu Val Gly Thr	
395 400 405	
caa acc agc atc acc aca gca tgt gct ggt acc cag act gca gtc atc	1301
Gln Thr Ser Ile Thr Thr Ala Cys Ala Gly Thr Gln Thr Ala Val Ile	
410 415 420 425	
acc agg ata gca agc tct caa acc acg att tgg tcc aga tcg acc act	1349





60	65	70	
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Ser Ser Ser Ser Ser Ser Pro Thr Ser Gly Ser Pro Arg Gly Ser His			
75	80	85	
tct agc gcc ctg gag agg cta gaa acc aag ctt cac ctc ctc agg caa			999
Ser Ser Ala Leu Glu Arg Leu Glu Thr Lys Leu His Leu Leu Arg Gln			
90	95	100	105
gag atg gtt aac ctc aga gcc aca gac gtc agg ctc atg cgc cag ttg			1047
Glu Met Val Asn Leu Arg Ala Thr Asp Val Arg Leu Met Arg Gln Leu			
110	115	120	
ctt gta atc aat gag agc atc gag tcc atc aag tgg atg atc gaa gaa			1095
Leu Val Ile Asn Glu Ser Ile Glu Ser Ile Lys Trp Met Ile Glu Glu			
125	130	135	
aaa gcc acc att acc agc aga ggc agc agc ctc agt ggc agc ctg tgc			1143
Lys Ala Thr Ile Thr Ser Arg Gly Ser Ser Leu Ser Gly Ser Leu Cys			
140	145	150	
agt ttg ttg gag agt cag agc acc tcc tta cgt ggc agc tac aac agc			1191
Ser Leu Leu Glu Ser Gln Ser Thr Ser Leu Arg Gly Ser Tyr Asn Ser			
155	160	165	
cta cac gat ggc agt gat ggg ctg gat ggc att tcc gtg gga agt tat			1239
Leu His Asp Gly Ser Asp Gly Leu Asp Gly Ile Ser Val Gly Ser Tyr			
170	175	180	185
ctg gac acg ttg gcg gat gat gtc cca ggc cat cag acc cct tca gac			1287
Leu Asp Thr Leu Ala Asp Asp Val Pro Gly His Gln Thr Pro Ser Asp			
190	195	200	
ttg gac caa ttc agt gac agc tcc ctc ata gag gac tca cag gca cta			1335
Leu Asp Gln Phe Ser Asp Ser Ser Leu Ile Glu Asp Ser Gln Ala Leu			
205	210	215	
cac aag cgt cct aaa ttg gat tct gaa tac tac tgc ttt ggc tag tga			1383
His Lys Arg Pro Lys Leu Asp Ser Glu Tyr Tyr Cys Phe Gly *			
220	225	230	
cagtttttttg catgggactg gtgtgcaatg aacttgtatt tatccttctt ctccgctgct			1443
atatttttttg tgtgattttt attttaataa gatgaccttt ttaaaagaag ctgattttga			1503
aactgcttaa tgggtattgct gttgctccta atacttctca tctgagctga tttatttttc			1563
tctgttacat ctctattttt tatttattac aatgattttc tcccttcttt tacagtagca			1623
caaacaaagt agggggaaaa gaataagcaa taattatggt tttgcttttg ttttcagagc			1683
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						Met
						1
aag gcc ttt ggt cct cca cat gag ggc ccc ctc caa gga ctc gtg gcc	166					
Lys Ala Phe Gly Pro Pro His Glu Gly Pro Leu Gln Gly Leu Val Ala						
5 10 15						
tcc cgc att gag act tat ggg ggc cgg cat cga gcc tct gct cag agc	214					
Ser Arg Ile Glu Thr Tyr Gly Gly Arg His Arg Ala Ser Ala Gln Ser						
20 25 30						
act act ggc aga ctc tat ccc cga gga tac cct gtg ctg gat ccc agt	262					
Thr Thr Gly Arg Leu Tyr Pro Arg Gly Tyr Pro Val Leu Asp Pro Ser						
35 40 45						
cgc cga cgc ctc cag cag tat gtc ccc ttt gcc agg ggt tct ggc cag	310					
Arg Arg Arg Leu Gln Gln Tyr Val Pro Phe Ala Arg Gly Ser Gly Gln						
50 55 60 65						
gcc cga ggc ctg tca ccc atg aga ctg cga gat cca gag ccc gag aag	358					
Ala Arg Gly Leu Ser Pro Met Arg Leu Arg Asp Pro Glu Pro Glu Lys						
70 75 80						
agg cac ggg ggc cat gtg ggg gct ggc ctg ctt cac tcc ccc aaa ctc	406					
Arg His Gly Gly His Val Gly Ala Gly Leu Leu His Ser Pro Lys Leu						
85 90 95						
aag gaa ctc acc aag gcc cat gag ctg gag gtg agg ctg cac act ttc	454					
Lys Glu Leu Thr Lys Ala His Glu Leu Glu Val Arg Leu His Thr Phe						
100 105 110						
agc atg ttt ggg atg ccc cgg ctg ccc cct gag gac cgg cgg cac tgg	502					
Ser Met Phe Gly Met Pro Arg Leu Pro Pro Glu Asp Arg Arg His Trp						
115 120 125						
gag ata gga gag ggt ggc gac agt ggc ctg acc atc gag aag tcc tgg	550					
Glu Ile Gly Glu Gly Gly Asp Ser Gly Leu Thr Ile Glu Lys Ser Trp						
130 135 140 145						
agg gag ctg gtg cct ggg cac aag gag atg agc cag gag ctc tgc cac	598					
Arg Glu Leu Val Pro Gly His Lys Glu Met Ser Gln Glu Leu Cys His						
150 155 160						





aac ctg cgc cca ttc tcc acc ctg gac ctg acg tcc ccc atg ctg ggg Asn Leu Arg Pro Phe Ser Thr Leu Asp Leu Thr Ser Pro Met Leu Gly 390 395 400	1318
gtt gca tct gag cac acc aga cag ctg ctg ctg gag ggg cct gtg cga Val Ala Ser Glu His Thr Arg Gln Leu Leu Leu Glu Gly Pro Val Arg 405 410 415	1366
gtg aag gag gga cga gaa ggg aag ctg gac gtg tac ctg ttc ctc ttc Val Lys Glu Gly Arg Glu Gly Lys Leu Asp Val Tyr Leu Phe Leu Phe 420 425 430	1414
tct gat gtg ctc ctt gtg acc aag ccc cag cgc aag gcg gac aaa gcc Ser Asp Val Leu Leu Val Thr Lys Pro Gln Arg Lys Ala Asp Lys Ala 435 440 445	1462
aag gtc atc cga ccc cct ctc atg ctg gag aag ctc gtg tgc caa ccc Lys Val Ile Arg Pro Pro Leu Met Leu Glu Lys Leu Val Cys Gln Pro 450 455 460 465	1510
ctg cga gac ccc aac agc ttc ctg ctg atc cac ctc act gaa ttc cag Leu Arg Asp Pro Asn Ser Phe Leu Leu Ile His Leu Thr Glu Phe Gln 470 475 480	1558
tgt gtc tcc agc gcc ctc ctt gtg cac tgt ccc agt cct aca gac cgt Cys Val Ser Ser Ala Leu Leu Val His Cys Pro Ser Pro Thr Asp Arg 485 490 495	1606
gcc cag tgg ctg gag aag acc cag cag gcc cag gcc gcc cta cag aag Ala Gln Trp Leu Glu Lys Thr Gln Gln Ala Gln Ala Ala Leu Gln Lys 500 505 510	1654
ctg aag gca gag gag tat gtt caa cag aag agg gag ctc ctg acc ctc Leu Lys Ala Glu Glu Tyr Val Gln Gln Lys Arg Glu Leu Leu Thr Leu 515 520 525	1702
tat cgg gac cag gac agg gag tcc ccc agc acc agg ccc tcc acg cct Tyr Arg Asp Gln Asp Arg Glu Ser Pro Ser Thr Arg Pro Ser Thr Pro 530 535 540 545	1750
tcc ctg gag ggc tct cag agc agc gca gag ggg agg act cct gag ttc Ser Leu Glu Gly Ser Gln Ser Ser Ala Glu Gly Arg Thr Pro Glu Phe 550 555 560	1798
tcg acc att atc ccc cac ctg gtg gtg aca gaa gac aca gat gaa gat Ser Thr Ile Ile Pro His Leu Val Val Thr Glu Asp Thr Asp Glu Asp 565 570 575	1846
gct ccc ctt gtg cca gat gat acc tca gac tct ggc tac ggc act ttg Ala Pro Leu Val Pro Asp Asp Thr Ser Asp Ser Gly Tyr Gly Thr Leu 580 585 590	1894
atc cca ggc acc ccc acg ggg tcc cgc tcc cca ctg agc cgt cta cgc Ile Pro Gly Thr Pro Thr Gly Ser Arg Ser Pro Leu Ser Arg Leu Arg 595 600 605	1942
caa aga gcc ctt cgg cgg gac cct cgc ctc acc ttc tcc acc ctg gaa	1990

Gln Arg Ala Leu Arg Arg Asp Pro Arg Leu Thr Phe Ser Thr Leu Glu	
610 615 620 625	
ctc cgg gac atc cct ctg cgt ccc cac cct ccc gac ccc caa gct cct	2038
Leu Arg Asp Ile Pro Leu Arg Pro His Pro Pro Asp Pro Gln Ala Pro	
630 635 640	
caa cgc cga agc gcc ccc gaa ctg ccg gaa gga atc cta aaa gga ggc	2086
Gln Arg Arg Ser Ala Pro Glu Leu Pro Glu Gly Ile Leu Lys Gly Gly	
645 650 655	
agt ctt ccc cag gaa gac cca cca acc tgg tct gag gaa gaa gat ggg	2134
Ser Leu Pro Gln Glu Asp Pro Pro Thr Trp Ser Glu Glu Glu Asp Gly	
660 665 670	
gcc tcc gag cga ggg aat gtg gtg gtg gaa aca ctc cac agg gcc cgg	2182
Ala Ser Glu Arg Gly Asn Val Val Val Glu Thr Leu His Arg Ala Arg	
675 680 685	
ctt cgg ggc cag ctt ccc tcc tcc cca acc cat gct gac tct gcc ggg	2230
Leu Arg Gly Gln Leu Pro Ser Ser Pro Thr His Ala Asp Ser Ala Gly	
690 695 700 705	
gaa agc ccc tgg gag tcc tca ggg gag gag gaa gaa gag ggg cct ctg	2278
Glu Ser Pro Trp Glu Ser Ser Gly Glu Glu Glu Glu Gly Pro Leu	
710 715 720	
ttc ctg aaa gct ggc cac aca tcc ctg cgc cca atg cgg gct gag gac	2326
Phe Leu Lys Ala Gly His Thr Ser Leu Arg Pro Met Arg Ala Glu Asp	
725 730 735	
atg ctc aga gag atc cgg gag gag ctg gcc agc caa agg att gag ggg	2374
Met Leu Arg Glu Ile Arg Glu Glu Leu Ala Ser Gln Arg Ile Glu Gly	
740 745 750	
gcc gag gag ccc cgg gac agc agg cca cgg aag ctg act cgg gcc cag	2422
Ala Glu Glu Pro Arg Asp Ser Arg Pro Arg Lys Leu Thr Arg Ala Gln	
755 760 765	
ctg cag agg atg cgg ggg ccc cac atc att cag ctg gac acc cct ctg	2470
Leu Gln Arg Met Arg Gly Pro His Ile Ile Gln Leu Asp Thr Pro Leu	
770 775 780 785	
tcc gca tca gag gta tga ggaatg cagaggacct ttggcatgca tctctcccag	2524
Ser Ala Ser Glu Val *	
790	
aggagatctc tccccagtag tgctggtcac cctccggcat ctgtgactct acctcaagga	2584
ccacatttcc caaaggaagc ctggcccagg caccctgcct cctgctctgt ttgggggatca	2644
agaactgtaa atttatgtat cataggtgca cctgagcccc acagaaagtt gtgcataaaa	2704
atgactgccc tggctgggca tggctgcctg taatcccagc actttggggag gctgaggtgg	2764
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2860

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cacgtgcata tgatcaactt tggacttctt ttgagattgc caggcgtttg ca atg	175
	Met
	1
gct gct act gtg aac ttg gaa ctt gat ccc att ttt ttg aaa gca cta	223
Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu	
5 10 15	
ggt ttc ttg cat tca aag agt aaa gat tct gct gaa aag cta aaa gca	271
Gly Phe Leu His Ser Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala	
20 25 30	
ctg ctt gat gaa tct ttg gct cgg ggc att gat tcc agt tac cgt cca	319
Leu Leu Asp Glu Ser Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro	
35 40 45	
tct caa aag gat gtg gag cca ccc aaa att tca agc aca aaa aac att	367
Ser Gln Lys Asp Val Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile	
50 55 60 65	
tcc att aag caa gag ccc aaa ata tca tcc agt ctt cct tct ggt aat	415
Ser Ile Lys Gln Glu Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn	
70 75 80	
aat aat ggc aag gtc ctc aca act gaa aag gta aag aag gaa gct gaa	463
Asn Asn Gly Lys Val Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu	
85 90 95	
aag aga cct gct gat aaa atg aaa tca gac atc act gaa gga gtt gat	511
Lys Arg Pro Ala Asp Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp	
100 105 110	
att cca aag aaa cct aga ttg gag aaa cca gaa aca cag tca tct ccc	559
Ile Pro Lys Lys Pro Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro	
115 120 125	
att act gtc caa agt agc aag gat tta cct atg gct gac ctt tcc agt	607
Ile Thr Val Gln Ser Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser	

130	135	140	145	
ttt gag gag acc agt gct gat gat ttt gcc atg gag atg gga ttg gcc				655
Phe Glu Glu Thr Ser Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala	150	155	160	
tgc gtt gtt tgt agg caa atg atg gtg gca tct ggc aat caa tta gta				703
Cys Val Val Cys Arg Gln Met Met Val Ala Ser Gly Asn Gln Leu Val	165	170	175	
gaa tgt cag gag tgc cat aat ctc tac cac cga gat tgt cat aaa ccc				751
Glu Cys Gln Glu Cys His Asn Leu Tyr His Arg Asp Cys His Lys Pro	180	185	190	
cag gtg aca gac aag gaa gcg aat gac cct cgc ctg gtg tgg tat tgt				799
Gln Val Thr Asp Lys Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys	195	200	205	
gcc cga tgt acc aga caa atg aaa aga atg gct caa aaa act cag aaa				847
Ala Arg Cys Thr Arg Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys	210	215	220	225
cca ccg cag aaa cca gcc cct gca gtt gtt tct gta act cca gct gtc				895
Pro Pro Gln Lys Pro Ala Pro Ala Val Val Ser Val Thr Pro Ala Val	230	235	240	
aaa gat cca ttg gtt aag aaa cca gaa act aaa ctg aaa caa gag aca				943
Lys Asp Pro Leu Val Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr	245	250	255	
act ttt cta gcg ttt aag aga aca gaa gtc aag aca tcc aca gtt att				991
Thr Phe Leu Ala Phe Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile	260	265	270	
tca gga aat tct tct agt gcc agc gtt tcc tcg tca gta act agt ggc				1039
Ser Gly Asn Ser Ser Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly	275	280	285	
tta act gga tgg gca gct ttt gca gcc aaa act tcc tct gct ggt cct				1087
Leu Thr Gly Trp Ala Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro	290	295	300	305
tca aca gca aaa ttg agt tca aca aca caa aac aat act ggg aaa cct				1135
Ser Thr Ala Lys Leu Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro	310	315	320	
gct act tcg tca gct aac cag aaa cct gtg ggt ttg act ggt ctg gca				1183
Ala Thr Ser Ser Ala Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala	325	330	335	
aca tca tcc aaa ggt gga ata ggt tcc aaa ata ggt tcc aat aac agc				1231
Thr Ser Ser Lys Gly Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser	340	345	350	
act acg ccc act gta cct tta aaa cca cct cca cct cta acc ttg ggt				1279
Thr Thr Pro Thr Val Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly	355	360	365	

aaa act ggc ctt agt cgc tca gtt agt tgt gac aat gtc agc aaa gta	1327
Lys Thr Gly Leu Ser Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val	
370 375 380 385	
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Gly Leu Pro Ser Pro Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu	
390 395 400	
agt ggg aat gga aat agt gga aca tca gga cct agt gga agt act acc	1423
Ser Gly Asn Gly Asn Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr	
405 410 415	
agc aaa act act tca gaa tcc agc agc tct ccc tca gca tcc ctt aaa	1471
Ser Lys Thr Thr Ser Glu Ser Ser Ser Pro Ser Ala Ser Leu Lys	
420 425 430	
ggc cca act tca caa gaa tca cag ctc aat gct atg aag cga tta cag	1519
Gly Pro Thr Ser Gln Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln	
435 440 445	
atg gtc aag aag aaa gct gcc caa aag aaa ctc aag aag taa tgtggcc	1568
Met Val Lys Lys Lys Ala Ala Gln Lys Lys Leu Lys Lys *	
450 455 460	
aagtagggttt ttgtatcata ttagcctaaa gatgaaaggc ttattattat gatataatct	1628
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tcgccagcga gggatgcgga gacgcccctg aacgacc atg gca tcg gcc gac gag	175
Met Ala Ser Ala Asp Glu	
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ctg acc ttc cat gaa ttc gag gag gcc act aat ctt ctg gct gac acc	223
Leu Thr Phe His Glu Phe Glu Glu Ala Thr Asn Leu Leu Ala Asp Thr	
10 15 20	
cca gat gca gcc acc acc agc aga agc gat cag ctg acc cca caa ggg	271
Pro Asp Ala Ala Thr Thr Ser Arg Ser Asp Gln Leu Thr Pro Gln Gly	
25 30 35	

cac gtg gct gtg gcc gtg ggc tca ggt ggc agc tat gga gcc gag gat	319
His Val Ala Val Ala Val Gly Ser Gly Gly Ser Tyr Gly Ala Glu Asp	
40 45 50	
gag gtg gag gag gag agt gac aag gcc gcg ctc ctg cag gag cag cag	367
Glu Val Glu Glu Glu Ser Asp Lys Ala Ala Leu Leu Gln Glu Gln Gln	
55 60 65 70	
cag cag cag cag ccg gga ttc tgg acc ttc agc tac tat cag agc ttc	415
Gln Gln Gln Gln Pro Gly Phe Trp Thr Phe Ser Tyr Tyr Gln Ser Phe	
75 80 85	
ttt gac gtg gac acc tca cag gtc ctg gac cgg atc aaa ggc tca ctg	463
Phe Asp Val Asp Thr Ser Gln Val Leu Asp Arg Ile Lys Gly Ser Leu	
90 95 100	
ctg ccc cgg cct ggc cac aac ttt gtg cgg cac cat ctg cgg aat cgg	511
Leu Pro Arg Pro Gly His Asn Phe Val Arg His His Leu Arg Asn Arg	
105 110 115	
ccg gat ctg tat ggc ccc ttc tgg atc tgt gcc acg ttg gcc ttt gtc	559
Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala Thr Leu Ala Phe Val	
120 125 130	
ctg gcc gtc act ggc aac ctg acg ctg gtg ctg gcc cag agg agg gac	607
Leu Ala Val Thr Gly Asn Leu Thr Leu Val Leu Ala Gln Arg Arg Asp	
135 140 145 150	
ccc tcc atc cac tac agc ccc cag ttc cac aag gtg acc gtg gca ggc	655
Pro Ser Ile His Tyr Ser Pro Gln Phe His Lys Val Thr Val Ala Gly	
155 160 165	
atc agc atc tac tgc tat gcg tgg ctg gtg ccc ctg gcc ctg tgg ggc	703
Ile Ser Ile Tyr Cys Tyr Ala Trp Leu Val Pro Leu Ala Leu Trp Gly	
170 175 180	
ttc ctg cgg tgg cgc aag ggt gtc cag gag cgc atg ggg ccc tac acc	751
Phe Leu Arg Trp Arg Lys Gly Val Gln Glu Arg Met Gly Pro Tyr Thr	
185 190 195	
ttc ctg gag act gtg tgc atc tac ggc tac tcc ctc ttt gtc ttc atc	799
Phe Leu Glu Thr Val Cys Ile Tyr Gly Tyr Ser Leu Phe Val Phe Ile	
200 205 210	
ccc atg gtg gtc ctg tgg ctc atc cct gtg cct tgg ctg cag tgg ctc	847
Pro Met Val Val Leu Trp Leu Ile Pro Val Pro Trp Leu Gln Trp Leu	
215 220 225 230	
ttt ggg gcg ctg gcc ctg ggc ctg tca gcc gcc ggg ctg gta ttc acc	895
Phe Gly Ala Leu Ala Leu Gly Leu Ser Ala Ala Gly Leu Val Phe Thr	
235 240 245	
ctc tgg ccc gtg gtc cgt gag gac acc agg ctg gtg gcc aca gtg ctg	943
Leu Trp Pro Val Val Arg Glu Asp Thr Arg Leu Val Ala Thr Val Leu	
250 255 260	

ctg tcc gtg gtc gtg ctg ctc cag gcc ctc ctg gcc atg ggc tgt gaa 991  
 Leu Ser Val Val Val Leu Leu Gln Ala Leu Leu Ala Met Gly Cys Glu  
 265 270 275

gtt gga ctt ctt ccg gtg tgc ctc ggg gac gtg gtc ctc ccc cca ttc 1039  
 Val Gly Leu Leu Pro Val Cys Leu Gly Asp Val Val Leu Pro Pro Phe  
 280 285 290

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 Ile Leu Pro \*  
 295

gcccttggac ccttgg 1110

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 Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser Trp Val  
 5 10 15

cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg gcc gtg 152  
 Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala Ala Val  
 20 25 30

gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg agc cga 200  
 Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu Ser Arg  
 35 40 45 50

gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat cac tgg 248  
 Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp His Trp  
 55 60 65

gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc tgg tca 296  
 Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg Trp Ser  
 70 75 80

gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc ttt ggc 344  
 Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala Phe Gly  
 85 90 95

ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg gaa gcc 392  
 Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu Glu Ala



100	105	110	
cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc ggg gcc			440
Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys Gly Ala			
115	120	125	130
acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg ctg gtg			488
Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg Leu Val			
	135	140	145
cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag ccg gcc			536
His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu Pro Gly			
	150	155	160
tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc cat gag			584
Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser His Glu			
	165	170	175
atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cag att ccc cgg			632
Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Gln Ile Pro Arg			
	180	185	190
ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc atg ggg			680
Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly Met Gly			
	195	200	205
cca ggg gag tct gga cag ccg ccc cca gcc tgc tga cccc cagctttcta			730
Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *			
	215	220	
cagacaccag atttgtgaat aaagttgggg aatggacagc ctaactggga cattgcagtg			790
gctgcttgct ggggccggga tttgcagggg aaccaggat ggcaactggcc catagggagc			850
tccaggtgtg gctggctgga cacatgggtca aagtcacaag gccgggagag tgggtgcctt			910
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<400> 63

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agggagccgg tccgccgccg gaacggggagc ctgggtgtgc gtgtggagtc cggactcgtg 180  
 ggagacgatac gcg atg aac acg gtg ctg tcg cgg gcg aac tca ctg ttc 229  
 Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe  
 1 5 10  
 gcc ttc tcg ctg agc gtg atg gcg gcg ctc acc ttc ggc tgc ttc atc 277  
 Ala Phe Ser Leu Ser Val Met Ala Ala Leu Thr Phe Gly Cys Phe Ile  
 15 20 25  
 acc acc gcc ttc aaa gac agg agc gtc ccg gtg cgg ctg cac gtc tcg 325  
 Thr Thr Ala Phe Lys Asp Arg Ser Val Pro Val Arg Leu His Val Ser  
 30 35 40  
 cgg atc ata cta aaa aat gta gaa gat ttc act gga cct aga gaa aga 373  
 Arg Ile Ile Leu Lys Asn Val Glu Asp Phe Thr Gly Pro Arg Glu Arg  
 45 50 55 60  
 agt gat ctg gga ttt atc aca ttt gat ata act gct gat cta gag aat 421  
 Ser Asp Leu Gly Phe Ile Thr Phe Asp Ile Thr Ala Asp Leu Glu Asn  
 65 70 75  
 ata ttt gat tgg aat gtt aag cag ttg ttt ctt tat tta tca gca gaa 469  
 Ile Phe Asp Trp Asn Val Lys Gln Leu Phe Leu Tyr Leu Ser Ala Glu  
 80 85 90  
 tat tca aca aaa aat aat gct ctg aac caa gtt gtc cta tgg gac aag 517  
 Tyr Ser Thr Lys Asn Asn Ala Leu Asn Gln Val Val Leu Trp Asp Lys  
 95 100 105  
 att gtt ttg aga ggt gat aat ccg aag ctg ctg ctg aaa gat atg aaa 565  
 Ile Val Leu Arg Gly Asp Asn Pro Lys Leu Leu Leu Lys Asp Met Lys  
 110 115 120  
 aca aaa tat ttt ttc ttt gac gat gga aat ggt ctc aag gga aac agg 613  
 Thr Lys Tyr Phe Phe Phe Asp Asp Gly Asn Gly Leu Lys Gly Asn Arg  
 125 130 135 140  
 aat gtc act ttg acc ctg tct tgg aac gtc gta cca aat gct gga att 661  
 Asn Val Thr Leu Thr Leu Ser Trp Asn Val Val Pro Asn Ala Gly Ile  
 145 150 155  
 cta cct ctt gtg aca gga tca gga cac gta tct gtc cca ttt cca gat 709  
 Leu Pro Leu Val Thr Gly Ser Gly His Val Ser Val Pro Phe Pro Asp  
 160 165 170  
 aca tat gaa ata acg aag agt tat taa attat tctgaatttg aaacaacata 761  
 Thr Tyr Glu Ile Thr Lys Ser Tyr \*  
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 ggttttgtttt ttggtttttgg g 842

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cattcaggct attttttaggg gaaagaaagc tagaagacat ttaaaaatga tgcatatagc      180
cgcaactctc attcagagga gatttagaac tctaattgatg agaagaagat tcctctctct      240
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cagaatgcac agattacata tgagatatca ggctttgaaa caggcctccg ttgtgatcca      480
acagcaatac caagcaaata gagctgcaaa actgcagagg cagcattatc tcagacaaaag      540
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aaacatgctt caattctaatt tcagcaacat tatcgaacat atagagctgc aaaattgcaa      960
agagaaaatt atatcagaca atggcattct gctgtgggta ttcagggtgc atataaagga     1020

atg aaa gca aga caa ctt tta agg gaa aaa cac aaa gct tct atc gta      1068
Met Lys Ala Arg Gln Leu Leu Arg Glu Lys His Lys Ala Ser Ile Val
  1             5             10            15

ata caa agc acc tac aga atg tat agg cag tat tgt ttc tac caa aag      1116
Ile Gln Ser Thr Tyr Arg Met Tyr Arg Gln Tyr Cys Phe Tyr Gln Lys
             20             25            30

ctt cag tgg gct aca aaa atc ata caa gaa aaa tat aga gca aat aaa      1164
Leu Gln Trp Ala Thr Lys Ile Ile Gln Glu Lys Tyr Arg Ala Asn Lys
             35             40            45

aag aaa cag aaa gta ttt caa cac aat gaa ctt aag aaa gag act tgt      1212

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Lys Leu Glu Thr Gln Lys Cys Ala Ala Leu Arg Ile Gln Phe Phe Leu			
290	295	300	
cag atg gct gtg tat cgg aga aga ttt gtt cag cag aaa aga gct gct			1980
Gln Met Ala Val Tyr Arg Arg Arg Phe Val Gln Gln Lys Arg Ala Ala			
305	310	315	320
atc act tta cag cat tat ttt agg acg tgg caa acc aga aaa cag ttt			2028
Ile Thr Leu Gln His Tyr Phe Arg Thr Trp Gln Thr Arg Lys Gln Phe			
	325	330	335
tta cta tat aga aaa gca gca gtg gtt tta caa aat cac tac aga gca			2076
Leu Leu Tyr Arg Lys Ala Ala Val Val Leu Gln Asn His Tyr Arg Ala			
	340	345	350
ttt ctg tct gca aaa cat caa aga caa gtc tat tta cag atc aga agc			2124
Phe Leu Ser Ala Lys His Gln Arg Gln Val Tyr Leu Gln Ile Arg Ser			
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agt gtt atc att att caa gct aga agt aaa gga ttt ata cag aaa cgg			2172
Ser Val Ile Ile Ile Gln Ala Arg Ser Lys Gly Phe Ile Gln Lys Arg			
	370	375	380
aag ttt cag gaa att aaa aat agc acc ata aaa att cag gct atg tgg			2220
Lys Phe Gln Glu Ile Lys Asn Ser Thr Ile Lys Ile Gln Ala Met Trp			
385	390	395	400
agg aga tat aga gcc aag aaa tat tta tgt aaa gtg aaa gct gcc tgc			2268
Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala Cys			
	405	410	415
aag att caa gcc tgg tat aga tgt tgg aga gca cac aaa gaa tat cta			2316
Lys Ile Gln Ala Trp Tyr Arg Cys Trp Arg Ala His Lys Glu Tyr Leu			
	420	425	430
gct gta tta aaa gct gtt aaa att att caa ggt tgc ttc tat acc aaa			2364
Ala Val Leu Lys Ala Val Lys Ile Ile Gln Gly Cys Phe Tyr Thr Lys			
	435	440	445
cta gag aga aca cgg ttt ttg aat gtg aga gca tca gca att atc att			2412
Leu Glu Arg Thr Arg Phe Leu Asn Val Arg Ala Ser Ala Ile Ile Ile			
	450	455	460
cag aga aaa tgg aga gct ata ctt cct gca aag ata gct cat gaa cac			2460
Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys Ile Ala His Glu His			
465	470	475	480
ttc tta atg ata aaa aga cat cga gct gct tgt ttg atc caa gca cat			2508
Phe Leu Met Ile Lys Arg His Arg Ala Ala Cys Leu Ile Gln Ala His			
	485	490	495
tat aga gga tat aaa gga agg cag gtc tct ctt cgg cag aaa tct gct			2556
Tyr Arg Gly Tyr Lys Gly Arg Gln Val Ser Leu Arg Gln Lys Ser Ala			
	500	505	510

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Ala Leu Ile Ile Gln Lys Tyr Ile Arg Ala Arg Glu Ala Gly Lys His	
515 520 525	
gaa agg ata aaa tat att gaa ttt aaa aaa tct aca gtt atc cta caa	2652
Glu Arg Ile Lys Tyr Ile Glu Phe Lys Lys Ser Thr Val Ile Leu Gln	
530 535 540	
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Ala Leu Val Arg Gly Trp Leu Val Arg Lys Arg Phe Leu Glu Gln Arg	
545 550 555 560	
gcc aaa att cga ctt ctt cac ttc act gca gct gca tat tat cac ctg	2748
Ala Lys Ile Arg Leu Leu His Phe Thr Ala Ala Ala Tyr Tyr His Leu	
565 570 575	
aat gct gtt aga att caa aga gcc tat aaa ctt tac ctg gct gtg aag	2796
Asn Ala Val Arg Ile Gln Arg Ala Tyr Lys Leu Tyr Leu Ala Val Lys	
580 585 590	
aat gct aac aag cag gtt aat tca gtc atc tgt att cag aga tgg ttt	2844
Asn Ala Asn Lys Gln Val Asn Ser Val Ile Cys Ile Gln Arg Trp Phe	
595 600 605	
cga gca aga tta caa gaa aag aga ttt att cag aaa tat cat agc atc	2892
Arg Ala Arg Leu Gln Glu Lys Arg Phe Ile Gln Lys Tyr His Ser Ile	
610 615 620	
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Lys Lys Ile Glu His Glu Gly Gln Glu Cys Leu Ser Gln Arg Asn Arg	
625 630 635 640	
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Ala Ala Ser Val Ile Gln Lys Ala Val Arg His Phe Leu Leu Arg Lys	
645 650 655	
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Lys Gln Glu Lys Phe Thr Ser Gly Ile Ile Lys Ile Gln Ala Leu Trp	
660 665 670	
aga ggc tat tct tgg agg aag aaa aat gat tgt aca aaa att aaa gct	3084
Arg Gly Tyr Ser Trp Arg Lys Lys Asn Asp Cys Thr Lys Ile Lys Ala	
675 680 685	
ata cga cta agt ctt caa gtt gtt aat agg gag att cga gaa gaa aac	3132
Ile Arg Leu Ser Leu Gln Val Val Asn Arg Glu Ile Arg Glu Glu Asn	
690 695 700	
aaa ctc tac aaa aga act gca ctt gca ctt cat tac ctt ttg aca tat	3180
Lys Leu Tyr Lys Arg Thr Ala Leu Ala Leu His Tyr Leu Leu Thr Tyr	
705 710 715 720	
aag cac ctt tct gcc att ctt gag gcc tta aaa cac cta gag gta gtt	3228
Lys His Leu Ser Ala Ile Leu Glu Ala Leu Lys His Leu Glu Val Val	
725 730 735	

act aga ttg tct cca ctt tgt tgt gag aac atg gcc cag agt gga gca	3276
Thr Arg Leu Ser Pro Leu Cys Cys Glu Asn Met Ala Gln Ser Gly Ala	
740 745 750	
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Ile Ser Lys Ile Phe Val Leu Ile Arg Ser Cys Asn Arg Ser Ile Pro	
755 760 765	
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Cys Met Glu Val Ile Arg Tyr Ala Val Gln Val Leu Leu Asn Val Ser	
770 775 780	
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Lys Tyr Glu Lys Thr Thr Ser Ala Val Tyr Asp Val Glu Asn Cys Ile	
785 790 795 800	
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Asp Ile Leu Leu Glu Leu Leu Gln Ile Tyr Arg Glu Lys Pro Gly Asn	
805 810 815	
aaa gtt gca gac aaa ggc gga agc att ttt aca aaa act tgt tgt ttg	3516
Lys Val Ala Asp Lys Gly Gly Ser Ile Phe Thr Lys Thr Cys Cys Leu	
820 825 830	
ttg gct att tta ctg aag aca aca aat aga gcc tct gat gta cga agt	3564
Leu Ala Ile Leu Leu Lys Thr Thr Asn Arg Ala Ser Asp Val Arg Ser	
835 840 845	
agg tcc aaa gtt gtt gac cgt att tac agt ctc tac aaa ctt aca gct	3612
Arg Ser Lys Val Val Asp Arg Ile Tyr Ser Leu Tyr Lys Leu Thr Ala	
850 855 860	
cat aaa cat aaa atg aat act gaa aga ata ctt tac aag caa aag aag	3660
His Lys His Lys Met Asn Thr Glu Arg Ile Leu Tyr Lys Gln Lys Lys	
865 870 875 880	
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Asn Ser Ser Ile Ser Ile Pro Phe Ile Pro Glu Thr Pro Val Arg Thr	
885 890 895	
aga ata gtt tca aga ctt aag cca gat tgg gtt ttg aga aga gat aac	3756
Arg Ile Val Ser Arg Leu Lys Pro Asp Trp Val Leu Arg Arg Asp Asn	
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915 920 925	
acg ctt ggc att cct tat tag ta aatgtaaaca ttttcagtat gtatagtgt	3857
Thr Leu Gly Ile Pro Tyr *	
930 935	
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tgaact	ccaa	gatcaa	atca	cccgt	gatgc	taatag	tttt	aaatct	ctgtg	atcagag	agg	420
tgtac	aggaa	gaaaaa	agtga	agaat	catga	ggatat	tttt	gattgt	ctcta	gggatt	tatt	480
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His Tyr Leu Thr Phe Leu Asn Asp Glu Thr Gln Leu Ser Gln Ala Ile		
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Asn Asp Ser Glu Met Arg Ala Ile Tyr Met Lys Ser Leu Arg Ser Pro		
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Met Met Asn Asn Lys Tyr Lys Met Ile His Lys Thr His Lys Asn Ile		
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Glu Glu Val Cys Val Asp Phe Asn Leu Ile Thr Asp Asp Cys Phe Ala		
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Asn Ser Lys Lys Tyr Lys Thr Arg Arg Ala Val Met Leu Lys Glu Met		
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Met Glu Gln Asn Cys Ala His Ser Lys Lys Lys Leu Ser Arg Ile Ile		
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Leu Pro Asp Asp Ser Ser Glu Glu Glu Asn Asn Val Asn Asp Lys Arg		
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gaa tct aat act gcg gtt aac cca agc act gtt aag aag aac aaa caa	1898	
Glu Ser Asn Thr Ala Val Asn Pro Ser Thr Val Lys Lys Asn Lys Gln		
	175 180 185	
cag gac cat tgt tta aat tca gtg cct tct gga tct tct gcg cag tcc	1946	
Gln Asp His Cys Leu Asn Ser Val Pro Ser Gly Ser Ser Ala Gln Ser		
	190 195 200	
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Lys Val Arg Ser Thr Pro Arg Val Asn Pro Leu Ala Lys Gln Ser Lys		
	205 210 215 220	





Glu	Pro	Ile	Cys	Gln	Ala	Ala	Tyr	Gln	Asn	Asp	Phe	Gly	Gln	Val	Trp	
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cgg	tgg	gtg	aaa	gaa	gac	agc	agc	tat	gcc	aac	gtt	caa	gat	ggc	ttt	450
Arg	Trp	Val	Lys	Glu	Asp	Ser	Ser	Tyr	Ala	Asn	Val	Gln	Asp	Gly	Phe	
			25				30						35			
aat	gga	gac	acg	ccc	ctg	atc	tgt	gct	tgc	agg	cga	ggg	cat	gtg	aga	498
Asn	Gly	Asp	Thr	Pro	Leu	Ile	Cys	Ala	Cys	Arg	Arg	Gly	His	Val	Arg	
			40				45						50			
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Ile	Val	Ser	Phe	Leu	Leu	Arg	Arg	Asn	Ala	Asn	Val	Asn	Leu	Lys	Asn	
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cag	aaa	gag	aga	acc	tgc	ttg	cat	tat	gct	gtg	aag	aaa	aaa	ttt	acc	594
Gln	Lys	Glu	Arg	Thr	Cys	Leu	His	Tyr	Ala	Val	Lys	Lys	Lys	Phe	Thr	
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ttc	att	gat	tat	cta	cta	att	atc	ctc	tta	atg	cct	gtt	ctg	ctt	att	642
Phe	Ile	Asp	Tyr	Leu	Leu	Ile	Ile	Leu	Leu	Met	Pro	Val	Leu	Leu	Ile	
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ggg	tat	ttc	ctc	atg	gta	tca	aag	aca	aag	cag	aat	gag	gct	ctt	gta	690
Gly	Tyr	Phe	Leu	Met	Val	Ser	Lys	Thr	Lys	Gln	Asn	Glu	Ala	Leu	Val	
			105				110						115			
cga	atg	cta	ctt	gat	gct	ggc	gtc	gaa	gtt	aat	gct	aca	gat	tgt	tat	738
Arg	Met	Leu	Leu	Asp	Ala	Gly	Val	Glu	Val	Asn	Ala	Thr	Asp	Cys	Tyr	
			120				125						130			
ggc	tgt	acc	gca	tta	cat	tat	gcc	tgt	gaa	atg	aaa	aac	cag	tct	ctt	786
Gly	Cys	Thr	Ala	Leu	His	Tyr	Ala	Cys	Glu	Met	Lys	Asn	Gln	Ser	Leu	
			135				140						145			150
atc	cct	ctg	ctc	ttg	gaa	gcc	cgt	gca	gac	ccc	aca	ata	aag	aat	aag	834
Ile	Pro	Leu	Leu	Leu	Glu	Ala	Arg	Ala	Asp	Pro	Thr	Ile	Lys	Asn	Lys	
			155				160						165			
cat	ggt	gag	agc	tca	ctg	gat	att	gca	cgg	aga	tta	aaa	ttt	tcc	cag	882
His	Gly	Glu	Ser	Ser	Leu	Asp	Ile	Ala	Arg	Arg	Leu	Lys	Phe	Ser	Gln	
			170				175						180			
att	gaa	tta	atg	cta	agg	aaa	gca	ttg	taa	t	cctt	gtgacc	acacc	gatgg		933
Ile	Glu	Leu	Met	Leu	Arg	Lys	Ala	Leu	*							
			185				190									
agatacagaa aaagttaacg actggattct atcttcattt tagacttttg gtctgtgggc																993
catttaacct ggatgccacc attttatggg gataatgatg cttaccatgg ttaatgtttt																1053
ggaagagctt tttattttata gcattgttta ctacgtcaag ttcaccatgg ccgtaatcct																1113
tctaagggaa aactaaagt tgtttagtc tccatttcag tcagaaactg atgtttcagc																1173
taggcacagt ggtacatgcc tgt																1196

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (209)..(403)

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 gcaaattact taatctcagt aggcctcagt tctctctttc accaaatcag gagaattatt 180  
 tttttaatca tcaactgtac attattat atg caa aac ata ctg gta ggc att 232  
 Met Gln Asn Ile Leu Val Gly Ile  
 1 5  
 atg tgg acc aaa aaa tat gac agc agg tgg tcc ttc cct ttt aag aaa 280  
 Met Trp Thr Lys Lys Tyr Asp Ser Arg Trp Ser Phe Pro Phe Lys Lys  
 10 15 20  
 cta aga tat aca cac atg aag act gct ggt ggt gca agg tgt gga gtc 328  
 Leu Arg Tyr Thr His Met Lys Thr Ala Gly Gly Ala Arg Cys Gly Val  
 25 30 35 40  
 att ggt gcc gtg ata gca gtg tgc agg tca gag cta gag agt cca gag 376  
 Ile Gly Ala Val Ile Ala Val Cys Arg Ser Glu Leu Glu Ser Pro Glu  
 45 50 55  
 aag gga ctt tgc tgt ggg ctg aag tga ccagg aagggctccg tggaggaagt 428  
 Lys Gly Leu Cys Cys Gly Leu Lys \*  
 60 65  
 ggggcccaag gatggacagg acatggatgt ggcaggaaga gggagagcct taccagatgg 488  
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 <213> Homo sapiens

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Ser Lys Tyr Arg Lys Asn Ile Trp Ile Lys Arg Gly Asp Phe Leu Ile  
55 60 65 70

gtt gac ccc att gaa gag gga gaa aag gtg aag gct gaa atc tcg ttt 352  
Val Asp Pro Ile Glu Gly Glu Lys Val Lys Ala Glu Ile Ser Phe  
75 80 85

gtg ctc tgc aag gac cac gtg cgc tct ctg cag aag gag ggg ttt tgg 400  
Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp  
90 95 100

cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga 448  
Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg  
105 110 115

caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag 496  
Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu  
120 125 130

tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga 544  
Ser Ser Ser Glu Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg  
135 140 145 150

cag tat cat gag agt gag gag gag agt gaa gag gag gag gca gcc tga 592  
Gln Tyr His Glu Ser Glu Glu Glu Ser Glu Glu Glu Glu Ala Ala \*  
155 160 165

gactccagga cccaattctc cacttgctca gggactggcc cctggctctt ctgggcttgg 652

acattcccag ggtgctctgc acatcttcac ccctgcatga ggacaaagca gggctcctct 712

ctgaactgat cttttgattc agagaattaa acccctgggtg gggttggtgaa aaaaaaaaaa 772

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aggag atg gcg gag tcg ttg agg tct ccg cgc cgc tcc ctg tac aaa 107  
Met Ala Glu Ser Leu Arg Ser Pro Arg Ser Leu Tyr Lys  
1 5 10

ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg 155  
Leu Val Gly Ser Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu  
15 20 25 30

gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag 203





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cgctgggacg tatgtgccga gggccgcggc gtctgacctc atggcgtaga gcctagcaac	180
agcgcaggct cccagccgag tccggtt atg gcc gct gcc gtc ccg aag agg atg	233
Met Ala Ala Ala Val Pro Lys Arg Met	
1 5	
agg ggg cca gca caa gcg aaa ctg ctg ccc ggg tcg gcc atc caa gcc	281
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala	
10 15 20 25	
ctt gtg ggg ttg gcg cgg ccg ctg gtc ttg gcg ctc ctg ctt gtg tcc	329
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val Ser	
30 35 40	
gcc gct cta tcc agt gtt gta tca cgg act gat tca ccg agc cca acc	377
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr	
45 50 55	
gta ctc aac tca cat att tct acc cca aat gtg aat gct tta aca cat	425
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His	
60 65 70	
gaa aac caa acc aaa cct tct att tcc caa atc agc acc acc ctc cct	473
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro	
75 80 85	
ccc acg acg agt acc aag aaa agt gga gga gca tct gtg gtc cct cat	521
Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro His	
90 95 100 105	
ccc tcg cct act cct ctg tct caa gag gaa gct gat aac aat gaa gat	569
Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu Asp	
110 115 120	
cct agt ata gag gag gag gat ctt ctc atg ctg aac agt tct cca tcc	617
Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro Ser	
125 130 135	
aca gcc aaa gac act cta gac aat ggc gat tat gga gaa cca gac tat	665
Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp Tyr	
140 145 150	
gac tgg acc acg ggc ccc agg gac gac gac gag tct gat gac acc ttg	713
Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr Leu	

155	160	165	
gaa gaa aac agg ggt tac atg gaa att gaa cag tca gtg aaa tct ttt			761
Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser Phe			
170	175	180	185
aag atg cca tcc tca aat ata gaa gag gaa gac agc cat ttc ttt ttt			809
Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe Phe			
	190	195	200
cat ctt att att ttt gct ttt tgc att gct gtt gtt tac att aca tat			857
His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr Tyr			
	205	210	215
cac aac aaa agg aag att ttt ctt ctg gtt caa agc agg aaa tgg cgt			905
His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp Arg			
	220	225	230
gat ggc ctt tgt tcc aaa aca gtg gaa tac cat cgc cta gat cag aat			953
Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln Asn			
	235	240	245
gtt aat gag gca atg cct tct ttg aag att acc aat gat tat att ttt			1001
Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile Phe			
	250	255	260
taa			1004
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<210> 72  
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 <212> DNA  
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aatagtaact ggcctgtttg gatactaaaa ttgaaaataa ctttttagcct cctccttatg	180
atagccgcca gagtaaattg tgagcattac tacagaaaag ccacaaacca agaattctacc	240
tgtttggaag gatcttttgc atctctgaag gtgcttaaag catacttagt gccttttcctt	300
ttaactggga agataaaaga agtatctgtc caagatatta atatgtaaga taacattgta	360
gacatgttct tctgataata caaggtttat tctatttgca ttaggatatt tgtggacatg	420

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tccatctaataataaaggaaa gttttttaat cattgaggca ttaggggctg agttatataa 480
ttagaaaact tctaaagata attggatgag aatatacata ttgacctgta tattatgact 540
aatcatgact cagatcttaa tacagggatg atctcatagc atttagatat cagaaaaggt 600
tttgacctat atgtctttaa tattgtttga atacatgtat aatctttatc attcctcagt 660
gtttcatttc tcaaattctg taaaaggaat ataagaggaa agacaattca tatacaaaga 720
caacgagatt aaaaatatgc agtaggaaaa ataattactt aaggggagat tttttttaca 780
tgaaatctgg gctttggatg tgtgtgtgtg tgtgtgtgtg cacatatgca ctgtggtggg 840
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attaaccaca gaattatagc aggtattcat aacttaagtt tgaaaatcaa tagcgtctgc 1080
aatggatta acagattaga gaatcaacag catcgaaaa taggttaatg catattgctt 1140
ctaacaagtg catgaagaaa tagaagaagc tatgtagctt tcagttctga cagaaaaggg 1200
tgaaggaggg tatcatttca agaaaaaaaa tagctatcac gca atg gtt atc tct 1255
                               Met Val Ile Ser
                               1
gaa aat att tgt att aag atg tgt ata cat ggc cag gca tgg tgg ctc 1303
Glu Asn Ile Cys Ile Lys Met Cys Ile His Gly Gln Ala Trp Trp Leu
  5              10              15              20
atg cct gta atc cca gca ctt tgg gag gca ggt gga tca cga ggt cag 1351
Met Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Gly Ser Arg Gly Gln
          25              30              35
gag atc aag acc atc ctg gcc aac atg gtg aaa cct cat ctc tac taa 1399
Glu Ile Lys Thr Ile Leu Ala Asn Met Val Lys Pro His Leu Tyr  *
          40              45              50
aaatacaaaaa atgagcgggg tgtggtggcc catgcctgta gtcccagctg ctcgggagac 1459
tgaatctctt gagcctggga agcagaggtt gcagtgaact gagatcgct cactgcactc 1519
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<210> 73  
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 <222> (1229)..(1432)

<220>  
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 <223> n = a,t,c or g

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aacaagaaac aataattcta agttagccag ccaatcaaac tacttcagta aatgatcata	180
ctacagcctg gaatcactca aacaaaaaat tcttctagtt ctcttttaaag atattttatcg	240
tttatttttt catgaaacca aagtaattga ttcaacaata ctaacagttc tagcatgcaa	300
caaaccatct actatctaata gtttaattctt cttaacatgt atattttcat tcctataaag	360
tttccataag aagcttgcaa tgacaataaa ggtaaataag tacagttgtc ccttggtatc	420
catgggggat tgggttcctgg accgtcccc caaccacag ataccaaaaa tccaagtata	480
ctcaagtccc ttacataaaa tgacatattt gtatataacc aacgcacatc cgctgtata	540
ctttatccct agactaatac ctaatgcaat gtaaatagcta tttaaataac tgttatactg	600
tatttttatt tgtattattt ttattttttc taatattttt gatctgcaat tggtttaatc	660
cacagatgca gagtacatgg atacagaggg ccaactgttt tgttacaggt acttcaaata	720
gcactacagt acatctttga caaaattttt acaatattcc acctttcaat atgaaacagc	780
ttaaaaaggc atgggtcaaa aataaagtat agtagtatca cttacgcaaa taaagtctca	840
gaatcataca agcacaacac tgtaggact ctccctgttt aggctgggaa aaacattata	900
caaaacattt tcttcaaata aaattacata aattgcttag aaaaatgcca aaatcaataa	960
tttcaaacat attaaggaga aaaccttgaa cattattgga aaatataaac tagttattcc	1020
ttgcttttaa cagatgagtt cttgacaagt tttgtgtaaa gcaaattctg taaaccatta	1080
tcttgcttgc actggaggaa catatctcaa ggaaacctaa gagaaagtg tctttaaagc	1140
atgtgattct cctgtttttg ctggatgtct gtatctacat aataaacagg cacacttcta	1200
catcactggg tatttttactc agactgtc atg ttt cat ctc tgt aaa tta aac	1252
Met Phe His Leu Cys Lys Leu Asn	
1 5	
cca agt tac tta aaa atc acc tgt ggt aaa aga agc aag cag atc acc	1300
Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr	
10 15 20	

ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca	1348
Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser	
25 30 35 40	
ggt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata	1396
Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile	
45 50 55	
gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc	1446
Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly *	
60 65	
ctctttttcag cttagaaaca taacggttca ttccttttat tgctagagaa tgtcattcct	1506
gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt	1566
tgtagtaaag aatatttccc aaatcataac agttctatct ggaatgatac ccacaactct	1626
acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca	1686
aggatcaaaa taaaattctt tagcaataga ctctgcaaa aataaaaact aaaactagac	1746
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aattattccn cctggaaaag gtaaactcat acgtattatg gaaaangcct atgggcactt	1986
agaaaaatat tcttgggtaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc	2046
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 <212> DNA  
 <213> Homo sapiens

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 <222> (267)..(866)

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agcgaccttg gccgttggcc tgaccatctt agtgctgtct gtcgtaacta tcatcatctg	180
cttcacctgc tctgctgct gcctttacaa gacgtgccgc cgaccacgtc cggttgtcac	240
caccaccaca tccaccactg tgggtgc atg ccc ctt atc ctc agc ctc caa gtg	293

Met Pro Leu Ile Leu Ser Leu Gln Val																
1								5								
tgc	cgc	cca	gct	acc	cgt	gga	cca	agc	tac	cag	ggc	tac	cac	acc	atg	341
Cys	Arg	Pro	Ala	Thr	Arg	Gly	Pro	Ser	Tyr	Gln	Gly	Tyr	His	Thr	Met	
10					15					20					25	
ccg	cct	cag	cca	ggg	atg	cca	gca	gcg	acc	cta	ccc	aat	gca	ggg	aag	389
Pro	Pro	Gln	Pro	Gly	Met	Pro	Ala	Ala	Thr	Leu	Pro	Asn	Ala	Gly	Lys	
				30					35					40		
atg	gcg	gac	att	cag	act	gag	cgt	gcc	tac	caa	aag	cag	ccg	acc	atc	437
Met	Ala	Asp	Ile	Gln	Thr	Glu	Arg	Ala	Tyr	Gln	Lys	Gln	Pro	Thr	Ile	
			45					50					55			
ttt	caa	aac	aag	aag	agg	gtc	ctg	ctg	gga	gaa	act	ggc	aag	gag	aag	485
Phe	Gln	Asn	Lys	Lys	Arg	Val	Leu	Leu	Gly	Glu	Thr	Gly	Lys	Glu	Lys	
		60					65					70				
ctc	ccg	cgg	tac	tac	aag	aac	atc	ggt	ctg	ggc	ttc	aag	aca	ccc	aag	533
Leu	Pro	Arg	Tyr	Tyr	Lys	Asn	Ile	Gly	Leu	Gly	Phe	Lys	Thr	Pro	Lys	
	75					80					85					
gag	gct	att	gag	ggc	acc	tac	att	gac	aag	aaa	tgc	ccc	ttc	act	ggt	581
Glu	Ala	Ile	Glu	Gly	Thr	Tyr	Ile	Asp	Lys	Lys	Cys	Pro	Phe	Thr	Gly	
90					95					100					105	
aat	gtg	tcc	att	cga	ggg	cgg	atc	ctc	tct	ggc	gtg	gtg	acc	aag	atg	629
Asn	Val	Ser	Ile	Arg	Gly	Arg	Ile	Leu	Ser	Gly	Val	Val	Thr	Lys	Met	
				110					115					120		
aag	atg	cag	agg	acc	att	gtc	atc	cgc	cga	gac	tat	ctg	cac	tac	atc	677
Lys	Met	Gln	Arg	Thr	Ile	Val	Ile	Arg	Arg	Asp	Tyr	Leu	His	Tyr	Ile	
			125					130					135			
cgc	aag	tac	aac	cgc	ttc	gag	aag	cgc	cac	aag	aac	atg	tct	gta	cac	725
Arg	Lys	Tyr	Asn	Arg	Phe	Glu	Lys	Arg	His	Lys	Asn	Met	Ser	Val	His	
		140					145					150				
ctg	tcc	ccc	tgc	ttc	agg	gac	gtc	cag	atc	ggt	gac	atc	gtc	aca	gtg	773
Leu	Ser	Pro	Cys	Phe	Arg	Asp	Val	Gln	Ile	Gly	Asp	Ile	Val	Thr	Val	
	155					160					165					
ggc	gag	tgc	cgg	cct	ctg	agc	aag	aca	gtg	cgc	ttc	aac	gtg	ctc	aag	821
Gly	Glu	Cys	Arg	Pro	Leu	Ser	Lys	Thr	Val	Arg	Phe	Asn	Val	Leu	Lys	
170					175					180					185	
gtc	acc	aag	gct	gcc	ggc	acc	aag	aag	cag	ttc	cag	aag	ttc	tga	ggc	869
Val	Thr	Lys	Ala	Ala	Gly	Thr	Lys	Lys	Gln	Phe	Gln	Lys	Phe	*		
			190					195					200			
tgga	catcgg	cccgc	tcccc	acaat	gaaat	aaagt	tattt	tctc	attccc	aaaaaaaa						929
aaaa																933

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 <211> 3093  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (446)..(2956)

<400> 75

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cgtgctccac ctctggccct tcaccatcca cgacctgcgg gcactcgggtg ctaagaagtt      180
ctacggggcgc ttctgcaccg gcaccctgga ccacatcagc atcaggcagc tccagctgct      240
tctgctgaag gtagcattgc tgctgggggt ggaaattcac tgggggtgtca ctttcaactgg      300
cctccagccc cctcctagga aggggagtgg ctggcgtgcc cagctccaac ccaaccccc      360
tgcccagctg gccaaactatg aatttgacgt ctttatctcg gctgcaggag gtaaattcgt      420
ccctgaaggc ttcaaagtgc gagaa  atg cga ggc aaa ctg gcc att ggc atc      472
                               Met Arg Gly Lys Leu Ala Ile Gly Ile
                               1                               5

aca gcc aac ttt gtg aat gga cgc acc gtg gag gag aca cag gtg ccg      520
Thr Ala Asn Phe Val Asn Gly Arg Thr Val Glu Glu Thr Gln Val Pro
10                               15                               20                               25

gag atc agt ggt gta gcc agg atc tac aac cag agc ttc ttc cag agc      568
Glu Ile Ser Gly Val Ala Arg Ile Tyr Asn Gln Ser Phe Phe Gln Ser
                               30                               35                               40

ctt ctc aaa gcc aca ggc att gat ctg gag aac att gtg tac tac aag      616
Leu Leu Lys Ala Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys
                               45                               50                               55

gac gac acc cac tac ttt gtg atg aca gcc aag aag cag tgc ctg ctg      664
Asp Asp Thr His Tyr Phe Val Met Thr Ala Lys Lys Gln Cys Leu Leu
60                               65                               70

cgg ctg ggg gtg ctg cgc cag gac tgg cca gac acc aat cgg ctg ctg      712
Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
75                               80                               85

ggc agt gcc aat gtg gtg ccc gag gct ctg cag cgc ttt acc cgg gca      760
Gly Ser Ala Asn Val Val Pro Glu Ala Leu Gln Arg Phe Thr Arg Ala
90                               95                               100                               105

gct gct gac ttt gcc acc cat ggc aag ctc ggg aaa cta gag ttt gcc      808
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
110                               115                               120
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atg Met	atg Met	cgg Arg 140	gca Ala	gag Glu	agt Ser	tct Ser	gct Ala 145	cgt Arg	gtg Val	caa Gln	gag Glu 150	aag Lys	cat His	ggc Gly	gcc Ala	904
cgc Arg	ctg Leu 155	ctg Leu	ctg Leu	gga Gly	ctg Leu	gtg Val 160	ggg Gly	gac Asp	tgc Cys	ctg Leu 165	gtg Val	gag Glu	ccc Pro	ttc Phe	tgg Trp	952
ccc Pro 170	ctg Leu	ggc Gly	act Thr	gga Gly	gtg Val 175	gca Ala	cgg Arg	ggc Gly	ttc Phe 180	ctg Leu	gca Ala	gcc Ala	ttt Phe	gat Asp	gca Ala 185	1000
gcc Ala	tgg Trp	atg Met	gtg Val 190	aag Lys	cgg Arg	tgg Trp	gca Ala	gag Glu	ggc Gly 195	gct Ala	gag Glu	tcc Ser	cta Leu 200	gag Glu	gtg Val	1048
ttg Leu	gct Ala	gag Glu	cgt Arg 205	gag Glu	agc Ser	ctg Leu	tac Tyr	cag Gln 210	ctt Leu	ctg Leu	tca Ser	cag Gln 215	aca Thr	tcc Ser	cca Pro	1096
gaa Glu	aac Asn 220	atg Met	cat His	cgc Arg	aat Asn	gtg Val 225	gcc Ala	cag Gln	tat Tyr	ggg Gly	ctg Leu	gac Asp 230	cca Pro	gcc Ala	acc Thr	1144
cgc Arg	tac Tyr 235	ccc Pro	aac Asn	ctg Leu	aac Asn	ctc Leu 240	cgg Arg	gca Ala	gtg Val	acc Thr 245	ccc Pro	aat Asn	cag Gln	gta Val	cga Arg	1192
gac Asp 250	ctg Leu	tat Tyr	gat Asp	gtg Val 255	cta Leu	gcc Ala	aag Lys	gag Glu	cct Pro 260	gtg Val	cag Gln	agg Arg	aac Asn	aac Asn	gac Asp 265	1240
aag Lys	aca Thr	gat Asp	aca Thr 270	ggg Gly	atg Met	cca Pro	gcc Ala	acc Thr	ggg Gly 275	tcg Ser	gca Ala	ggc Gly	acc Thr 280	cag Gln	gag Glu	1288
gag Glu	ctg Leu	cta Leu	cgc Arg 285	tgg Trp	tgc Cys	cag Gln	gag Glu 290	cag Gln	aca Thr	gct Ala	ggg Gly	tac Tyr 295	ccg Pro	gga Gly	gtc Val	1336
cac His	gtc Val 300	tcc Ser	gat Asp	ttg Leu	tct Ser	tcc Ser	tcc Ser 305	tgg Trp	gct Ala	gat Asp	ggg Gly 310	cta Leu	gct Ala	ctg Leu	tgt Cys	1384
gcc Ala	ctg Leu 315	gtg Val	tac Tyr	cgg Arg	ctg Leu	cag Gln 320	cct Pro	ggc Gly	ctg Leu	ctg Leu 325	gaa Glu	ccc Pro	tca Ser	gag Glu	ctg Leu	1432
cag Gln 330	ggg Gly	ctg Leu	gga Gly	gct Ala	ctg Leu 335	gaa Glu	gca Ala	act Thr	gct Ala 340	tgg Trp	gca Ala	cta Leu	aag Lys	gtg Val	gca Ala 345	1480
gag	aat	gag	ctg	ggc	atc	aca	ccg	gtg	gtg	tct	gca	cag	gcc	gtg	gta	1528



Glu	Asn	Glu	Leu	Gly	Ile	Thr	Pro	Val	Val	Ser	Ala	Gln	Ala	Val	Val	
				350					355					360		
gca	ggg	agt	gac	cca	ctg	ggc	ctc	att	gcc	tac	ctc	agc	cac	ttc	cac	1576
Ala	Gly	Ser	Asp	Pro	Leu	Gly	Leu	Ile	Ala	Tyr	Leu	Ser	His	Phe	His	
			365					370					375			
agt	gcc	ttc	aag	agc	atg	gcc	cac	agc	cca	ggc	cct	gtc	agc	cag	gcc	1624
Ser	Ala	Phe	Lys	Ser	Met	Ala	His	Ser	Pro	Gly	Pro	Val	Ser	Gln	Ala	
		380					385					390				
tcc	cca	ggg	acc	tcc	agt	gct	gta	tta	ttc	ctt	agt	aaa	ctt	cag	agg	1672
Ser	Pro	Gly	Thr	Ser	Ser	Ala	Val	Leu	Phe	Leu	Ser	Lys	Leu	Gln	Arg	
	395					400					405					
acc	ctg	cag	cga	tcc	cgg	gcc	aag	gaa	aat	gca	gag	gat	gct	ggt	ggc	1720
Thr	Leu	Gln	Arg	Ser	Arg	Ala	Lys	Glu	Asn	Ala	Glu	Asp	Ala	Gly	Gly	
410					415				420					425		
aag	aag	ctg	cgc	ttg	gag	atg	gag	gcc	gag	acc	cca	agt	act	gag	gtg	1768
Lys	Lys	Leu	Arg	Leu	Glu	Met	Glu	Ala	Glu	Thr	Pro	Ser	Thr	Glu	Val	
				430					435					440		
cca	cct	gac	cca	gag	cct	ggg	gta	ccc	ctg	aca	ccc	cca	tcc	caa	cac	1816
Pro	Pro	Asp	Pro	Glu	Pro	Gly	Val	Pro	Leu	Thr	Pro	Pro	Ser	Gln	His	
			445					450					455			
cag	gag	gcc	ggg	gct	ggg	gac	ctg	tgt	gca	ctt	tgt	ggg	gaa	cac	ctc	1864
Gln	Glu	Ala	Gly	Ala	Gly	Asp	Leu	Cys	Ala	Leu	Cys	Gly	Glu	His	Leu	
		460					465					470				
tat	gtc	ctg	gaa	cgc	ctc	tgt	gtc	aac	ggc	cat	ttc	ttc	cac	cgg	agc	1912
Tyr	Val	Leu	Glu	Arg	Leu	Cys	Val	Asn	Gly	His	Phe	Phe	His	Arg	Ser	
	475					480					485					
tgc	ttc	cgc	tgc	cat	acc	tgt	gag	gcc	aca	ctg	tgg	cca	ggt	ggc	tac	1960
Cys	Phe	Arg	Cys	His	Thr	Cys	Glu	Ala	Thr	Leu	Trp	Pro	Gly	Gly	Tyr	
490					495				500					505		
gag	cag	cac	cca	gga	gat	gga	cat	tcc	tac	tgc	ctc	cag	cac	ctg	ccc	2008
Glu	Gln	His	Pro	Gly	Asp	Gly	His	Ser	Tyr	Cys	Leu	Gln	His	Leu	Pro	
			510						515					520		
cag	aca	gac	cac	aaa	gag	gaa	ggc	agc	gat	aga	ggc	cct	gag	agt	ccg	2056
Gln	Thr	Asp	His	Lys	Glu	Glu	Gly	Ser	Asp	Arg	Gly	Pro	Glu	Ser	Pro	
			525					530					535			
gag	ctc	ccc	aca	cca	agt	gag	aat	agc	atg	cca	cca	ggc	ctc	tca	act	2104
Glu	Leu	Pro	Thr	Pro	Ser	Glu	Asn	Ser	Met	Pro	Pro	Gly	Leu	Ser	Thr	
		540					545					550				
ccc	aca	gcc	tcg	cag	gag	ggg	gcc	ggg	cct	gtt	cca	gat	ccc	agc	cag	2152
Pro	Thr	Ala	Ser	Gln	Glu	Gly	Ala	Gly	Pro	Val	Pro	Asp	Pro	Ser	Gln	
	555					560					565					
ccc	acc	cgt	cgg	cag	atc	cgc	ctc	tcc	agc	ccg	gag	cgc	cag	cgg	ttg	2200
Pro	Thr	Arg	Arg	Gln	Ile	Arg	Leu	Ser	Ser	Pro	Glu	Arg	Gln	Arg	Leu	

570	575	580	585	
tcc tcc ctt aac ctt acc cct gac ccg gaa atg gag cct cca ccc aag				2248
Ser Ser Leu Asn Leu Thr Pro Asp Pro Glu Met Glu Pro Pro Pro Lys	590	595	600	
cct ccc cgc agc tgc tcc gcc ttg gcc cgc cac gcc ctg gag agc agc				2296
Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala Leu Glu Ser Ser	605	610	615	
ttt gtg ggc tgg ggc ctg cca gtc cag agc cct caa gct ctt gtg gcc				2344
Phe Val Gly Trp Gly Leu Pro Val Gln Ser Pro Gln Ala Leu Val Ala	620	625	630	
atg gag aag gag gaa aaa gag agt ccc ttc tcc agt gaa gag gaa gaa				2392
Met Glu Lys Glu Glu Lys Glu Ser Pro Phe Ser Ser Glu Glu Glu Glu	635	640	645	
gaa gat gtg cct ttg gac tca gat gtg gaa cag gcc ctg cag acc ttt				2440
Glu Asp Val Pro Leu Asp Ser Asp Val Glu Gln Ala Leu Gln Thr Phe	650	655	660	665
gcc aag acc tca ggc acc atg aat aac tac cca aca tgg cgt cgg act				2488
Ala Lys Thr Ser Gly Thr Met Asn Asn Tyr Pro Thr Trp Arg Arg Thr	670	675	680	
ctg ctg cgc cgt gcg aag gag gag gag atg aag agg ttc tgc aag gcc				2536
Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg Phe Cys Lys Ala	685	690	695	
cag acc atc caa cgg cga cta aat gag att gag gct gcc ttg agg gag				2584
Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala Ala Leu Arg Glu	700	705	710	
cta gag gcc gag ggc gtg aag ctg gag ctg gcc ttg agg cgc cag agc				2632
Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu Arg Arg Gln Ser	715	720	725	
agt tcc cca gaa cag caa aag aaa cta tgg gta gga cag ctg cta cag				2680
Ser Ser Pro Glu Gln Gln Lys Lys Leu Trp Val Gly Gln Leu Leu Gln	730	735	740	745
ctc gtt gac aag aaa aac agc ctg gtg gct gag gag gcc gag ctc atg				2728
Leu Val Asp Lys Lys Asn Ser Leu Val Ala Glu Glu Ala Glu Leu Met	750	755	760	
atc acg gtg cag gaa ttg aat ctg gag gag aaa cag tgg cag ctg gac				2776
Ile Thr Val Gln Glu Leu Asn Leu Glu Glu Lys Gln Trp Gln Leu Asp	765	770	775	
cag gag cta cga ggc tac atg aac cgg gaa gaa aac cta aag aca gct				2824
Gln Glu Leu Arg Gly Tyr Met Asn Arg Glu Glu Asn Leu Lys Thr Ala	780	785	790	
gct gat cgg cag gct gag gac cag gtc ctg agg aag ctg gtg gat ttg				2872
Ala Asp Arg Gln Ala Glu Asp Gln Val Leu Arg Lys Leu Val Asp Leu	795	800	805	

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100 105 110	
aag gcg gga aaa tgg gaa gtc cct ctg cct aaa gta cgt gcc cag gga	562
Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly	
115 120 125	
gaa aca gaa gta tta aaa gtt att cga aca gga aag aga aag aag aag	610
Glu Thr Glu Val Leu Lys Val Ile Arg Thr Gly Lys Arg Lys Lys Lys	
130 135 140	
gca tgg aag aga atg gtt act aaa gtg tgc ttt gtt gga gat ggc ttt	658
Ala Trp Lys Arg Met Val Thr Lys Val Cys Phe Val Gly Asp Gly Phe	
145 150 155 160	
aca aga aaa cca cct aaa tat gaa aga ttc atc agg cca atg ggc ttg	706
Thr Arg Lys Pro Pro Lys Tyr Glu Arg Phe Ile Arg Pro Met Gly Leu	
165 170 175	
cgt ttc aag aaa gcc cat gta aca cat cct gaa ctg aaa gcc acc ttt	754
Arg Phe Lys Lys Ala His Val Thr His Pro Glu Leu Lys Ala Thr Phe	
180 185 190	
tgc cta cca ata ctt ggt gta aag aag aat ccc tca tcc cca ctg tat	802
Cys Leu Pro Ile Leu Gly Val Lys Lys Asn Pro Ser Ser Pro Leu Tyr	
195 200 205	
aca act ttg ggt gtt att acc aaa ggt act gtc att gaa gta aat gtg	850
Thr Thr Leu Gly Val Ile Thr Lys Gly Thr Val Ile Glu Val Asn Val	
210 215 220	
agc gaa ttg ggc ctt gtg aca caa gga ggc aaa gtt att tgg gga aaa	898
Ser Glu Leu Gly Leu Val Thr Gln Gly Gly Lys Val Ile Trp Gly Lys	
225 230 235 240	
tat gcc cag gtt acc aac aat cct gaa aat gat gga tgt ata aat gca	946
Tyr Ala Gln Val Thr Asn Asn Pro Glu Asn Asp Gly Cys Ile Asn Ala	
245 250 255	
gtc tta ctg gtt tga cagcaatttc atatataatt attgaggact acacaccaat	1001
Val Leu Leu Val *	
260	
tgaagaaact gccattactg tgatgtttct gaatactacc aaacagccat acatgtctgc	1061
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<220>

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	1 5	
agt gct tcc ctt att gac aga acc atc aag atg aga aaa gaa aca gag	100	
Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys Glu Thr Glu		
10 15 20		
gct agg aaa gtg gtc tta gcc tgg gga ctc cta aat gta tct atg gct	148	
Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val Ser Met Ala		
25 30 35 40		
gga atg ata tat act gaa atg act gga aaa ttg att agt tca tac tac	196	
Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr Tyr		
45 50 55		
aat gtg aca tac tgg ccc ctc tgg tat att gag ctt gcc ctt gca tct	244	
Asn Val Thr Tyr Trp Pro Leu Trp Tyr Ile Glu Leu Ala Leu Ala Ser		
60 65 70		
ctc ttc agc ctt aat gcc tta ttt gat ttt tgg aga tat ttc aaa tat	292	
Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg Tyr Phe Lys Tyr		
75 80 85		
act gtg gca cca aca agt ctg gtt gtt agt cct gga cag caa aca ctt	340	
Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly Gln Gln Thr Leu		
90 95 100		
tta ggg ttg aaa aca gct gtt gta cag act acg cct cca cat gat ctg	388	
Leu Gly Leu Lys Thr Ala Val Val Gln Thr Thr Pro Pro His Asp Leu		
105 110 115 120		
gca gca acc caa atc cct ccc gct cca cct tcc cct tca att cag ggt	436	
Ala Ala Thr Gln Ile Pro Pro Ala Pro Pro Ser Pro Ser Ile Gln Gly		
125 130 135		
cag agt gtg ttg agt tat agc cct tct cgt tcg ccc agt acc agt ccc	484	
Gln Ser Val Leu Ser Tyr Ser Pro Ser Arg Ser Pro Ser Thr Ser Pro		
140 145 150		
aag ttc acc acc agc tgt atg act ggt tac agc cct cag ctg caa ggt	532	
Lys Phe Thr Thr Ser Cys Met Thr Gly Tyr Ser Pro Gln Leu Gln Gly		
155 160 165		
ctg tcc tca ggt ggc agt ggt tct tat agc cct gga gtg acc tac tcg	580	
Leu Ser Ser Gly Gly Ser Gly Ser Tyr Ser Pro Gly Val Thr Tyr Ser		
170 175 180		
ccc gtc agt ggt tat aat aag ttg gcg agc ttt agc ccc tct cct cct	628	
Pro Val Ser Gly Tyr Asn Lys Leu Ala Ser Phe Ser Pro Ser Pro Pro		
185 190 195 200		
tct ccg tac cct acc act gtt gga cca gtg gag agc agt gga ttg aga	676	

Ser	Pro	Tyr	Pro	Thr	Thr	Val	Gly	Pro	Val	Glu	Ser	Ser	Gly	Leu	Arg		
				205					210					215			
tct	cgc	tac	cgt	tct	tca	cct	acc	gtc	tac	aac	tca	cct	act	gac	aaa		724
Ser	Arg	Tyr	Arg	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Pro	Thr	Asp	Lys		
			220					225					230				
gaa	gac	tac	atg	acc	gac	cta	cga	act	ttg	gat	act	ttt	ctc	aga	agt		772
Glu	Asp	Tyr	Met	Thr	Asp	Leu	Arg	Thr	Leu	Asp	Thr	Phe	Leu	Arg	Ser		
		235					240					245					
gaa	gag	gag	aaa	cag	cat	agg	gtt	aag	ctg	ggg	agc	cca	gat	tct	acc		820
Glu	Glu	Glu	Lys	Gln	His	Arg	Val	Lys	Leu	Gly	Ser	Pro	Asp	Ser	Thr		
	250					255					260						
tct	cct	tcc	agc	agt	cct	act	ttc	tgg	aac	tat	agt	cgt	tct	atg	ggg		868
Ser	Pro	Ser	Ser	Ser	Pro	Thr	Phe	Trp	Asn	Tyr	Ser	Arg	Ser	Met	Gly		
265					270				275						280		
gat	tat	gca	caa	act	tta	aag	aag	ttt	cag	tat	cag	ctt	gcc	tgt	agg		916
Asp	Tyr	Ala	Gln	Thr	Leu	Lys	Lys	Phe	Gln	Tyr	Gln	Leu	Ala	Cys	Arg		
				285				290						295			
tct	cag	gcc	cca	tgt	gct	aac	aaa	gat	gaa	gcc	gat	ctc	agc	tct	aaa		964
Ser	Gln	Ala	Pro	Cys	Ala	Asn	Lys	Asp	Glu	Ala	Asp	Leu	Ser	Ser	Lys		
			300					305					310				
caa	gcc	gca	gaa	gag	gtc	tgg	gca	aga	gtg	gct	atg	aat	aga	caa	ctt		1012
Gln	Ala	Ala	Glu	Glu	Val	Trp	Ala	Arg	Val	Ala	Met	Asn	Arg	Gln	Leu		
		315					320					325					
ctt	gat	cat	atg	gat	tca	tgg	aca	gct	aaa	ttt	aga	aat	tgg	atc	aat		1060
Leu	Asp	His	Met	Asp	Ser	Trp	Thr	Ala	Lys	Phe	Arg	Asn	Trp	Ile	Asn		
	330					335					340						
gag	aca	ata	tta	gtg	cca	ctt	gtt	caa	gag	att	gag	tct	gtc	agc	aca		1108
Glu	Thr	Ile	Leu	Val	Pro	Leu	Val	Gln	Glu	Ile	Glu	Ser	Val	Ser	Thr		
345				350					355						360		
cag	atg	aga	cga	atg	ggg	tgt	cca	gag	cta	cag	ata	gga	gag	gct	agt		1156
Gln	Met	Arg	Arg	Met	Gly	Cys	Pro	Glu	Leu	Gln	Ile	Gly	Glu	Ala	Ser		
				365					370					375			
att	act	agc	ttg	aaa	caa	gct	gcc	ctg	gtt	aaa	gcg	cct	ctc	att	ccg		1204
Ile	Thr	Ser	Leu	Lys	Gln	Ala	Ala	Leu	Val	Lys	Ala	Pro	Leu	Ile	Pro		
			380					385					390				
act	ttg	aac	aca	atc	gtt	cag	tat	cta	gac	ctt	act	cca	aat	cag	gaa		1252
Thr	Leu	Asn	Thr	Ile	Val	Gln	Tyr	Leu	Asp	Leu	Thr	Pro	Asn	Gln	Glu		
		395				400						405					
tac	ttg	ttt	gaa	agg	atc	aaa	gaa	cta	tct	cag	gga	ggg	tgt	atg	agc		1300
Tyr	Leu	Phe	Glu	Arg	Ile	Lys	Glu	Leu	Ser	Gln	Gly	Gly	Cys	Met	Ser		
	410					415					420						
tca	ttt	cga	tgg	aac	aga	ggg	ggc	gac	ttc	aaa	gga	cga	aag	tgg	gat		1348
Ser	Phe	Arg	Trp	Asn	Arg	Gly	Gly	Asp	Phe	Lys	Gly	Arg	Lys	Trp	Asp		

425	430	435	440	
aca gac ctg ccc acc gat tct gct atc atc atg cat gta ttt tgc acc				1396
Thr Asp Leu Pro Thr Asp Ser Ala Ile Ile Met His Val Phe Cys Thr	445	450	455	
tac ctt gat tcc aga tta cct cca cat ccg aag tat ccc gac gga aaa				1444
Tyr Leu Asp Ser Arg Leu Pro Pro His Pro Lys Tyr Pro Asp Gly Lys	460	465	470	
act ttt act tct cag cac ttt gtt cag aca cca aat aaa cca gat gtt				1492
Thr Phe Thr Ser Gln His Phe Val Gln Thr Pro Asn Lys Pro Asp Val	475	480	485	
aca aat gag aat gtt ttt tgc att tat cag agt gct atc aac cct ccc				1540
Thr Asn Glu Asn Val Phe Cys Ile Tyr Gln Ser Ala Ile Asn Pro Pro	490	495	500	
cat tat gag ctg atc tac cag cgt cat gta tac aac ctg cca aag ggc				1588
His Tyr Glu Leu Ile Tyr Gln Arg His Val Tyr Asn Leu Pro Lys Gly	505	510	515	520
aga aat aat atg ttt cat aca ttg ttg atg ttt ctg tac atc ata aag				1636
Arg Asn Asn Met Phe His Thr Leu Leu Met Phe Leu Tyr Ile Ile Lys	525	530	535	
acc aaa gag tca gga atg ctt ggg aga gtt aat ctt ggt cta tct ggt				1684
Thr Lys Glu Ser Gly Met Leu Gly Arg Val Asn Leu Gly Leu Ser Gly	540	545	550	
gtg aat ata ttg tgg atc ttt ggc gag tag c aagtcataata tttaattctg				1735
Val Asn Ile Leu Trp Ile Phe Gly Glu *	555	560		
acatttagac tatttcactg aaccagaagt cgaaactaaa catctctgag ccactgactc				1795
ttctgaaata aaatacacat ggggtgtaaaa aaaaaaaaaa				1835

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 <212> DNA  
 <213> Homo sapiens

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aattgaagaa aaaaggccaa gttaaaatag gaaaacaaat ggttttcatt tgggtggcagt	180

tgaaatcaaa gtatacatgt gtatacattc taatccgtca tctatcccat gtggcatttt	240
ccaagggtttt aagagtctac caggccaaac cctttgccac tttcactgct tttgctttgc	300
ttttcccctt tcttttctct cgctttgcct tcagcctttt tctttgcctt tggttcatcc	360
atattgggta ctgtccatgc tggtcggcgt gagcgtgagg tgtgggtggt cgtttctcag	420
gtaaaac atg gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt	469
Met Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg	
1 5 10	
gct gaa aag aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa	517
Ala Glu Lys Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys	
15 20 25 30	
agt att ctc aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag	565
Ser Ile Leu Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu	
35 40 45	
ata gca act gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg	613
Ile Ala Thr Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met	
50 55 60	
caa tgt gag gta aaa gat gaa aaa gat gac atg aaa atg gag act gat	661
Gln Cys Glu Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp	
65 70 75	
att aag aga aac aaa aag act ctt cta gac cag cat gga cag tac cca	709
Ile Lys Arg Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro	
80 85 90	
ata tgg atg aac caa agg caa aga aaa agg ctg aag gca aag cga gag	757
Ile Trp Met Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu	
95 100 105 110	
aaa aga aag ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt	805
Lys Arg Lys Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly	
115 120 125	
ttg gcc tgg tag act cttaaaacct tggaaaatgc cacatgggat agatgacgga	860
Leu Ala Trp *	
130	
ttagaatgta tacacatgta tacttttgatt tcaactgccca ccaaataaaa accatttggt	920
ttcctatttt aacttggcct tttttcttca attcaaacc cgcataactc ctcaagtttg	980
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<210> 79

<211> 5476

<212> DNA

<213> Homo sapiens



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 <222> (188)..(5149)

<400> 79

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Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr	
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Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala	
225 230 235	
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Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln *	
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agggccaggg gaatagagct attttttttaa caaaacaaaa tgaagacaaa aatatggact	1192
gatgtatcct cgcttgact cagggcaggt gccgtgggtt ctccagagac cccagcacct	1252
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tct tcc cga atg gtg gtg cca aag gca gcc att tac caa aca cag gcc Ser Ser Arg Met Val Val Pro Lys Ala Ala Ile Tyr Gln Thr Gln Ala 220 225 230			962
ttc tat gcc aaa ggg aaa atg aag gaa gta aaa cag ctt gtg gct aac Phe Tyr Ala Lys Gly Lys Met Lys Glu Val Lys Gln Leu Val Ala Asn 235 240 245			1010
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aag ttg ctg aaa att cca cca gtt tct ccc tct atc ctc gac tgt agt Lys Leu Leu Lys Ile Pro Pro Val Ser Pro Ser Ile Leu Asp Cys Ser 270 275 280			1106
ata atc cgc gtg gaa tat tca cta atg gta tat gtg gat att cct gga Ile Ile Arg Val Glu Tyr Ser Leu Met Val Tyr Val Asp Ile Pro Gly 285 290 295			1154
gct atg gat tta ttt ctt aat ttg cca ctt gtc atc ggt acc att cct Ala Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro 300 305 310			1202
cta cat cca ttt ggt agc aga acc tca agt gta agc agt cag tgt agc Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser 315 320 325			1250
atg aat atg aac tgg ctc agt tta tca ctt cct gaa aga cct gaa gca Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu Arg Pro Glu Ala 330 335 340 345			1298
cca ccc agc tat gca gaa gtg gta aca gag gaa caa agg cgg aac aat Pro Pro Ser Tyr Ala Glu Val Val Thr Glu Glu Gln Arg Arg Asn Asn 350 355 360			1346
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cca ctg ttt gca tat atc cag gag ttt cga ttc ttg cct cca cct ctt Pro Leu Phe Ala Tyr Ile Gln Glu Phe Arg Phe Leu Pro Pro Pro Leu 380 385 390			1442
tat tca gag att gat cca aat cct gat cag tca gca gat gat aga cca Tyr Ser Glu Ile Asp Pro Asn Pro Asp Gln Ser Ala Asp Asp Arg Pro 395 400 405			1490
tcc tgc ccc tct cgt tga aggaac acttggttga atcaagttga tgtgggttcc Ser Cys Pro Ser Arg * 410 415			1544

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gaactgtatc tcttccggct gaggacagag aagtatcttg gagacacggt tcagaggaag 1604
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tttaaaactg gcacatactc agagcagtct tcttagccta tggtcgtacg tgtcaagaca 1784
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agtgtaaacta tatccccacc tctgcttgct ttctttccct cccctccaat gataaagaaa 180
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ttattcaggt tctaaccctt tgctgtacac aagcagacag aaatgcatct gttacataaa 480
tgagaaaaaag ctattatgct gatggagc atg ctt ttt aaa tcc ttt aaa aac 532
Met Leu Phe Lys Ser Phe Lys Asn
1 5

act cac cat ata aac ttg cat ttg agc ttg tgt gtt ctt ttg tta atg 580
Thr His His Ile Asn Leu His Leu Ser Leu Cys Val Leu Leu Leu Met
10 15 20

tgt aga gtt ctc ctt tct cga aat tgc cag tgt gta ctt ggc tta act 628
Cys Arg Val Leu Leu Ser Arg Asn Cys Gln Cys Val Leu Gly Leu Thr
25 30 35 40

caa gaa cag ttt ctt ctg gat tcc tta ttt gat tta ttt aac cta att 676
Gln Glu Gln Phe Leu Leu Asp Ser Leu Phe Asp Leu Phe Asn Leu Ile
45 50 55

ata ttc taa tattgca aatattacca taagtgggta aaagtaaaat tcctcttctg 732

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Ile Phe \*

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gcaactgcag gggctcgaga ccagccagca gtatctcatc cttcgataca ggggatatac 180  
tgtacagtcc tttttctaga agtgagacat acaagattac tctacaagag gaagattcca 240  
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atctaaaaca aagttctgtg ttaatgagtt acagaattca cgtggaagtc aatgtcactt 360  
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ataaggaaat tttctccttg aaatcacgat accaaatagg aaaa atg atc tac aag 596  
Met Ile Tyr Lys  
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tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg 644  
Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met  
5 10 15 20  
cat cag aaa att cac aca gct gag aag ccc cat aaa tgt gac aag tgt 692  
His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys  
25 30 35  
gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac 740  
Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp  
40 45 50  
cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt 788  
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe  
55 60 65



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Ser Thr Thr Thr Lys Leu Asn Arg His Lys Lys Ile His Thr Val Glu	
70 75 80	
aag ccc tat aaa tgt tac gag tgt ggc aaa gcc ttc aat tgg agc tcc	884
Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe Asn Trp Ser Ser	
85 90 95 100	
cat ctt caa att cat atg aga gtt cat aca ggt gag aaa ccg tat gtc	932
His Leu Gln Ile His Met Arg Val His Thr Gly Glu Lys Pro Tyr Val	
105 110 115	
tgt agt gag tgt gga agg ggc ttt agt aat agt tca aac ctt tgc atg	980
Cys Ser Glu Cys Gly Arg Gly Phe Ser Asn Ser Ser Asn Leu Cys Met	
120 125 130	
cat cag aga gtc cac acc gga gag aag ccc ttt aaa tgt gaa gag tgt	1028
His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys Cys Glu Glu Cys	
135 140 145	
ggg aag gcc ttc agg cac acc tcc agc ctc tgc atg cat caa aga gtc	1076
Gly Lys Ala Phe Arg His Thr Ser Ser Leu Cys Met His Gln Arg Val	
150 155 160	
cac aca gga gag aaa ccc tat aaa tgt tat gag tgt ggg aag gcg ttc	1124
His Thr Gly Glu Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe	
165 170 175 180	
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Ser Gln Ser Ser Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu	
185 190 195	
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Lys Pro Tyr Arg Cys Cys Gly Cys Gly Lys Ala Phe Ser Gln Ser Ser	
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Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys	
215 220 225	
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Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Ser Leu Cys Ile	
230 235 240	
cac cag aga gtc cac aca aag gag aga aac cat ctc aaa ata tca gtt	1364
His Gln Arg Val His Thr Lys Glu Arg Asn His Leu Lys Ile Ser Val	
245 250 255 260	
ata taa aacgttttgc taagagttta aaatcttaaa acccataagt gccactagga	1420
Ile *	
aggaaaccct gtatatacct acattgaccc aagaaatatt tacgcaatcc ctagcagaac	1480
attgtttctg aggaggcata tgtgagattg atttgttggt tcatgcccaag tgtgttccac	1540

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<212> DNA
<213> Homo sapiens

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<220>
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<222> (66)..(1382)

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Asp	Lys	Asn	Thr	Leu	Lys	Asp	His	Met	Arg	Lys	Lys	Gln	His	Arg	Lys	
			225					230					235			
att	aat	cct	aag	aac	aga	gaa	tat	gac	aga	ttt	tat	gtc	atc	aat	tat	827
Ile	Asn	Pro	Lys	Asn	Arg	Glu	Tyr	Asp	Arg	Phe	Tyr	Val	Ile	Asn	Tyr	
			240					245					250			
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Leu	Glu	Leu	Gly	Lys	Ser	Trp	Glu	Glu	Val	Gln	Leu	Glu	Asp	Asp	Arg	
255						260					265				270	
gag	ttg	ctg	gac	cat	cag	gaa	gat	gac	tgg	tct	gat	tgg	gaa	gaa	cac	923
Glu	Leu	Leu	Asp	His	Gln	Glu	Asp	Asp	Trp	Ser	Asp	Trp	Glu	Glu	His	
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cct	gcc	tct	gca	gtc	tgc	tta	ttt	tgt	gaa	aag	caa	gca	gaa	aca	att	971
Pro	Ala	Ser	Ala	Val	Cys	Leu	Phe	Cys	Glu	Lys	Gln	Ala	Glu	Thr	Ile	
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Glu	Lys	Leu	Tyr	Val	His	Met	Glu	Asp	Ala	His	Glu	Phe	Asp	Leu	Leu	
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aaa	ata	aag	tca	gaa	ctt	gga	tta	aat	ttc	tat	cag	caa	gtg	aaa	ctg	1067
Lys	Ile	Lys	Ser	Glu	Leu	Gly	Leu	Asn	Phe	Tyr	Gln	Gln	Val	Lys	Leu	
				320			325					330				
gtc	aat	ttt	att	cgg	agg	caa	gtt	cac	caa	tgc	aga	tgt	tat	ggc	tgc	1115
Val	Asn	Phe	Ile	Arg	Arg	Gln	Val	His	Gln	Cys	Arg	Cys	Tyr	Gly	Cys	
335					340					345					350	
cat	gtg	aag	ttc	aaa	tcc	aaa	gca	gac	tta	aga	act	cac	atg	gaa	gaa	1163
His	Val	Lys	Phe	Lys	Ser	Lys	Ala	Asp	Leu	Arg	Thr	His	Met	Glu	Glu	
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act	aaa	cac	act	tcg	ctg	ctc	ccc	gat	aga	aag	acg	tgg	gat	caa	ctg	1211
Thr	Lys	His	Thr	Ser	Leu	Leu	Pro	Asp	Arg	Lys	Thr	Trp	Asp	Gln	Leu	
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gag	tat	tat	ttt	cca	acc	tat	gaa	aat	gac	act	ctc	ctg	tgt	aca	cta	1259
Glu	Tyr	Tyr	Phe	Pro	Thr	Tyr	Glu	Asn	Asp	Thr	Leu	Leu	Cys	Thr	Leu	
				385				390					395			
tct	gac	agt	gaa	agt	gac	ctg	aca	gct	cag	gaa	caa	aat	gaa	aat	gtt	1307
Ser	Asp	Ser	Glu	Ser	Asp	Leu	Thr	Ala	Gln	Glu	Gln	Asn	Glu	Asn	Val	
				400			405						410			
ccc	atc	atc	agt	gaa	gat	aca	tct	aaa	ctg	tat	gct	ttg	aaa	caa	agc	1355
Pro	Ile	Ile	Ser	Glu	Asp	Thr	Ser	Lys	Leu	Tyr	Ala	Leu	Lys	Gln	Ser	
415					420					425					430	
agt	att	ttg	aac	cag	ttg	cta	cta	taa	gagta	cttgaaaacc	tagaagaaac					1407
Ser	Ile	Leu	Asn	Gln	Leu	Leu	Leu	*								

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Met Glu Ala Leu Asn Thr Ala Gln Gly Ala Arg Asp Phe Ile Tyr Ser  
1 5 10 15  
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Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe  
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Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr  
35 40 45  
cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata 250  
Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile  
50 55 60  
ggg ttt ggc ttt ttg gat aat gca att atg att gtt gct gga acc cat 298  
Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His  
65 70 75 80  
att gaa atg tct att gga att att ttg gga att tca act atg gca gct 346  
Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala  
85 90 95  
gct gct ttg gga aat ctt gtg tca gat cta gct gga ctt gga ctt gca 394  
Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala  
100 105 110  
ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat 442  
Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp  
115 120 125

ctc aca cca aag caa gtt gac atg tgg caa aca cgt ctt agt aca cat 490  
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cct tta att ttc ttt gga gga ggt gaa gaa gat gaa aaa ctg gaa acg 586  
 Pro Leu Ile Phe Phe Gly Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr  
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 Lys Ser \*

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aataatntag catgtattat ggaaaacact aacttattgt ggcttgatct tcttaggaca 762

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 Met Arg Phe Arg Val Ser Ser  
 1 5

ggg ctt tcg gga cgc ggc cga gga ggg tcg ctg tcc acc cgg ggg cgt Gly Leu Ser Gly Arg Gly Arg Gly Ser Leu Ser Thr Arg Gly Arg	340
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25 30 35	
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40 45 50 55	
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60 65 70	
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75 80 85	
gtc tca ggc ttc ctg ctt ttc cga agc ctt ccc cga cat acc ttc gga Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly	580
90 95 100	
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120 125 130 135	
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Variable	Mean	SD	Min	Max
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Marital status (Married/Single)	10/10	0	0	20
Occupation (Student/Professional)	10/10	0	0	20
Religion (Muslim/Hindu)	10/10	0	0	20
Education (High school/College)	10/10	0	0	20
Income (Low/Medium/High)	10/10/0	0	0	20
Health status (Good/Bad)	10/10	0	0	20
Smoking status (Smoker/Non-smoker)	10/10	0	0	20
Alcohol consumption (Yes/No)	10/10	0	0	20
Exercise frequency (Regular/Irregular)	10/10	0	0	20
Stress level (Low/Medium/High)	10/10/0	0	0	20
Sleep quality (Good/Bad)	10/10	0	0	20
Dietary habits (Healthy/Unhealthy)	10/10	0	0	20
Family size (Small/Large)	10/10	0	0	20
Urban/Rural residence	10/10	0	0	20
Health insurance (Yes/No)	10/10	0	0	20
Chronic diseases (Yes/No)	10/10	0	0	20
Genetic predisposition (Yes/No)	10/10	0	0	20
Environmental factors (Yes/No)	10/10	0	0	20
Lifestyle changes (Yes/No)	10/10	0	0	20
Healthcare access (Yes/No)	10/10	0	0	20
Healthcare costs (Low/High)	10/10	0	0	20
Healthcare quality (Good/Bad)	10/10	0	0	20
Healthcare satisfaction (Yes/No)	10/10	0	0	20
Healthcare utilization (High/Low)	10/10	0	0	20
Healthcare equity (Yes/No)	10/10	0	0	20
Healthcare innovation (Yes/No)	10/10	0	0	20
Healthcare research (Yes/No)	10/10	0	0	20
Healthcare policy (Yes/No)	10/10	0	0	20
Healthcare regulation (Yes/No)	10/10	0	0	20
Healthcare funding (Yes/No)	10/10	0	0	20
Healthcare infrastructure (Yes/No)	10/10	0	0	20
Healthcare workforce (Yes/No)	10/10	0	0	20
Healthcare technology (Yes/No)	10/10	0	0	20
Healthcare communication (Yes/No)	10/10	0	0	20
Healthcare education (Yes/No)	10/10	0	0	20
Healthcare training (Yes/No)	10/10	0	0	20
Healthcare certification (Yes/No)	10/10	0	0	20
Healthcare accreditation (Yes/No)	10/10	0	0	20
Healthcare compliance (Yes/No)	10/10	0	0	20
Healthcare safety (Yes/No)	10/10	0	0	20
Healthcare security (Yes/No)	10/10	0	0	20
Healthcare privacy (Yes/No)	10/10	0	0	20
Healthcare confidentiality (Yes/No)	10/10	0	0	20
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Healthcare accountability (Yes/No)	10/10	0	0	20
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Healthcare network (Yes/No)	10/10	0	0	20
Healthcare system (Yes/No)	10/10	0	0	20
Healthcare organization (Yes/No)	10/10	0	0	20
Healthcare institution (Yes/No)	10/10	0	0	20
Healthcare facility (Yes/No)	10/10	0	0	20
Healthcare service (Yes/No)	10/10	0	0	20
Healthcare program (Yes/No)	10/10	0	0	20
Healthcare initiative (Yes/No)	10/10	0	0	20
Healthcare project (Yes/No)	10/10	0	0	20
Healthcare effort (Yes/No)	10/10	0	0	20
Healthcare action (Yes/No)	10/10	0	0	20
Healthcare step (Yes/No)	10/10	0	0	20
Healthcare measure (Yes/No)	10/10	0	0	20
Healthcare approach (Yes/No)	10/10	0	0	20
Healthcare method (Yes/No)	10/10	0	0	20
Healthcare technique (Yes/No)	10/10	0	0	20
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 785 790 795

aaa aaa aaa ggg cgg ccg ctc tag agtatccctc gaggggcccc agcttacgcg 2694  
 Lys Lys Lys Gly Arg Pro Leu \*  
 800 805

taccagctt tctgtacaa agtggctcct atagtgagtc gtattataag ctggcgccctg 2754

cgcagctagt caacctctca cctt 2778

<210> 90  
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 <212> DNA  
 <213> Homo sapiens



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<220>  
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 <223> n = a,t,c or g

<400> 90

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accattcctg ctggggcgcag tggctcatgc ctttaatccc agtcattaag gaggctgagg	180
tgggaagatt gcttgaaacc aggagattgc ctcaggcctg ggcaacatgg tgagacctct	240
tatctcaaaa aatcaaaata aaaaattagc tgggcatggt ggctcatccc tgtagcccca	300
gcttctcaag aggctgaggt gggaggatag cttcagccta ggagacagaa gctgcagtga	360
gctatgatca caccactaca ctccagcctg gacaacagaa agagaccttg tctctaaaaa	420
caaaacaaaa caatcaaaca aaaaagtact cctgaattta agtattgatg gctatgggaa	480
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tcagtgaagc tttgttaaag ggaatgagga gtttaggccc cagcaggcaa accacttcac	600
agtgctagga tgaagagctc acactcaggg acttcgagag tgaatcaact actttcgtta	660
actcaatggt aaatgagaat aacatcaacc ttggatggtt gtggtgagaa tcaaatgaaa	720
tgacat    atg gga aaa cct ttg tca cat gtt aca caa ttg acg gca act	768
Met Gly Lys Pro Leu Ser His Val Thr Gln Leu Thr Ala Thr	
1                    5                    10	
aca gct tta ggt aga att tca act tct aat ttt tac tac tat gca aat	816
Thr Ala Leu Gly Arg Ile Ser Thr Ser Asn Phe Tyr Tyr Tyr Ala Asn	
15                    20                    25                    30	
tat cag aat att tat gat gtt aac ttt tta aaa agg ttt tta aat aga	864
Tyr Gln Asn Ile Tyr Asp Val Asn Phe Leu Lys Arg Phe Leu Asn Arg	
35                    40                    45	
aac ttt att taa ata aatgaactct tctcaacccc aaaaccagc ttctgatctt	919
Asn Phe Ile    *	
50	
gactaagttc ataattactc agggaaaaac actgctggtt ccttataagc cactgtgctg	979
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attaagtata ttcacttaac atattaattt a	1070

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 <213> Homo sapiens

<220>  
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<400> 91

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ataaaaacgga aaatttgcta gaatcaaga  atg atg gat cca tgt tca gtt gga      173
                               Met Met Asp Pro Cys Ser Val Gly
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gtc cag ctt cgt act aca aat gag tgc cat aaa acc tac tat act cgc      221
Val Gln Leu Arg Thr Thr Asn Glu Cys His Lys Thr Tyr Tyr Thr Arg
      10                               15                               20

cac aca ggt ttt aag act ttg caa gaa ttg tca tca aat gat atg ctt      269
His Thr Gly Phe Lys Thr Leu Gln Glu Leu Ser Ser Asn Asp Met Leu
      25                               30                               35                               40

tta ctt caa ctt aga act gga atg aca ctt tct ggg aac aat aca att      317
Leu Leu Gln Leu Arg Thr Gly Met Thr Leu Ser Gly Asn Asn Thr Ile
                               45                               50                               55

tgc ttt cat cat gta aaa att tac att gac aga ttt gag gat tta cag      365
Cys Phe His His Val Lys Ile Tyr Ile Asp Arg Phe Glu Asp Leu Gln
                               60                               65                               70

aag tca tgt tgt gac cca ttt aac ata cac aag aaa tta gcc aaa aaa      413
Lys Ser Cys Cys Asp Pro Phe Asn Ile His Lys Lys Leu Ala Lys Lys
      75                               80                               85

aat ttg cat gta att gac tta gat gat gcc act ttt ctg agt gct aaa      461
Asn Leu His Val Ile Asp Leu Asp Asp Ala Thr Phe Leu Ser Ala Lys
      90                               95                               100

ttt gga aga cag ctt gta cct ggt tgg aag ctt tgt cca aaa tgc aca      509
Phe Gly Arg Gln Leu Val Pro Gly Trp Lys Leu Cys Pro Lys Cys Thr
      105                               110                               115                               120

cag ata atc aat gga agt gtg gat gtt gat act gaa gac cgc cag aaa      557
Gln Ile Ile Asn Gly Ser Val Asp Val Asp Thr Glu Asp Arg Gln Lys
                               125                               130                               135

agg aaa cct gag tca gat gga aga act gct aaa gct ttg agg tca tta      605
Arg Lys Pro Glu Ser Asp Gly Arg Thr Ala Lys Ala Leu Arg Ser Leu
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<210> 92  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 92  
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 cattttttcc agcaaagggtg gtttttgaaa gtaacctaat gaaaccctgg ctgccatggg 180  
 cattttaatt ctggactgag aagaagcgac tctgcgttgt gctgttggcc caggcctgca 240  
 tgcctgagga ctggtggccg ttacagttcc ttgctgtggt cgccggtctc tctgtattct 300  
 gccactgctc tcatgtggca tttggcagaa gtactacgta gatttctgtg ctactgaaaa 360  
 aaataaaaac agtgggttcct tttaatagcc ctgatttgag acttaggaga ggggtcaagag 420  
 tccctacctg atttatgagg agagaagatt ttttaaaaac ctcatgtgat gctgtcatac 480  
 atagttcaaa gagcttcctt taattcactt catttacctt tttttccatt ttcgcttgag 540  
 aactagagaa gtttgtgttc tgttggaacc ctctgtagaa cactttacac tcagttctga 600  
 tggacctttt caggggcgat tttttaaaaa ccgctctcga aagtagtctt aaaatgagag 660  
 cactttattg atggcttttc aggactgtgt tgggtatttt catgcagtgt atttgtcagc 720  
 ttacattttt cagttgagct acctgatgct actgacacac atatgatttt cctatcttac 780  
 caggcaaata ctactgttaa cgttttaata gtaagtctac ttatgcacat tgattttact 840  
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 tatttcttaa tgcagat atg aaa aac agt agc tcc gta tcg aat aca ttg 1010  
 Met Lys Asn Ser Ser Ser Val Ser Asn Thr Leu  
 1 5 10  
 aca aat gga tgt gtc atc aat gga cat ttg gac ttc ccc tcc acg acc 1058  
 Thr Asn Gly Cys Val Ile Asn Gly His Leu Asp Phe Pro Ser Thr Thr  
 15 20 25  
 ccg ctc agt ggg atg gaa agc agg aat ggc cag tgc ttg aca gga act 1106  
 Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr Gly Thr  
 30 35 40

aac gga att agc agt gga tta gcc cca gga cag ccg ttt ccg agt agc	1154
Asn Gly Ile Ser Ser Gly Leu Ala Pro Gly Gln Pro Phe Pro Ser Ser	
45 50 55	
cag ggt tct ctc tgc att agt ggg act gag gag cca gag aag acc ctg	1202
Gln Gly Ser Leu Cys Ile Ser Gly Thr Glu Glu Pro Glu Lys Thr Leu	
60 65 70 75	
aga gct aac cct gag ttg tgc ggt tct ctg cac ctg aac ggg agt cca	1250
Arg Ala Asn Pro Glu Leu Cys Gly Ser Leu His Leu Asn Gly Ser Pro	
80 85 90	
agt agc tgc ata gcc agt agg cct tcc tgg gtg gaa gac att ggg gat	1298
Ser Ser Cys Ile Ala Ser Arg Pro Ser Trp Val Glu Asp Ile Gly Asp	
95 100 105	
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Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala Glu Ser	
110 115 120	
atc cca gaa ctg aac agt gtg gtc gag cat tcc aag tcc gtg aag gtg	1394
Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val Lys Val	
125 130 135	
cag gag cgg tac gac agt gcc gtg ctg ggc acc atg cac ctg cac cac	1442
Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu His His	
140 145 150 155	
ggc tcc tag agacgct gacctggctc tcggaaacgc aggagtcctt cctggtagcc	1498
Gly Ser *	
agctcagaat acccatgtag cagcaacttg aacgaatgtc acaacttgta ctttttttat	1558
atacttcaac tttctgaaaa agtaaaacttc gacaagttcc cagcaactgc ttgtttgtgc	1618
atgagtaggg cttactaagt gcatagatgt ttctacagtg aggtgtcctt ttataaagg	1678
gcacttttgg agtttttctg atgccaatct caacattgtc tttttaatac tgtcaccaga	1738
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cagggtgcctg gtaatttatc tctttgcaca tgggcatcat tttaaaaagc ttgcttccac	1858
tcttttctgt agaatttgac ggaacacagc tatttcccta tgcaaggtag agccttacia	1918
agatttctgc agtgatttgt gtgaagaaga gaatgtttgt ctttttcaat gaagctttgc	1978
agatcaccat gtgggtgaag gtttttagttg tggacacagt ggtccctcct taatgatgaa	2038
gatcactgcc ttgggcttca tggaaaacag gccagcctg gggctgcgtt tggatttatt	2098
gtttttattc cacacttcct acttgggtctc tggaagtttt accacatgta acagattcct	2158
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ataccactat gtatatccag ttaactgaga gaattttgac tctcttaata aaactgcatt 2338  
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cacaaattga ataaaaaact ctcacactca aaaaaaaaaa a 2559

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<212> DNA  
<213> Homo sapiens

<220>  
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tttactgcag tttcatcatg gggtttgttg atgtgcagtc catttattgc cctgtcttgc 180  
ttaaatattc ttgttgagaa cagctggagg ctttgactgg gttcctagtt ctgttttctg 240  
ggaaggcaac gtggattctg tttttagac attaatgagc tttaa atg gga att 294  
Met Gly Ile  
1  
ggg gat gat gta tgt cta caa aaa aaa agt tgg agc ggc cgc caa 342  
Gly Asp Asp Val Cys Leu Gln Lys Lys Lys Ser Trp Ser Gly Arg Gln  
5 10 15  
ctt agg ggc cac gtg agc cac ggc cac ggc cgc ata ggc aag cac cgg 390  
Leu Arg Gly His Val Ser His Gly His Gly Arg Ile Gly Lys His Arg  
20 25 30 35  
aag cac ccc ggc ggc cgc ggt aat gct ggt ggt ctg cat cac cac cgg 438  
Lys His Pro Gly Gly Arg Gly Asn Ala Gly Gly Leu His His His Arg  
40 45 50  
atc aac ttc gac aaa tac cac cca ggc tac ttt ggg aaa gtt ggt atg 486  
Ile Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met  
55 60 65  
aag cat tac cac tta aag agg aac cag agc ttc tgc cca act gtc aac 534  
Lys His Tyr His Leu Lys Arg Asn Gln Ser Phe Cys Pro Thr Val Asn  
70 75 80  
ctt gac aaa ttg tgg act ttg gtc agt gaa cag aca cgg gtg aat gct 582

Leu	Asp	Lys	Leu	Trp	Thr	Leu	Val	Ser	Glu	Gln	Thr	Arg	Val	Asn	Ala		
85						90					95						
gct aaa aac aag act ggg gct gct ccc atc att gat gtg gtg cga tcg 630																	
Ala	Lys	Asn	Lys	Thr	Gly	Ala	Ala	Pro	Ile	Ile	Asp	Val	Val	Arg	Ser		
100					105					110					115		
ggc tac tat aaa gtt ctg gga aag gga aag ctc cca aag cag cct gtc 678																	
Gly	Tyr	Tyr	Lys	Val	Leu	Gly	Lys	Gly	Lys	Leu	Pro	Lys	Gln	Pro	Val		
			120						125					130			
atc gtg aag gcc aaa ttc ttc agc aga aga gct gag gag aag att aag 726																	
Ile	Val	Lys	Ala	Lys	Phe	Phe	Ser	Arg	Arg	Ala	Glu	Glu	Lys	Ile	Lys		
			135					140						145			
agt gtt ggg ggg gcc tgt gtc ctg gtg gct tga agccacat ggagggagtt 777																	
Ser	Val	Gly	Gly	Ala	Cys	Val	Leu	Val	Ala	*							
		150					155										
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<210> 94  
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 <213> Homo sapiens  
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 <222> (737)..(1003)

<400> 94																	
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ttccatgtgt	aagttttaca	tttgtatttt	ctacaattaa	gtaaatctaa	atgttaaatt											180	
ttaacacata	tatccaatta	tgtacacaat	tacaatgtca	atttataagt	caagcttact											240	
taacaatcat	aaattacaaa	aaacgcacta	tgaataat	ttgttctagaa	gtatcacatc											300	
aactcatatg	atctaggtga	acccaaaagt	aaaaaataat	gattataaat	tatggtagtg											360	
tctgtaaaac	cctgttataa	aggaggtatt	cttttaaaat	atgtacctta	tatataaaag											420	
ctcctgactc	cttttaagga	ccaaaattat	tttcagtcta	accattttca	ttaaagcgct											480	
tatttataaaa	gtatcacctt	ataaaactga	gtatataaaa	tacaatgcag	cccttgatag											540	
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tgggttgatt	ttttttcttc	ctctaaatta	agtggcccta	gactaatata	tttgttcagt											660	
tattctgttt	tcttccttac	tgccatttca	catctccatc	agtgagttcc	tcaggatttg											720	

cctttatgtt acaact	atg aaa gtc ttc aat cca att ccc tgc ttc cac	769
	Met Lys Val Phe Asn Pro Ile Pro Cys Phe His	
	1 5 10	
aca aag gac aaa gaa agc cta aac ttt cct ttt ttc tgg gct cca ata	817	
Thr Lys Asp Lys Glu Ser Leu Asn Phe Pro Phe Phe Trp Ala Pro Ile		
	15 20 25	
gga agc agc att tac aac gtg tct ggc ttg gtg gga gga aga ttg tca	865	
Gly Ser Ser Ile Tyr Asn Val Ser Gly Leu Val Gly Gly Arg Leu Ser		
	30 35 40	
att gag gta tca tgt gtg ttc acc tgc ctc tct tgc cct att tct ttg	913	
Ile Glu Val Ser Cys Val Phe Thr Cys Leu Ser Cys Pro Ile Ser Leu		
	45 50 55	
gtt gct ata aat ttc ctg ctt ctc aaa tat ctg gat ttt tgg cta cct	961	
Val Ala Ile Asn Phe Leu Leu Leu Lys Tyr Leu Asp Phe Trp Leu Pro		
	60 65 70 75	
att tgg ctt ccg tct ttg gtg ttt ata tct gtc tgg ttt tag caggtct	1010	
Ile Trp Leu Pro Ser Leu Val Phe Ile Ser Val Trp Phe *		
	80 85	
ctctgattcc tgaccacag ctccctcct tctctaatat tcaagtatgc tgcttccta	1070	
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tattaaatta ataaccctta taacaatttc aaatgtaata ctatctggat ttgaacttca	1370	
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<211> 1217

<212> DNA

<213> Homo sapiens



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 <222> (353)..(472)

<400> 95

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taagtttttg tattccacta ctttcagttc aataaaacct agagttgttt catctgcgcc      180
taaagtgtat ggcacaattt tcttaagaat taggggaacc aggtgcctac agttaaagga      240
acgtttcagt tcctttcatt cattcctggg tttttctttt attttctaag aaggttgaag      300
aaggatgagt gatagagaag aaagcaacac cattgatttt tttttttaag aa      atg      355
                                     Met
                                     1

ata tat ata tgt ata tgt ttg tgt gtg tgt gtg tgt gtg tgt gta ttc      403
Ile Tyr Ile Cys Ile Cys Leu Cys Val Cys Val Cys Val Cys Val Phe
          5                      10                      15

tgt gca tta ttt tgt cat gat ctc aat tct ctt ctt tcc acc aaa gtt      451
Cys Ala Leu Phe Cys His Asp Leu Asn Ser Leu Leu Ser Thr Lys Val
          20                      25                      30

tgt cgt aat att ttc tcc tga ag gtgcattctg gtccttttaa attagtcagt      504
Cys Arg Asn Ile Phe Ser      *
          35                      40

gttatattgt aggagactgt catggaaaaa aggactcagt ttactttcgt cattttcaca      564
ggggaacctt ttaaaacaat cttttcagca gcagatacct ttaaccctaa taatctcagg      624
ccttgatgaa aatactatat tttgtagatt atgggttaaag ggggaaaatt actagttccg      684
taagataaat atgagctcca tttgacttct gatgtctggt ttagcattac ataatatggt      744
gatcttacac tctgcttttg tccaaataaa atgcaatagt atcaatatca atttcagaaa      804
aatggactga atatgctttt ttggtgatga aatctcatgt acgatattta tagtgatgtg      864
cttttatttt ctcatgagat actaaatatt aattgtgttg tacatttggt cttagcatat      924
attaaagttt tgaaccaaat gtgttaaagc ttacgctttg ccatgtaa atccccagaag      984
ttgttgagct caaatgtatc ctacatccag ctgtagaaat ttgtcagaaa ttgttttaat      1044
tttgatatata attgtactgt ttaattctag ccattgcgct gaacagtatt tgagttacca      1104
tataatatgg ctttacacaa ggaaatgtgt ggcttttggt ttgtatTTTT tcagtataga      1164
agttcctgtg tcttatttta ataaagttaa tagtaaaaact gaaaaaaaaa aaa      1217

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<210> 96  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 96

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gcttgcaatt gaacatcacc ccccaactgg aagagcctca catcctggac gaatgaccaa      180

ggcgccagga gaaagactgt gttttctccc acgctacctg ccgcccgcctc ttctcttggc      240

tctctgcaaa cacctgaagc tgtgaccacc agaaagggca caggcttgct ttctcagac      300

tacaggatca tcaatggcaa aagtggaact caggacatcc agcctggccc tctttttaat      360

aataatgctg atggagtggc cacagatata acttctacca gatccttaaa ttacaaaagc      420

actagcagcg gtcacagaga aatatcatca cctaggattc aggatgctgg acctgcttcc      480

cgagatgtcc aggccactgg cagaatcgca gatgatgctg acccaagagt agcacttggt      540

aacgattctt tatctgatgt cacaagtacc acatcttcta ggggtggatga tcatgactca      600

gaggaaatth gtcttgacca tctgtgtaag ggttggtccgc ttaatggtag ctgcagcaaa      660

gtccacttcc atctgcctta ccggtggcag      atg ctt att ggt aaa acc tgg      711
                               Met Leu Ile Gly Lys Thr Trp
                               1                               5

acg gac ttt gag cac atg gag acg atc gag aaa ggc tac tgt aac ccc      759
Thr Asp Phe Glu His Met Glu Thr Ile Glu Lys Gly Tyr Cys Asn Pro
          10                15                20

gga atc cac ctc tgt tct gta gga agt tat aca atc aat ttt cgg gta      807
Gly Ile His Leu Cys Ser Val Gly Ser Tyr Thr Ile Asn Phe Arg Val
          25                30                35

atg agt tgt gat tcc ttt ccc atc cga cgc ctc tcc act cct tct tct      855
Met Ser Cys Asp Ser Phe Pro Ile Arg Arg Leu Ser Thr Pro Ser Ser
          40                45                50                55

gtc acc aag cca gcc aat tct gtc ttc acc acc aaa tgg att tgg tat      903
Val Thr Lys Pro Ala Asn Ser Val Phe Thr Thr Lys Trp Ile Trp Tyr
          60                65                70

tgg aag aat gaa tct ggc aca tgg att cag tat gga gaa gag aaa gac      951
Trp Lys Asn Glu Ser Gly Thr Trp Ile Gln Tyr Gly Glu Glu Lys Asp
          75                80                85

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aaa cgg aaa aat tca aac gtc gac tct tca tac ctg gag tct ctc tat      999
Lys Arg Lys Asn Ser Asn Val Asp Ser Ser Tyr Leu Glu Ser Leu Tyr
          90                      95                      100

caa tcc tgt ccg agg gga gtt gtg cca ttt cag gcg ggc tca cgg aac      1047
Gln Ser Cys Pro Arg Gly Val Val Pro Phe Gln Ala Gly Ser Arg Asn
          105                      110                      115

tat gag ctg agt ttc caa ggg atg att cag aca aac ata gct tcc aaa      1095
Tyr Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys
          120                      125                      130                      135

act caa aag gat gtc atc aga aga cca aca ttt gtg cct cag tgg tat      1143
Thr Gln Lys Asp Val Ile Arg Arg Pro Thr Phe Val Pro Gln Trp Tyr
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Val Gln Gln Met Lys Arg Gly Pro Glu *
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attttgtcct gtgtccttac cggcaaaacg atgtataaat gaaagaaatt gagatgggtgc      240

acgatgcaca gttgaagtga acttgcgggg tttttcagta tctacgattc atagatctgg      300

aattcgcggc cgcgtcgacg aaatatctct ttcaataatg aaagaataag aaaaagaaat      360

agaagagctg gaaacaatag gtaaagttta ggctaggcct tagacttctc ctgcattgta      420

atccttctgg ttgccacat atgcatgctg tcaggaagtt gatgaggt atg tac agg      477
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 His Leu Leu Asn Val Ser Ser Gln Ala Ile Leu Pro Ile Gly Ala Arg  
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 Ser Arg Gln Phe Val Asn Val Ser \*  
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gcagtttgaa gagcattttg tttagtgaag tcaacaaata caaagtcagt gaaagaaacc 925

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gag gtg cac att gga ggc gtg atg ctt aag ctg gtg gag aaa ctc gat Glu Val His Ile Gly Gly Val Met Leu Lys Leu Val Glu Lys Leu Asp 40 45 50	318
gta aaa aaa gat tgg tct gac cat gct ctc tgg tgg gaa aag aag aga Val Lys Lys Asp Trp Ser Asp His Ala Leu Trp Trp Glu Lys Lys Arg 55 60 65	366
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gca gat gct aag ctt cag ttc acc cct cag cac aaa ctg ctc cgc ctg Ala Asp Ala Lys Leu Gln Phe Thr Pro Gln His Lys Leu Leu Arg Leu 90 95 100	462
cag ctt ccc aac atg aag tat gtg aag gtg aaa gtg aat ttc tct gat Gln Leu Pro Asn Met Lys Tyr Val Lys Val Lys Val Asn Phe Ser Asp 105 110 115	510
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gca aaa atc aac caa gga tgg ctt gat tcc tca aga tct ctc atg gaa	942





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Ala Val Ile Asp Ser Ile Phe Val Trp Phe Ile Phe Ile Ser Leu Ala  
20 25 30 35



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Leu Tyr Arg His Phe Lys Asn Thr Leu Ile Phe Ala Val Leu Ala Ser	
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Ile Val Phe Met Gly Trp Thr Thr Lys Thr Phe Arg Ile Ala Lys Cys	
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Gln Ser Asp Trp Met Glu Arg Trp Val Asp Asp Ala Phe Trp Ser Phe	
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Leu Phe Ser Leu Ile Leu Ile Val Ile Met Phe Leu Trp Arg Pro Ser	
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Asp Glu Ile Glu Glu Phe Met Val Thr Ser Glu Asn Leu Thr Glu Gly	
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Ile Lys Leu Arg Ala Ser Lys Ser Val Ser Asn Gly Thr Ala Lys Pro	
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Ser Glu Lys Ile Met *	
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His Gly Pro Leu Pro Pro Pro Gly Tyr Gly Thr Pro Leu Asn Cys Asn	
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Leu Pro Asp Ser Pro Pro Asp Ser Gly Ser Glu Ala Tyr Ser Pro Gln	
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Cys His Val Gly Val Pro Ser Arg Leu Glu His Pro Pro Pro Pro Pro	
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Ala His Leu Pro Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro His Tyr	
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His Tyr Ala Ala Met Gly Gln Gly Leu Val Pro Thr Asp Leu His His	
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Pro Ser Thr Leu Asn Ala Gln Met Leu Asn Gly Met Ile Lys Gln Glu	
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Tyr	Leu	Asp	Pro	Asn	Tyr	Gln	Ser	Ile	Lys	Trp	Gln	Pro	His	Gln	Gln	
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Asn	Lys	Trp	Ala	Thr	Leu	Tyr	Asp	Ala	Asn	Tyr	Lys	Glu	Leu	Pro	Met	
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Asp	Asp	Ala	Phe	Val	Cys	Gln	Lys	Lys	Asn	His	Phe	Gln	Val	Thr	Val	
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aac	aac	atg	cgt	aag	aag	ggc	aag	ccc	aac	ccg	gac	cag	agg	tac	ttc	1603
Asn	Asn	Met	Arg	Lys	Lys	Gly	Lys	Pro	Asn	Pro	Asp	Gln	Arg	Tyr	Phe	
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Met	Leu	Val	Val	Ala	Leu	Gln	Ala	His	Ala	Gln	Asn	Gln	Asn	Tyr	Thr	
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ctg	gcc	gcc	cag	atc	tca	gag	cgc	atc	att	gtg	cgg	gcc	tcc	aac	cca	1699
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Val Gly Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Glu Pro Val	
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Met Leu Thr Gln Leu Lys	
1 5	
gca aaa tca gag ggg aag ctt gca aaa cag att tgc aaa gtt gtg ttg	163
Ala Lys Ser Glu Gly Lys Leu Ala Lys Gln Ile Cys Lys Val Val Leu	
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gat cat ttt gaa aaa cag tat tcc aaa gaa ctc gga gat gcc tgg aat	211
Asp His Phe Glu Lys Gln Tyr Ser Lys Glu Leu Gly Asp Ala Trp Asn	
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Leu Leu Asn Arg Phe Asn Tyr Pro Phe Glu Leu Glu Lys Asp Leu His	
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ttg aag ggc tat cac aca ctc tct cag gga tct tta ccc aac tat cct	355
Leu Lys Gly Tyr His Thr Leu Ser Gln Gly Ser Leu Pro Asn Tyr Pro	
75 80 85	
aaa tca gtg aag tgt tac ctt agc aga act ccg ggc cga atc cct tca	403
Lys Ser Val Lys Cys Tyr Leu Ser Arg Thr Pro Gly Arg Ile Pro Ser	
90 95 100	
gaa aga cac caa att gga aac ctg aaa aaa tat tat ctc cta aat gct	451
Glu Arg His Gln Ile Gly Asn Leu Lys Lys Tyr Tyr Leu Leu Asn Ala	
105 110 115	
gct tct ctt ctc cca gtg ttg gct ctg gaa tta agg gat ggg gag aag	499
Ala Ser Leu Leu Pro Val Leu Ala Leu Glu Leu Arg Asp Gly Glu Lys	
120 125 130	
gtt ctg gat ctc tgt gct gct cct gga ggg aaa tta ata gct ctg ctg	547
Val Leu Asp Leu Cys Ala Ala Pro Gly Gly Lys Leu Ile Ala Leu Leu	
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gat gcc cag cct gaa atg ttt gac aag gtg tta gtg gat gct ccg tgt Asp Ala Gln Pro Glu Met Phe Asp Lys Val Leu Val Asp Ala Pro Cys 200 205 210	739
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Leu Ala Leu Arg Gln Lys Pro His Ser Thr Gly Thr Ile His Glu Val  
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act gcc cag ctc atg atg tcc gtg agg ctg tcc ttt tgg cca gta gcc 206  
Thr Ala Gln Leu Met Met Ser Val Arg Leu Ser Phe Trp Pro Val Ala  
30 35 40  
gtg tgc agc tgt gtg gca cag atg gct tgc ttc atc ctg atc aag gcc 254  
Val Cys Ser Cys Val Ala Gln Met Ala Ser Phe Ile Leu Ile Lys Ala  
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cca cct cag cca cag cag tcc ccc caa cct gtg ttg tcc acc cta tta 302  
Pro Pro Gln Pro Gln Gln Ser Pro Gln Pro Val Leu Ser Thr Leu Leu  
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ttc atg tac ctg cca ggc cct gct aga tag c acccgtggc attacataac 353  
Phe Met Tyr Leu Pro Gly Pro Ala Arg \*  
75 80  
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cag ctc ttc aat gga gga tgc cca ccc cct cct cct gtc ctg aat ggt      163
Gln Leu Phe Asn Gly Gly Cys Pro Pro Pro Pro Val Leu Asn Gly
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gag gac gtg ctt cct gac ctg aac ctc ctc cca ccc ctt caa ccg ccc      211
Glu Asp Val Leu Pro Asp Leu Asn Leu Leu Pro Pro Leu Gln Pro Pro
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ctt cca ggg ctt ctg cct tct gaa aag gag gct cct gct cca atg ggg      259
Leu Pro Gly Leu Leu Pro Ser Glu Lys Glu Ala Pro Ala Pro Met Gly
          35                      40                      45

gcc tca ctc att gca aac tta aag cag ctg cac ctg tcc ccg ccc ccg      307
Ala Ser Leu Ile Ala Asn Leu Lys Gln Leu His Leu Ser Pro Pro Pro
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ccc cca cca cag gcc cca gcg gag gga cct tca gtc cag ccc ggt ccc      355
Pro Pro Pro Gln Ala Pro Ala Glu Gly Pro Ser Val Gln Pro Gly Pro
          70                      75                      80

ctc agg ccc atg gag gaa gag ctg cca cct ccc ccg gca gaa cct gtt      403
Leu Arg Pro Met Glu Glu Glu Leu Pro Pro Pro Pro Ala Glu Pro Val
          85                      90                      95

gag aaa ggg gca tcc aca gac atc tgt gcc ttc tgc cac aag acc gtg      451
Glu Lys Gly Ala Ser Thr Asp Ile Cys Ala Phe Cys His Lys Thr Val
          100                      105                      110

ttc ccc cga gag ctg gct gtg gag gcc atg aag agg cag tac cat gcc      499
Phe Pro Arg Glu Leu Ala Val Glu Ala Met Lys Arg Gln Tyr His Ala
          115                      120                      125

cag tgc ttc acg tgc cgc acc tgc cgc cgc cag ctg gct ggg cag agc      547
Gln Cys Phe Thr Cys Arg Thr Cys Arg Arg Gln Leu Ala Gly Gln Ser
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Ile Arg Ala Leu Gly Gln Ala Phe His Pro Ser Cys Phe Thr Cys Val	
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Asn Glu Val Tyr Cys Leu Asp Asp Phe Tyr Arg Lys Phe Ala Pro Val	
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Cys Ser Ile Cys Glu Asn Pro Ile Ile Pro Arg Asp Gly Lys Asp Ala	
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Phe Lys Ile Glu Cys Met Gly Arg Asn Phe His Glu Asn Cys Tyr Arg	
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Cys Glu Asp Cys Arg Ile Leu Leu Ser Val Glu Pro Thr Asp Gln Gly	
260 265 270	
tgc tac ccc ctg aac aac cat ctc ttc tgc aag cca tgc cat gtg aag	979
Cys Tyr Pro Leu Asn Asn His Leu Phe Cys Lys Pro Cys His Val Lys	
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Leu Asn Val Asp Met Glu Trp Leu Tyr Gly Ala Ser Glu Ser Ser Asn			
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Met Glu Val Asp Ile Gly Tyr Ile Pro Gln Met Glu Leu Glu Ala Thr			
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Gly Pro Ser Val Pro Ser Val Ile Leu Asp Glu Asp Gly Ser Met Ile			
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Phe Ile Ser Lys Cys Pro Gly Phe Arg Phe Thr Phe Arg Leu Val Met			
115	120	125	
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Leu Val Asp *			
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1509

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cctgttttcc tgtgaagata ctttgagtgg cagccattct ctccacgtga accacacgtc      720
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Ser Pro Val Phe Ala Arg Asp Thr Val Leu Glu Val Glu Val Leu Leu
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Tyr Ser Ser Leu Arg Phe Ala His Cys Ser Val Asp Thr Arg Arg Pro
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gcg ttc tgt tcc cta taa atggaa gcgtgctctg agcctgtctg cctccctcgg      978
Ala Phe Cys Ser Leu *
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50

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gctca      atg aca gtc gag ctt tgg cta agg ctc cgg gga aag ggt cta 287
            Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu
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Trp Pro Leu Leu Pro Ala Leu Leu Gly Pro Pro Arg Ala Leu Ser Ser	
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ctg gca gcc aaa atg ggg gag tat cgc aag atg tgg aac ccc agg gag	431
Leu Ala Ala Lys Met Gly Glu Tyr Arg Lys Met Trp Asn Pro Arg Glu	
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ccc cgc gac tgg gcc cag cag tac cgc gag cgc ttc att ccc ttc tcc	479
Pro Arg Asp Trp Ala Gln Gln Tyr Arg Glu Arg Phe Ile Pro Phe Ser	
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Lys Glu Gln Leu Leu Arg Leu Leu Ile Gln Val Thr Gly Ile Pro Leu	
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Glu Ser Gly Arg Glu Gly Gly Phe Gly Gly Val Leu Ser Pro Arg Gly	
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Leu Leu His Pro Val Pro Leu Pro Pro Asn Pro Gly Pro Ala Ala Gly	
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Met Asn Phe Lys Leu Gly Asn Phe Ser Tyr Gln Lys Asn  
1 5 10  
cca ctg aaa ttg gga gag ctt caa gga aac cac ttc act gtt gtt ctc 756  
Pro Leu Lys Leu Gly Glu Leu Gln Gly Asn His Phe Thr Val Val Leu  
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Arg Asn Ile Thr Gly Thr Asp Asp Gln Val Gln Gln Ala Met Asn Ser  
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ctc aag gag att gga ttt att aac tac tat gga atg caa aga ttt gga 852  
Leu Lys Glu Ile Gly Phe Ile Asn Tyr Tyr Gly Met Gln Arg Phe Gly  
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acc aca gct gtc cct acg tat cag gtt gga aga gct ata cta caa aat	900
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Asp Pro Thr Ala Ala Leu Arg Lys Leu Pro Val Lys Arg Cys Val Glu	
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Ala Tyr Asp Asp Pro Lys Ile Pro Leu Phe Asn Thr Asp Val Asp Asn	
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Lys Glu Leu Lys Lys Ile Cys Lys Ser Ser Glu Glu Gln Leu Ser Arg		
30 35 40		
gcc tac cgc ctc ctc ata gac ccg aac tgt agt ggc cac agc ccg cgc		195
Ala Tyr Arg Leu Leu Ile Asp Pro Asn Cys Ser Gly His Ser Pro Arg		
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acc gcc cgg cac gca cct gcg gtc cgg aag ttc tcc cct gac ctt aag		243
Thr Ala Arg His Ala Pro Ala Val Arg Lys Phe Ser Pro Asp Leu Lys		
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Ser Lys Asp Arg Lys Val Leu Tyr Thr Gly Ala Glu Arg Asp Val Arg		
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Ala Glu Cys Gly Leu Leu Leu Ser Pro Val Ser Gly Asp Val His Ala		
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Cys Pro Phe Gly Gly Ser Val Gly Asp Gly Val Gly Ile Gly Gly Glu		
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Cys Leu Leu Ala Ile Tyr Ser Leu Leu Trp Ile Val Cys Ile Pro Tyr	
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Leu Leu Ser Ile Gly Leu Cys Val Asp Ile Leu Phe Leu Phe Val Gln	
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Gln Pro Gln Pro Pro Asp Glu Asp Gly Asp His Ser Asp Lys Glu Asp			
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Lys Lys Pro Asn Glu Asp Glu Val Asn Gln Asp Ser Val Lys Lys Asn			
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Met Val Val Ser Lys Met Asn			
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Thr Pro Lys Gly Arg Ala Leu Val Pro Asp Ser Val Lys Lys Glu Leu
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Leu Gln Arg Ile Arg Thr Phe Leu Ala Gln His Ala Ser Leu *
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gctggtgacg cacacgctgc gccggaagtg tgaactgtct gcctccgggc tttgtc      476
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Met Ala Ala Ala Ala Ala Arg Trp Asn His Val Trp Val Gly Thr Glu
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Phe	Thr	Ala	Gly	Gly	Gln	Pro	Arg	Arg	Glu	Glu	Ala	Val	Ser	Ala	Leu	
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Cys	Trp	Gly	Thr	Gly	Gly	Glu	Thr	Gln	Met	Leu	Val	Gly	Cys	Ala	Asp	
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Arg	Thr	Val	Lys	His	Phe	Ser	Thr	Glu	Asp	Gly	Ile	Phe	Gln	Gly	Gln	
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Arg	His	Cys	Pro	Gly	Gly	Glu	Gly	Met	Phe	Arg	Gly	Leu	Ala	Gln	Ala	
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Asp	Gly	Thr	Leu	Ile	Thr	Cys	Val	Asp	Ser	Gly	Ile	Leu	Arg	Val	Trp	
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His	Asp	Lys	Asp	Lys	Asp	Thr	Ser	Ser	Asp	Pro	Leu	Leu	Glu	Leu	Arg	
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Trp	Leu	Asp	Leu	Arg	Val	Pro	Ile	Trp	Asp	Gln	Asp	Ile	Gln	Phe	Leu	
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Val	Tyr	Asp	Pro	Ala	Ser	Pro	Gln	Arg	Arg	Pro	Val	Leu	Glu	Thr	Thr	
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Tyr	Gly	Glu	Tyr	Pro	Leu	Thr	Ala	Met	Thr	Leu	Thr	Pro	Gly	Gly	Asn	
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Ser	Val	Ile	Val	Gly	Asn	Thr	His	Gly	Gln	Leu	Ala	Glu	Ile	Asp	Leu	



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Arg Gln Gly Arg Leu Leu Gly Cys Leu Lys Gly Leu Ala Gly Ser Val			
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Arg Gly Leu Gln Cys His Pro Ser Lys Pro Leu Leu Ala Ser Cys Gly			
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Leu Asp Arg Val Leu Arg Ile His Arg Ile Gln Asn Pro Arg Gly Leu			
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Glu His Lys Val Tyr Leu Lys Ser Gln Leu Asn Cys Leu Leu Leu Ser			
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ggc agg gac aac tgg gag gat gag ccc caa gag cct caa gaa ccc aac			1484
Gly Arg Asp Asn Trp Glu Asp Glu Pro Gln Glu Pro Gln Glu Pro Asn			
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Lys Val Pro Leu Glu Asp Thr Glu Thr Asp Glu Leu Trp Ala Ser Leu			
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agttggcagc ggcaagcgcg ctgcggttcc ggtggcgcc atg tcg ttc tgc agc 174  
 Met Ser Phe Cys Ser  
 1 5

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 Phe Phe Gly Gly Glu Val Phe Gln Asn His Phe Glu Pro Gly Val Tyr  
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gtg tgt gcc aag tgt ggc tat gag ctg ttc tcc agc cgc tcg aag tat	270
Val Cys Ala Lys Cys Gly Tyr Glu Leu Phe Ser Ser Arg Ser Lys Tyr	
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gca cac tcg tct cca tgg ccg gcg ttc acc gag acc att cac gcc gac	318
Ala His Ser Ser Pro Trp Pro Ala Phe Thr Glu Thr Ile His Ala Asp	
40 45 50	
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Ser Val Ala Lys Arg Pro Glu His Asn Arg Ser Glu Ala Leu Lys Val	
55 60 65	
tcc tgt ggc aag tgt ggc aat ggg ttg ggc cac gag ttc ctg aac gac	414
Ser Cys Gly Lys Cys Gly Asn Gly Leu Gly His Glu Phe Leu Asn Asp	
70 75 80 85	
ggc ccc aag ccg ggg cag tcc cga ttc tga a tattcagcag ctgctgaag	465
Gly Pro Lys Pro Gly Gln Ser Arg Phe *	
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Met Glu Met Arg Leu Pro Ile Arg Ser Pro Ile Lys Arg	
1 5 10	
gac ttt tta tca gga att cag att gaa ttt aag cag tct tct cac cag	156
Asp Phe Leu Ser Gly Ile Gln Ile Glu Phe Lys Gln Ser Ser His Gln	
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Arg Ser Leu Arg Ala Arg Leu Tyr Trp Leu Gln Val Asp Asn Gln Leu	
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Pro Gly Ala Met Phe Pro Val Val Phe His Pro Val Ala Pro Pro Lys	
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Ser Ile Ala Leu Asp Ser Glu Pro Lys Pro Phe Ile Asp Val Ser Val	
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Ile Thr Arg Phe Asn Glu Tyr Ser Lys Val Leu Gln Phe Lys Tyr Phe	
80 85 90	
atg gtc ctc att cag gaa atg gcc tta aaa att gat caa ggg ttt cta	396
Met Val Leu Ile Gln Glu Met Ala Leu Lys Ile Asp Gln Gly Phe Leu	
95 100 105	
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Gly Ala Ile Ile Ala Leu Phe Thr Pro Thr Thr Asp Pro Glu Ala Glu	
110 115 120 125	
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Arg Arg Arg Thr Lys Leu Ile Gln Gln Asp Ile Asp Ala Leu Asn Ala	
130 135 140	
gaa tta atg gag act tca atg act gat atg tca att ctt agt ttc ttt	540
Glu Leu Met Glu Thr Ser Met Thr Asp Met Ser Ile Leu Ser Phe Phe	
145 150 155	
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Glu His Phe His Ile Ser Pro Val Lys Leu His Leu Ser Leu Ser Leu	
160 165 170	
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Gly Ser Gly Gly Glu Glu Ser Asp Lys Glu Lys Gln Glu Met Phe Ala	

175	180	185	
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Val His Ser Val Asn Leu Leu Lys Ser Ile Gly Ala Thr Leu Thr			
190	195	200	205
gat gtg gat gac ctt ata ttc aaa ctt gct tat tat gaa att cga tat			732
Asp Val Asp Asp Leu Ile Phe Lys Leu Ala Tyr Tyr Glu Ile Arg Tyr			
	210	215	220
cag ttc tac aag aga gat cag ctt ata tgg agt gtt gtt agg cat tac			780
Gln Phe Tyr Lys Arg Asp Gln Leu Ile Trp Ser Val Val Arg His Tyr			
	225	230	235
agt gaa cag ttc ttg aaa cag atg tat gtc ctt gta ttg ggg tta gat			828
Ser Glu Gln Phe Leu Lys Gln Met Tyr Val Leu Val Leu Gly Leu Asp			
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gta ctt gga aac cca ttt gga tta att aga ggt ctg tct gaa gga gtt			876
Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Gly Leu Ser Glu Gly Val			
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gaa gct tta ttc tat gaa ccc ttc cag ggt gct gtt caa ggc cct gaa			924
Glu Ala Leu Phe Tyr Glu Pro Phe Gln Gly Ala Val Gln Gly Pro Glu			
	270	275	280
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Glu Phe Ala Glu Gly Leu Val Ile Gly Val Arg Ser Leu Phe Gly His			
	290	295	300
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Thr Val Gly Gly Ala Ala Gly Val Val Ser Arg Ile Thr Gly Ser Val			
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ggg aaa ggt ttg gca gca att aca atg gac aag gaa tat cag caa aaa			1068
Gly Lys Gly Leu Ala Ala Ile Thr Met Asp Lys Glu Tyr Gln Gln Lys			
	320	325	330
aga aga gaa gag ttg agt cga cag ccc aga gat ttt gga gac agc ctg			1116
Arg Arg Glu Glu Leu Ser Arg Gln Pro Arg Asp Phe Gly Asp Ser Leu			
	335	340	345
gcc aga gga gga aag ggc ttt ctg cga gga gtt gtt ggt gga gtg act			1164
Ala Arg Gly Gly Lys Gly Phe Leu Arg Gly Val Val Gly Gly Val Thr			
	350	355	360
gga ata ata aca aaa cct gtg gaa ggt gcc aaa aag gaa gga gct gct			1212
Gly Ile Ile Thr Lys Pro Val Glu Gly Ala Lys Lys Glu Gly Ala Ala			
	370	375	380
gga ttc ttt aaa gga att gga aaa ggg ctt gtg ggt gct gtg gcc cgt			1260
Gly Phe Phe Lys Gly Ile Gly Lys Gly Leu Val Gly Ala Val Ala Arg			
	385	390	395
cca act ggt gga atc gta gat atg gcc agt agt acc ttc caa ggc att			1308
Pro Thr Gly Gly Ile Val Asp Met Ala Ser Ser Thr Phe Gln Gly Ile			
	400	405	410

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tct gag ggc tct gac tta ctt gag aat cat atc aaa aag ttg gaa gga Ser Glu Gly Ser Asp Leu Leu Glu Asn His Ile Lys Lys Leu Glu Gly 450 455 460	1452
gag act tac cga tac cac tgt gct att cct gga agc aag aag aca atc Glu Thr Tyr Arg Tyr His Cys Ala Ile Pro Gly Ser Lys Lys Thr Ile 465 470 475	1500
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ctg ggc ctt atg tgt gta gac tgg caa tgt cca ttt gaa gat ttt gta Leu Gly Leu Met Cys Val Asp Trp Gln Cys Pro Phe Glu Asp Phe Val 495 500 505	1596
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cag ggt ctg ttc cac aaa aaa gac agt gcc aat caa ggc tgt gtt cga Gln Gly Leu Phe His Lys Lys Asp Ser Ala Asn Gln Gly Cys Val Arg 530 535 540	1692
aaa gtt tac ctg aag gac acc gcc aca gca gag aga gca tgt aat gcc Lys Val Tyr Leu Lys Asp Thr Ala Thr Ala Glu Arg Ala Cys Asn Ala 545 550 555	1740
att gag gat gca cag tca acg aga cag cag caa aaa ttg atg aag cag Ile Glu Asp Ala Gln Ser Thr Arg Gln Gln Gln Lys Leu Met Lys Gln 560 565 570	1788
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attgggtttt ctagtttttt caccttttag tttttactct aattttgtaa ccatgtatat	2017
gctagcagtc cacttctacg ccaccacca aatgggtcag acccttgaag aaacgtcact	2077
tcaaactcag aatgaaattt tcattaatat taaaattgtg aagcaaagggt caataggctt	2137
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<400> 118

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cccagggtcat gcacacagcc agcagtgaca catccaatgg gacactccag gatgaaacct      180
gagaaaggag gtctgggata tgggatattg taatgggaga gcaggaaatt taaggtcgga      240
ggtatttggt taggatacct cagtattcta gagctatggg atttattttg ctttgaagtc      300
cagaggtatt tagctttatt ctaaaagcg  atg aag ttc ctc tta att aaa gac      353
                               Met Lys Phe Leu Leu Ile Lys Asp
                               1                               5

gct cct gga aaa aaa aaa agg aaa aat tta atg ctg tct ttt aaa agg      401
Ala Pro Gly Lys Lys Lys Arg Lys Asn Leu Met Leu Ser Phe Lys Arg
      10                               15                               20

aaa cat gcc aaa ggc cag gat ttg ttt gat cag att gtg tac cac ttg      449
Lys His Ala Lys Gly Gln Asp Leu Phe Asp Gln Ile Val Tyr His Leu
      25                               30                               35                               40

gac ctt gtg gaa aca gat tac ttt ggc ctc cag ttc ctc gac tct gcc      497
Asp Leu Val Glu Thr Asp Tyr Phe Gly Leu Gln Phe Leu Asp Ser Ala
                               45                               50                               55

cag gtt gcg cac tgg ctg gat cat gcc aaa ccc ata aaa aag cag atg      545
Gln Val Ala His Trp Leu Asp His Ala Lys Pro Ile Lys Lys Gln Met
                               60                               65                               70

aaa att gga cct gct tat gct tta cac ttt cga gtt aaa tac tat tct      593
Lys Ile Gly Pro Ala Tyr Ala Leu His Phe Arg Val Lys Tyr Tyr Ser
      75                               80                               85

tca gaa cca aac aac ctt cgt gag gag ttt aca agg tac ctg ttt gtt      641
Ser Glu Pro Asn Asn Leu Arg Glu Glu Phe Thr Arg Tyr Leu Phe Val
      90                               95                               100

tta caa ctc agg cat gac att ctt tct gga aaa ttg aaa tgc cct tat      689
Leu Gln Leu Arg His Asp Ile Leu Ser Gly Lys Leu Lys Cys Pro Tyr
      105                               110                               115                               120

gaa aca gct gtg gaa tta gct gct ctc tgt cta caa gcg gag ctt ggg      737
Glu Thr Ala Val Glu Leu Ala Ala Leu Cys Leu Gln Ala Glu Leu Gly

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140	145	150																		
ttc att cca aat cag aca gaa gca atg gaa ttt gat atc ttc cag aga	833																			
Phe Ile Pro Asn Gln Thr Glu Ala Met Glu Phe Asp Ile Phe Gln Arg																				
155	160	165																		
tgg aaa gag tgc agg gga aag agc cct gcc cag gcg gaa ctc tcc tat	881																			
Trp Lys Glu Cys Arg Gly Lys Ser Pro Ala Gln Ala Glu Leu Ser Tyr																				
170	175	180																		
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gtc agg gga aga gat ggc tgt gaa tat tct ctt gga ctg acc ccg aca	977																			
Val Arg Gly Arg Asp Gly Cys Glu Tyr Ser Leu Gly Leu Thr Pro Thr																				
205	210	215																		
ggc ata tta atc ttt gaa gga gct aac aaa ata ggc tta ttc ttt tgg	1025																			
Gly Ile Leu Ile Phe Glu Gly Ala Asn Lys Ile Gly Leu Phe Phe Trp																				
220	225	230																		
cct aaa att acc aaa atg gat ttt aaa aag agc aaa ttg aca ctc gtg	1073																			
Pro Lys Ile Thr Lys Met Asp Phe Lys Lys Ser Lys Leu Thr Leu Val																				
235	240	245																		
gtg gtc gag gat gat gat cag gga cgt gag caa gag cac acg ttt gtg	1121																			
Val Val Glu Asp Asp Asp Gln Gly Arg Glu Gln Glu His Thr Phe Val																				
250	255	260																		
ttc cgg tta gac agt gcc agg acc tgc aaa cac ctt tgg aag tgt gca	1169																			
Phe Arg Leu Asp Ser Ala Arg Thr Cys Lys His Leu Trp Lys Cys Ala																				
265	270	275	280																	
gtt gag cac cac gca ttc ttc cga ctg cgg acg cca gga aac agc aaa	1217																			
Val Glu His His Ala Phe Phe Arg Leu Arg Thr Pro Gly Asn Ser Lys																				
285	290	295																		
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Ser Asn Arg Ser Asp Phe Ile Arg Leu Gly Ser Arg Phe Arg Phe Ser																				
300	305	310																		
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Gly Arg Thr Glu Tyr Gln Ala Thr His Gly Ser Arg Leu Arg Arg Thr																				
315	320	325																		
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Ser Thr Phe Glu Arg Lys Pro Ser Lys Arg Tyr Pro Ser Arg Arg His																				
330	335	340																		
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345	350	355	360																	

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Lys Thr Asn Pro Glu Val His Asn Tyr Gln Pro Gln Tyr His Pro Asn	
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Pro Ser Phe Gln Asp Asp Arg Ser His Trp Lys Ala Ser Ala Ser Gly	
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Asp Asp Ser His Phe Asp Tyr Val His Asp Gln Asn Gln Lys Asn Leu	
410 415 420	
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 Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His  
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cag gac caa gtg gac cgc aac atc aag gag gct cgt gag aag ctg gag Gln Asp Gln Val Asp Arg Asn Ile Lys Glu Ala Arg Glu Lys Leu Glu 290 295 300			1152

atg gag atg gaa gct gca cgc cat gag cac cag gtc atg cta atg aga Met Glu Met Glu Ala Ala Arg His Glu His Gln Val Met Leu Met Arg 305 310 315	1200
cag gat ttg atg agg cgc caa gaa gaa ctt cgg agg atg gaa gag ctg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu 320 325 330	1248
cac aac caa gag gtg caa aaa cga aag caa ctg gag ctc agg cag gag His Asn Gln Glu Val Gln Lys Arg Lys Gln Leu Glu Leu Arg Gln Glu 335 340 345 350	1296
gaa gag cgc agg cgc cgt gaa gaa gag atg cgg cgg cag caa gaa gaa Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Arg Arg Gln Gln Glu Glu 355 360 365	1344
atg atg cgg cga cag cag gaa gga ttc aag gga acc ttc cct gat gcg Met Met Arg Arg Gln Gln Glu Gly Phe Lys Gly Thr Phe Pro Asp Ala 370 375 380	1392
aga gag cag gag att cgg atg ggt cag atg gct atg gga ggt gct atg Arg Glu Gln Glu Ile Arg Met Gly Gln Met Ala Met Gly Gly Ala Met 385 390 395	1440
ggc ata aac aac aga ggt gcc atg ccc cct gct cct gtg cca gct ggt Gly Ile Asn Asn Arg Gly Ala Met Pro Pro Ala Pro Val Pro Ala Gly 400 405 410	1488
acc cca gct cct cca gga cct gcc act atg atg ccg gat gga act ttg Thr Pro Ala Pro Pro Gly Pro Ala Thr Met Met Pro Asp Gly Thr Leu 415 420 425 430	1536
gga ttg acc cca cca aca act gaa cgc ttt ggt cag gct gct aca atg Gly Leu Thr Pro Pro Thr Thr Glu Arg Phe Gly Gln Ala Ala Thr Met 435 440 445	1584
gaa gga att ggg gca att ggt gga act cct cct gca ttc aac cgt gca Glu Gly Ile Gly Ala Ile Gly Gly Thr Pro Pro Ala Phe Asn Arg Ala 450 455 460	1632
gct cct gga gct gaa ttt gcc cca aac aaa cgt cgc cga tac taa taa Ala Pro Gly Ala Glu Phe Ala Pro Asn Lys Arg Arg Arg Tyr * 465 470 475	1680
gttcgagtgt ctagtttctc aaaaccctta aaagaaggac ccttttttggga ctagccagaa	1740
ttctaccctg gaaaagtgtt agggattcct tccaatagtt agatctaccc tgccctgtact	1800
actctagggga gtatgctgga ggcagagggc aagggagggg tggtattaaa caagtcaatt	1860
ctgaaaaaaaa aaaaa	1875

<210> 120

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<220>  
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 <222> (54)..(686)

<400> 120

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Gly Gly Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu Ser		
5 10 15		
tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga agc		152
Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg Ser		
20 25 30		
aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg gcc		200
Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro Ala		
35 40 45		
gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag gat		248
Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu Asp		
50 55 60 65		
gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat aac		296
Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr Asn		
70 75 80		
atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat gag		344
Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr Glu		
85 90 95		
ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg aac		392
Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Pro Gly Asn		
100 105 110		
cct gga ggg gcc ttc ctc atc cgg gag agc cag acc agg aga ggc tct		440
Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly Ser		
115 120 125		
tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg atc		488
Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg Ile		
130 135 140 145		
aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc tca		536
Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile Ser		
150 155 160		
ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg ggg gac cat tac tct		584
Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Gly Asp His Tyr Ser		
165 170 175		

gag ggc tgg ccc gct ccc tgg caa gga tat acc cct acc tgt gac tgt	632
Glu Gly Trp Pro Ala Pro Trp Gln Gly Tyr Thr Pro Thr Cys Asp Cys	
180 185 190	
gca gag gac acc act caa ctg gaa aga gct gga cag ctc cct cct gtt	680
Ala Glu Asp Thr Thr Gln Leu Glu Arg Ala Gly Gln Leu Pro Pro Val	
195 200 205	
ttc tga agctgccaca ggggaggagt ctcttctcag tgaggggtctc cgggaggtccc	736
Phe *	
210	
tcagcttcta catcagcctg aatgacgagg ctgtctcttt ggatgatgcc taggccccaaa	796
ggagaggcca aaagggaaac caaggctgca cacctagaac cccaattcag cctcctgggc	856
acccagagg caaggctgtg cactcagga gggaggggtgg gacacagagg tgcattctagg	916
gtcccacctg tacccttgct ctttctcttc ttagccctta gaagtcacct acttctcttc	976
agtgccatga tcccacctgc gacctctagt gcgagtgcag agaaggtggg accagggcca	1036
gggttccaaa aagagaataa gcctcctggg gggctctgacc tagttagttc ttgagtttgg	1096
ggtttccagt accatctgga tgccctgcct gttgagcccc attctacatc cccaccatta	1156
accagggccc accacaagg tagaaacaac ccctagagtc aacgagaaaag tcattttcag	1216
aaaatctaca agtctcgttg agaccaccac catacctcag aaggtaggac tgtggcctag	1276
aagggaaagg aaagctgaga tgatgtctta ccgtagcagc agatcttgga tgggtccaggc	1336
tctatgtgac ctccagagca aagagaaaga cttcggacag tctaggtcct caaatgtccc	1396
ccattgagga caacagc	1413

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (164)..(2323)

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tgcgacagc tccgccacc cctccctgcc tccttttctt cctcagcggg tccggggccc	120
gctactctcc gggagggggcg cttcccgcag ccaagacaaa agg atg cca cgg aga	175
	Met Pro Arg Arg



aag aaa aaa gtt aaa gaa gtc tcc gaa tct cgg aac ctg gag aag aag	223
Lys Lys Lys Val Lys Glu Val Ser Glu Ser Arg Asn Leu Glu Lys Lys	
5 10 15 20	
gat gtg gaa act acc agt tct gtc agt gtg aag agg aag cgt aga ctt	271
Asp Val Glu Thr Thr Ser Ser Val Ser Val Lys Arg Lys Arg Arg Leu	
25 30 35	
gag gat gca ttc att gtg ata tcc gat agt gat gga gag gaa cca aag	319
Glu Asp Ala Phe Ile Val Ile Ser Asp Ser Asp Gly Glu Glu Pro Lys	
40 45 50	
gag gaa aat ggg ttg cag aaa acg aag aca aaa cag tcg aat aga gca	367
Glu Glu Asn Gly Leu Gln Lys Thr Lys Thr Lys Gln Ser Asn Arg Ala	
55 60 65	
aag tgt ttg gcc aaa aga aaa att gca cag atg aca gaa gaa gaa cag	415
Lys Cys Leu Ala Lys Arg Lys Ile Ala Gln Met Thr Glu Glu Glu Gln	
70 75 80	
ttt gct ctg gct ctc aaa atg agt gag cag gaa gct agg gag gtg aac	463
Phe Ala Leu Ala Leu Lys Met Ser Glu Gln Glu Ala Arg Glu Val Asn	
85 90 95 100	
agc cag gag gag gaa gaa gag gag ctc ttg agg aaa gcc att gct gaa	511
Ser Gln Glu Glu Glu Glu Glu Glu Leu Leu Arg Lys Ala Ile Ala Glu	
105 110 115	
agc ctg aat agt tgc cgg cct tct gat gct tcc gct acc aga tct cga	559
Ser Leu Asn Ser Cys Arg Pro Ser Asp Ala Ser Ala Thr Arg Ser Arg	
120 125 130	
cct ctg gcc act gga ccg tct tcc cag tcc cat caa gag aaa acc aca	607
Pro Leu Ala Thr Gly Pro Ser Ser Gln Ser His Gln Glu Lys Thr Thr	
135 140 145	
gac tct ggg ctc act gaa ggc ata tgg cag ctg gta cct cca tca ctg	655
Asp Ser Gly Leu Thr Glu Gly Ile Trp Gln Leu Val Pro Pro Ser Leu	
150 155 160	
ttt aaa ggc tca cat atc agt cag gga aac gag gct gag gaa aga gag	703
Phe Lys Gly Ser His Ile Ser Gln Gly Asn Glu Ala Glu Glu Arg Glu	
165 170 175 180	
gag cct tgg gac cac act gaa aaa act gaa gag gag ccg gtc tct ggc	751
Glu Pro Trp Asp His Thr Glu Lys Thr Glu Glu Glu Pro Val Ser Gly	
185 190 195	
agc tca gga agc tgg gac cag tca agc cag cca gtg ttt gag aat gtg	799
Ser Ser Gly Ser Trp Asp Gln Ser Ser Gln Pro Val Phe Glu Asn Val	
200 205 210	
aac gtt aaa tct ttt gac aga tgt act ggc cac tcg gct gag cac aca	847
Asn Val Lys Ser Phe Asp Arg Cys Thr Gly His Ser Ala Glu His Thr	
215 220 225	
cag tgt ggg aag cca cag gaa agt act ggg agg ggt tct gct ttt ctc	895

Gln Cys Gly Lys Pro Gln Glu Ser Thr Gly Arg Gly Ser Ala Phe Leu	
230 235 240	
aaa gct gtc cag ggt agc ggg gac aca tct agg cac tgt cta cct acc	943
Lys Ala Val Gln Gly Ser Gly Asp Thr Ser Arg His Cys Leu Pro Thr	
245 250 255 260	
cta gca gat gcc aaa ggt ctc cag gac act ggg ggc act gtg aac tat	991
Leu Ala Asp Ala Lys Gly Leu Gln Asp Thr Gly Gly Thr Val Asn Tyr	
265 270 275	
ttc tgg ggt att cca ttc tgc cct gat gga gta gac cct aac cag tat	1039
Phe Trp Gly Ile Pro Phe Cys Pro Asp Gly Val Asp Pro Asn Gln Tyr	
280 285 290	
acc aag gtc att ctc tgc cag ttg gag gtt tat caa aag agc ctg aaa	1087
Thr Lys Val Ile Leu Cys Gln Leu Glu Val Tyr Gln Lys Ser Leu Lys	
295 300 305	
atg gct cag agg cag ctc ctt aat aaa aaa ggt ttt ggg gaa cca gtg	1135
Met Ala Gln Arg Gln Leu Leu Asn Lys Lys Gly Phe Gly Glu Pro Val	
310 315 320	
tta cct aga cct ccc tct ctg atc cag aat gaa tgt ggc caa gga gag	1183
Leu Pro Arg Pro Pro Ser Leu Ile Gln Asn Glu Cys Gly Gln Gly Glu	
325 330 335 340	
cag gct agt gag aaa aat gaa tgc atc tca gaa gat atg gga gat gaa	1231
Gln Ala Ser Glu Lys Asn Glu Cys Ile Ser Glu Asp Met Gly Asp Glu	
345 350 355	
gac aaa gag gag agg cag gag tct agg gca tct gac tgg cac tca aaa	1279
Asp Lys Glu Glu Arg Gln Glu Ser Arg Ala Ser Asp Trp His Ser Lys	
360 365 370	
acc aag gat ttc cag gaa agc tca att aaa agc ttg aaa gag aaa ctt	1327
Thr Lys Asp Phe Gln Glu Ser Ser Ile Lys Ser Leu Lys Glu Lys Leu	
375 380 385	
ttg ttg gag gaa gaa cca aca acc agt cat ggt cag tct tcc caa ggg	1375
Leu Leu Glu Glu Glu Pro Thr Thr Ser His Gly Gln Ser Ser Gln Gly	
390 395 400	
att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct tca caa	1423
Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala Ser Gln	
405 410 415 420	
agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg cca gag	1471
Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met Pro Glu	
425 430 435	
agt tct gca gaa gaa atc act gtt tgt cct gag aca cag cta agt tcc	1519
Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu Ser Ser	
440 445 450	
tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc aga gat	1567
Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser Arg Asp	

455	460	465	
atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt ggt aac Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val Gly Asn 470 475 480			1615
aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca tcc agt Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser Ser Ser 485 490 495 500			1663
aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc aca aag Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro Thr Lys 505 510 515			1711
att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa gat aca Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu Asp Thr 520 525 530			1759
gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac agt ggg Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp Ser Gly 535 540 545			1807
aca gct gcc cag act tct cta gac att gac aag aat gag aag tgt tac Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys Cys Tyr 550 555 560			1855
ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat gtg gac Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His Val Asp 565 570 575 580			1903
tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct gaa ggg Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro Glu Gly 585 590 595			1951
agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag agg ctg Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln Arg Leu 600 605 610			1999
aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt agt ttc Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu Ser Phe 615 620 625			2047
ttg gaa cag tct gag cac aag act tca gat gca gac atc aag tct tca Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys Ser Ser 630 635 640			2095
gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag gca ggc Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu Ala Gly 645 650 655 660			2143
tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta aat gaa Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu Asn Glu 665 670 675			2191
tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat tgc tta Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp Cys Leu 680 685 690			2239

gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg aca cgg	2287
Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg	
695 700 705	
acc aaa gct ggc aga gga aga agg aga aaa ttc tga attt ctagggtcca	2337
Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe *	
710 715 720	
aaagttgaca aaaccattag taggaggggt gggccatggt cattaagcca tagtgggtccc	2397
tagttcattg ttgagcaagt tttagccctg cagtttttcac caccagcacc taccagcat	2457
tctgggttttt atgttttttta tgatctatgc agacaactgt gtattctgtt ttataacagt	2517
ttgtttgaat ttacttacag ttaaaaaatt taaatat	2554

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (599)..(1648)

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cctgcgcaca gtcgcgcca cccctccctg cctccttttc ttcctcagcg ggtccgcggc	180
ccgtactct ccgggagggg cgcttcccga cgccaagaca aaaggatgcc acggagaaag	240
aaaaaagtta aagaagtctc cgaatctcgg aacctggaga agaaggatgt ggaaactacc	300
agttctgtca gtgtgaagag gaagcgtaga cttgaggatg cattcattgt gatatccgat	360
agtgatggag aggaaccaa ggaggaaaat gggttgcaga aaacgaagac aaaacagtcg	420
aatagagcaa agtgtttggc caaaagaaaa atcgcacaga tgacagaaga agaacagttt	480
gctctggctc tcaaatgag tgagcaggaa gctagggagg tgaacagcca ggaggaggaa	540
gaagaggagc tcttgaggaa agccattgct gaaagcctga atagttgccg gccttctg	598
atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc	646
Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro	
1 5 10 15	
agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc	694
Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser	
20 25 30	

caa ggg att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct	742
Gln Gly Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala	
35 40 45	
tca caa agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg	790
Ser Gln Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met	
50 55 60	
cca gag agt tct gca gaa gaa atc act gtt tgt cct gag acc cag cta	838
Pro Glu Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu	
65 70 75 80	
agt tcc tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc	886
Ser Ser Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser	
85 90 95	
aga gat atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt	934
Arg Asp Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val	
100 105 110	
ggt aac aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca	982
Gly Asn Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser	
115 120 125	
tcc agt aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc	1030
Ser Ser Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro	
130 135 140	
aca aag att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa	1078
Thr Lys Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu	
145 150 155 160	
gat aca gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac	1126
Asp Thr Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp	
165 170 175	
agt ggg aca gct gcc cag act tct cta gac att gac aag aat gag aag	1174
Ser Gly Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys	
180 185 190	
tgt tac ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat	1222
Cys Tyr Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His	
195 200 205	
gtg gac tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct	1270
Val Asp Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro	
210 215 220	
gaa ggg agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag	1318
Glu Gly Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln	
225 230 235 240	
agg ctg aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt	1366
Arg Leu Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu	
245 250 255	
agt ttc ttg gaa cag tct gag cac aag act tca gat gca gac atc aag	1414

Ser	Phe	Leu	Glu	Gln	Ser	Glu	His	Lys	Thr	Ser	Asp	Ala	Asp	Ile	Lys	
			260					265					270			
tct	tca	gaa	aca	gga	gcc	ttc	agg	gtg	cct	tca	cca	ggg	atg	gaa	gag	1462
Ser	Ser	Glu	Thr	Gly	Ala	Phe	Arg	Val	Pro	Ser	Pro	Gly	Met	Glu	Glu	
		275					280					285				
gca	ggc	tgc	agc	aga	gag	atg	cag	agt	tct	ttc	aca	cgt	cgt	gac	tta	1510
Ala	Gly	Cys	Ser	Arg	Glu	Met	Gln	Ser	Ser	Phe	Thr	Arg	Arg	Asp	Leu	
	290					295					300					
aat	gaa	tct	ccc	gtc	aag	tct	ttt	gtt	tcc	att	tca	gaa	gcc	aca	gat	1558
Asn	Glu	Ser	Pro	Val	Lys	Ser	Phe	Val	Ser	Ile	Ser	Glu	Ala	Thr	Asp	
305					310					315					320	
tgc	tta	gtg	gac	ttt	aaa	aag	caa	gtt	act	gtc	cag	cca	ggt	agt	cgg	1606
Cys	Leu	Val	Asp	Phe	Lys	Lys	Gln	Val	Thr	Val	Gln	Pro	Gly	Ser	Arg	
			325					330						335		
aca	cgg	acc	aaa	gct	ggc	aga	gga	aga	agg	aga	aaa	ttc	tga	atttcta		1655
Thr	Arg	Thr	Lys	Ala	Gly	Arg	Gly	Arg	Arg	Lys	Phe	*				
		340					345					350				
gggtccaaaa	ggtgacaaaa	ccattagtag	gaggggtggg	ccatgttcat	taagccatag											1715
tggtccctag	ttcattgttg	agcaagtttt	agccctgcag	ttttcaccac	cagcacctac											1775
ccagcattct	ggtttttatg	ttttttatga	tctatgcaga	caactgtgta	ttctgtttta											1835
taacagtttg	tttgaattta	cttacagtta	aaaaatttaa	atat												1879

<210> 123  
 <211> 2288  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (208)..(663)

<220>  
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 <222> (1)...(2288)  
 <223> n = a,t,c or g

<400> 123																
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tgttttgcta	ggcaaagtta	caagtgcact	aatgggagct	caaagtgtgtg	tgtgtctctc											120
tgtgtgtttg	tgtgtgtgtg	tgcaactcaag	acctctaaca	gcctcgaagc	ctgggggtggc											180
atcccggcct	tgccattagc	atgcctc	atg cat cat	cag atg aca	agg aca											231
			Met His	His Gln	Met Thr	Arg Thr										

acc ctc atg acg aag caa cat gaa tta ggg ggc ctc ttg gcc ttg gtc 279  
 Thr Leu Met Thr Lys Gln His Glu Leu Gly Gly Leu Leu Ala Leu Val  
 10 15 20

caa aat tgt caa tca gaa atg aac ata aag gac tcc aga gca gtg gga 327  
 Gln Asn Cys Gln Ser Glu Met Asn Ile Lys Asp Ser Arg Ala Val Gly  
 25 30 35 40

ctg tct gtc aaa aga ctc tgt ata tct ttt gtg gat gag ttt tgt gag 375  
 Leu Ser Val Lys Arg Leu Cys Ile Ser Phe Val Asp Glu Phe Cys Glu  
 45 50 55

aga aca gag aga cca ttg tac ctg gca caa ggg ctc ttc atg aaa agg 423  
 Arg Thr Glu Arg Pro Leu Tyr Leu Ala Gln Gly Leu Phe Met Lys Arg  
 60 65 70

gag act tac tgg gag gtg caa gac agt ggc att tct cct ctc ctc ttg 471  
 Glu Thr Tyr Trp Glu Val Gln Asp Ser Gly Ile Ser Pro Leu Leu Leu  
 75 80 85

ctg ctc agc aca gcc ctg gat tgc agc ccc gag gct gag acc aga caa 519  
 Leu Leu Ser Thr Ala Leu Asp Cys Ser Pro Glu Ala Glu Thr Arg Gln  
 90 95 100

agc ccg gga ggc aga aag atg ctc caa gaa cca aca cta tca atg tct 567  
 Ser Pro Gly Gly Arg Lys Met Leu Gln Glu Pro Thr Leu Ser Met Ser  
 105 110 115 120

ttg caa atc ctc aca gga ttc ctg tgg gtc cag ctt tgg aac tgg gaa 615  
 Leu Gln Ile Leu Thr Gly Phe Leu Trp Val Gln Leu Trp Asn Trp Glu  
 125 130 135

acc ttt ctt cgg atc cgc act cat tcc act gat gcc agc tgc ccc tga 663  
 Thr Phe Leu Arg Ile Arg Thr His Ser Thr Asp Ala Ser Cys Pro \*  
 140 145 150

aggatgccag tactgtggtg tgtgagtctc agcagccgcc cacacgctcc taactctgct 723

gcatggcaga tgcctaggtg gaaatagcaa aaacaaggcc caggctgggg ccagggccag 783

aggggaaggc cctggattct cactcatgtg agatcttgaa tctctttctt tgttctgttt 843

gtttagtttag tatcatctgg taaaatagtt aaaaaacaac aaaaaactct gtatctgttt 903

ctagcatgtg ctgcattgac tctattaatc acatttcaaa ttcaccctac attcctctcc 963

tcttcactag cctctctgaa ggtgtcctgg ccagccctgg agaagcactg gtgtctgcag 1023

caccctcag ttctgtgtcc tcagcccaca ggccactgtg ataatggtct gtttagcact 1083

tctgtattta ttgtaagaat gattataatg aagatacaca ctgtaactac aagaaattat 1143

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Thr	Glu	Val	Val	Leu	Leu	Ala	Cys	Gly	Ser	Phe	Asn	Pro	Ile	Thr	Asn		
			10					15					20				
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Met	His	Leu	Arg	Leu	Phe	Glu	Leu	Ala	Lys	Asp	Tyr	Met	Asn	Gly	Thr		
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gga	agg	tac	aca	gtt	gtc	aaa	ggc	atc	atc	tct	cct	gtt	ggg	gat	gcc	256	
Gly	Arg	Tyr	Thr	Val	Val	Lys	Gly	Ile	Ile	Ser	Pro	Val	Gly	Asp	Ala		
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tac	aag	aag	aaa	gga	ctc	att	cct	gcc	tat	cac	cgg	gtc	atc	atg	gca	304	
Tyr	Lys	Lys	Lys	Gly	Leu	Ile	Pro	Ala	Tyr	His	Arg	Val	Ile	Met	Ala		
	55				60				65					70			
gaa	ctt	gct	acc	aag	aat	tct	aaa	tgg	gtg	gaa	gtt	gat	aca	tgg	gaa	352	
Glu	Leu	Ala	Thr	Lys	Asn	Ser	Lys	Trp	Val	Glu	Val	Asp	Thr	Trp	Glu		
			75				80					85					
agt	ctt	cag	aag	gag	tgg	aaa	gag	act	ctg	aag	gtg	cta	aga	cac	cat	400	
Ser	Leu	Gln	Lys	Glu	Trp	Lys	Glu	Thr	Leu	Lys	Val	Leu	Arg	His	His		
		90					95					100					
caa	gag	aaa	ttg	gag	gct	agt	gac	tgt	gat	cac	cag	cag	aac	tca	cct	448	
Gln	Glu	Lys	Leu	Glu	Ala	Ser	Asp	Cys	Asp	His	Gln	Gln	Asn	Ser	Pro		
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act	cta	gaa	agg	cct	gga	agg	aag	agg	aag	tgg	act	gaa	aca	caa	gat	496	
Thr	Leu	Glu	Arg	Pro	Gly	Arg	Lys	Arg	Lys	Trp	Thr	Glu	Thr	Gln	Asp		
	120				125					130							
tct	agt	caa	aag	aaa	tcc	cta	gag	cca	aaa	aca	aaa	gct	gtg	cca	aag	544	
Ser	Ser	Gln	Lys	Lys	Ser	Leu	Glu	Pro	Lys	Thr	Lys	Ala	Val	Pro	Lys		
	135				140				145					150			
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Val	Lys	Leu	Leu	Cys	Gly	Ala	Asp	Leu	Leu	Glu	Ser	Phe	Ala	Val	Pro		
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Asn	Leu	Trp	Lys	Ser	Glu	Asp	Ile	Thr	Gln	Ile	Val	Ala	Asn	Tyr	Gly		
		170					175					180					
ctc	ata	tgt	gtt	act	cgg	gct	gga	aat	gat	gct	cag	aag	ttt	atc	tat	688	
Leu	Ile	Cys	Val	Thr	Arg	Ala	Gly	Asn	Asp	Ala	Gln	Lys	Phe	Ile	Tyr		
	185						190					195					
gaa	tcg	gat	gtg	ctg	tgg	aaa	cac	cgg	agc	aac	att	cac	gtg	gtg	aat	736	
Glu	Ser	Asp	Val	Leu	Trp	Lys	His	Arg	Ser	Asn	Ile	His	Val	Val	Asn		
	200					205				210							
gaa	tgg	atc	gct	aat	gac	atc	tca	tcc	aca	aaa	atc	cgg	aga	gcc	ctc	784	
Glu	Trp	Ile	Ala	Asn	Asp	Ile	Ser	Ser	Thr	Lys	Ile	Arg	Arg	Ala	Leu		
	215				220				225					230			
aga	agg	ggc	cag	agc	att	cgc	tac	ttg	gta	cca	gat	ctt	gtc	caa	gaa	832	
Arg	Arg	Gly	Gln	Ser	Ile	Arg	Tyr	Leu	Val	Pro	Asp	Leu	Val	Gln	Glu		

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                235                240                245
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Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser Glu Ser Glu Asp Arg Asn
                250                255                260

gct ggg gtc atc ctg gcc cct ttg cag aga aac act gca gaa gct aag      928
Ala Gly Val Ile Leu Ala Pro Leu Gln Arg Asn Thr Ala Glu Ala Lys
                265                270                275

aca tag gaattctaca gcatgatatt tcagacttcc catttgggga tctgaaacaa      984
Thr *
                280

tctgggagtt aataactggg gaaagaagtt gtgatctgtt gcctaaacta aagcttaaaa    1044

gtt                                                                    1047

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Leu Arg Gly Lys Lys Lys Glu Leu Leu Lys Gln Leu Asp Asp Leu
                10                15                20

aag gtg gag ctg tcc cag ctg cgc gtc gcc aaa gtg aca ggc ggt gcg      147
Lys Val Glu Leu Ser Gln Leu Arg Val Ala Lys Val Thr Gly Gly Ala
                25                30                35                40

gcc tcc aag ctc tct aag atc cga gtc gtc cgg aaa tcc att gcc cgt      195
Ala Ser Lys Leu Ser Lys Ile Arg Val Val Arg Lys Ser Ile Ala Arg
                45                50                55

gtt ctc aca gtt att aac cag act cag aaa gaa aac ctc agg aaa ttc      243
Val Leu Thr Val Ile Asn Gln Thr Gln Lys Glu Asn Leu Arg Lys Phe
                60                65                70

tac aag ggc aag aag tac aag ccc ctg gac ctg cgg cct aag aag aca      291
Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp Leu Arg Pro Lys Lys Thr
                75                80                85

cgt gcc atg cgc cgc cgg ctc aac aag cac gag gag aac ctg aag acc      339
Arg Ala Met Arg Arg Arg Leu Asn Lys His Glu Glu Asn Leu Lys Thr

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90	95	100	
aag aag cag cag cgg aag gag cgg ctg tac ccg ctg cag aag tac aca			387
Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr Pro Leu Gln Lys Tyr Thr			
105	110	115	120
gtg aac gcc tga acg tcacatgggt tcataaaaga gagctggccg aagagaacaa			442
Val Asn Ala *			
aagaaaagtg tgtattttaat atgcaattct gt			474

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ccagaacaca ctgctacaag gtcccag atg gcc acg tct ctg gat ttt aaa	171
Met Ala Thr Ser Leu Asp Phe Lys	
1 5	
act tat gta gat cag gca tgt aga gct gct gag gag ttt gtc aat att	219
Thr Tyr Val Asp Gln Ala Cys Arg Ala Ala Glu Glu Phe Val Asn Ile	
10 15 20	
tac tat gag aca atg gat aaa aga aga cgg gca cta acc agg ctg tat	267
Tyr Tyr Glu Thr Met Asp Lys Arg Arg Arg Ala Leu Thr Arg Leu Tyr	
25 30 35 40	
ctg gac aag gcc acc tta ata tgg aat gga aat gct gtt tca ggg ctg	315
Leu Asp Lys Ala Thr Leu Ile Trp Asn Gly Asn Ala Val Ser Gly Leu	
45 50 55	
gat gcc cta aat aat ttt ttt gac aca ttg cct tct agt gag ttc cag	363
Asp Ala Leu Asn Asn Phe Phe Asp Thr Leu Pro Ser Ser Glu Phe Gln	
60 65 70	
gtc aat atg tta gat tgc caa cca gtt cat gag caa gca act cag tcc	411
Val Asn Met Leu Asp Cys Gln Pro Val His Glu Gln Ala Thr Gln Ser	
75 80 85	
caa act aca gtt ctt gtt gtg acc agt gga act gtg aag ttt gat gga	459
Gln Thr Thr Val Leu Val Val Thr Ser Gly Thr Val Lys Phe Asp Gly	
90 95 100	

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aac aaa caa cat ttc ttc aac cag aac ttc ctg ctg act gct cag tcc      507
Asn Lys Gln His Phe Phe Asn Gln Asn Phe Leu Leu Thr Ala Gln Ser
105                      110                      115                      120

act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt      555
Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe
                      125                      130                      135

caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt      608
Gln Asp Trp Ser Ser Ser  *
                      140

agttccagca attgaaatTT atgtgaatta ttttgattgt agaagcacta taatatgtgc      668

tgaaactaaa tttctttaat attttctatt cctgtcagca ccttttctag cagctgccag      728

tttgagagcat tgccctctaa gagctttaaa actatTTTTT tacatgcctt atatacattc      788

cactaatgac attottataa taatattaaa cacatgatct tggTactaac atactcactg      848

tgaaccCagc ctattgcaaa aataaaatct ttttataata ttatctatgg gatgtcagca      908

caatataaca ctctgggaag aagtggagtt ttttggttat taggttaatt ttctagtaaa      968

acacattgcc tgTTTTcagt taacactggT aatgccattt taatatatgg cTTTTtcaaa    1028

tcagttcagt gaaaatagta cagatttagg tttacataac tactctgaca tactggaatt    1088

gcatatagag atgttcagtg gtcgtTTTTc atTTtaagta atTTTTgttt tggcattTTTT    1148

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caggtctata catttaggta atgaatggta gtagaactaa tagctTTtaac aggagaatag    1328

ggaatgagaa atagaaatcc aaggctgaag ccaaaagtaa ggaggggtggc caaatggtaa    1388

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ttttttccca gtgctttgta ctgtcaactg cattatcttt aattattTta aggtagaatt    1808

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tgttcccgct atgtggataa ctcttctttt taaaaagaaa atagagaata gcaaattctc    1928

atgataatcc tcaaaagaac aaaatgctta actttatctc ttaatttcta aaggtaaata    1988

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 ttgggcaaag gagaaattca gttttcagta gcatcattgg aagtattatg acttgtgctt 180  
 aaactttttac cagtgcattc ttttgataaa tagaaatagt aacaaaat atg aat ttt 237  
 Met Asn Phe  
 1  
 aaa tat gtg ggg aga tac ata aag aac att gct tat ttg ttc ttg aaa 285  
 Lys Tyr Val Gly Arg Tyr Ile Lys Asn Ile Ala Tyr Leu Phe Leu Lys  
 5 10 15  
 ata aca gtg att caa ata ttt cat tca gat tta cct atg cct aat gaa 333  
 Ile Thr Val Ile Gln Ile Phe His Ser Asp Leu Pro Met Pro Asn Glu  
 20 25 30 35  
 aaa aat gat gca gaa ctt gat tct cca cct tca aag aaa aaa aga tta 381  
 Lys Asn Asp Ala Glu Leu Asp Ser Pro Pro Ser Lys Lys Lys Arg Leu  
 40 45 50

ggt ttt ttc cag act tat gat aca gaa tat tta aaa gtt ggt ttt att Gly Phe Phe Gln Thr Tyr Asp Thr Glu Tyr Leu Lys Val Gly Phe Ile 55 60 65	429
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tgt gga gag atc tta tcc agt gaa aac atg aag cca gca aat ctt tct Cys Gly Glu Ile Leu Ser Ser Glu Asn Met Lys Pro Ala Asn Leu Ser 85 90 95	525
cat cat ttg aag aca aaa cat tca gaa tta gaa aac aaa cca gta gat His His Leu Lys Thr Lys His Ser Glu Leu Glu Asn Lys Pro Val Asp 100 105 110 115	573
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aaa aag tgt tta cta gtt gaa aag tca ctt gtg aaa gct tct tat tta Lys Lys Cys Leu Leu Val Glu Lys Ser Leu Val Lys Ala Ser Tyr Leu 135 140 145	669
att gct ttc caa act gct gca agc aag aag cca ttc tcc att gct gaa Ile Ala Phe Gln Thr Ala Ala Ser Lys Lys Pro Phe Ser Ile Ala Glu 150 155 160	717
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tca agt gct gga gac aaa atg aaa act att cca ctt tct aat gtt aca Ser Ser Ala Gly Asp Lys Met Lys Thr Ile Pro Leu Ser Asn Val Thr 180 185 190 195	813
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Lys Tyr Ile Asp Ser Lys Ser Leu Asn Trp Lys His Cys Val Gly Leu	
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tgt acc gat ggg gct gca agc atg act ggc agg tat tct ggt tta aaa	1149
Cys Thr Asp Gly Ala Ala Ser Met Thr Gly Arg Tyr Ser Gly Leu Lys	
295 300 305	
gca aaa att caa gaa gtt gcc atg aat aca gcg gca ttt aca cat tgt	1197
Ala Lys Ile Gln Glu Val Ala Met Asn Thr Ala Ala Phe Thr His Cys	
310 315 320	
ttt att cac cgt gaa cgt tta gtg gca gaa aag ttg tct cca tgt tta	1245
Phe Ile His Arg Glu Arg Leu Val Ala Glu Lys Leu Ser Pro Cys Leu	
325 330 335	
cat aaa att ctt ttg cag tca gca caa att tta agt ttt ata aag agc	1293
His Lys Ile Leu Leu Gln Ser Ala Gln Ile Leu Ser Phe Ile Lys Ser	
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Asn Ala Leu Asn Ser Arg Met Leu Thr Ile Leu Cys Glu Glu Met Gly	
360 365 370	
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Ser Glu His Val Ser Leu Pro Leu His Ala Glu Val Arg Trp Ile Ser	
375 380 385	
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Arg Gly Arg Met Leu Lys Arg Leu Phe Glu Leu Arg His Glu Ile Glu	
390 395 400	
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Ile Phe Leu Ser Gln Lys His Ser Asp Leu Ala Lys Tyr Phe His Asp	
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Glu Glu Trp Val Gly Lys Leu Ala Tyr Leu Ser Asp Ile Phe Ser Leu	
420 425 430 435	
ata aat gaa tta aat tta agt ctc caa gga act ttg act act ttc ttc	1581
Ile Asn Glu Leu Asn Leu Ser Leu Gln Gly Thr Leu Thr Thr Phe Phe	
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Asn Leu Cys Asn Lys Ile Asp Val Phe Lys Arg Lys Leu Lys Met Trp	
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Glu Phe Ser Asn Ser Ser Gly Leu Asn Met Thr Asp Ile Thr Arg Ile	
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<222> (97)..(798)

<400> 128

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gag gaa gag gaa gcc ggc gag gag gcg gag ggg gag gaa gag gag gac	162
Glu Glu Glu Glu Ala Gly Glu Glu Ala Glu Gly Glu Glu Glu Glu Asp	
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Asp Ser Phe Leu Leu Leu Gln Gln Ser Val Thr Leu Gly Ser Ser Gly	
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Glu Val Asp Arg Leu Val Ala Gln Ile Gly Glu Thr Leu Gln Leu Asp	
40 45 50	
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Ala Ala Gln Asp Ser Pro Ala Ser Pro Cys Ala Pro Pro Gly Val Pro	
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ctg cgg gcc ccg ggg ccc ctg gct gcg gcg gtg ccg acg gac aag gcc	354
Leu Arg Ala Pro Gly Pro Leu Ala Ala Ala Val Pro Thr Asp Lys Ala	
75 80 85	
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Arg Pro Pro Ala Val Pro Leu Leu Leu Pro Pro Ala Ser Ala Glu Thr	
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Val Gly Pro Ala Pro Ser Gly Ala Leu Arg Cys Ala Leu Gly Asp Arg	
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Gly Arg Val Arg Gly Arg Ala Ala Pro Tyr Cys Val Ala Glu Val Ala	
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Ala Gly Pro Ser Ala Leu Pro Gly Pro Cys Arg Arg Gly Trp Leu Arg	
135 140 145 150	
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Asp Ala Val Thr Ser Arg Arg Leu Gln Gln Arg Arg Trp Thr Gln Ala	
155 160 165	
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Gly Ala Arg Ala Gly Asp Asp Asp Pro His Arg Leu Leu Gln Gln Leu	
170 175 180	
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Val Leu Ser Gly Asn Leu Ile Lys Glu Ala Val Arg Arg Leu Gln Arg	
185 190 195	

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Gly Gly Gly Arg Ser Gly Pro Asp Arg Ile Ala Leu Gln Pro Ser Gly	
215 220 225 230	
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Ser Leu Leu *	
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tggcttggtc atcctccaga tgtagctatt gatgtacact tcgcaacgga gtgtctgaaa	2101
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      Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu
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ccg ccg cgt ttt ctg gag gcc ttc ggg cgg ctg tgg cag gta cag agc      159
Pro Pro Arg Phe Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser
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cgt ctg ggt agc ggc tcc tcc gcc tgc gtg tat cgg gtt cgc tgc tgc      207
Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys
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ggc aac cct ggc tgc ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca      255
Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro
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gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa      303
Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys
                60                65                70                75

gag agg gcg gcg ctg gaa cag ttg cag ggt cac aga aac atc gtg act      351
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr
                80                85                90

ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc      399
Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg
                95                100                105

tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tgc gaa ttg ctc tta      447
Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu
                110                115                120

tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc      495
Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala
                125                130                135

cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc      543
Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val
                140                145                150                155

cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa      591

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Cys	Phe	Lys	Leu	Ile	Asp	Phe	Gly	Leu	Ser	Phe	Lys	Glu	Gly	Asn	Gln	
			175					180					185			
gat	gta	aag	tat	att	cag	aca	gac	ggg	tat	cgg	gct	cca	gaa	gca	gaa	687
Asp	Val	Lys	Tyr	Ile	Gln	Thr	Asp	Gly	Tyr	Arg	Ala	Pro	Glu	Ala	Glu	
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Leu	Gln	Asn	Cys	Leu	Ala	Gln	Ala	Gly	Leu	Gln	Ser	Asp	Thr	Glu	Cys	
	205					210					215					
acc	tca	gct	gtt	gat	ctg	tgg	agc	cta	gga	atc	att	tta	ctg	gaa	atg	783
Thr	Ser	Ala	Val	Asp	Leu	Trp	Ser	Leu	Gly	Ile	Ile	Leu	Leu	Glu	Met	
220				225						230					235	
ttc	tca	gga	atg	aaa	ctg	aaa	cat	aca	gtc	aga	tct	cag	gaa	tgg	aag	831
Phe	Ser	Gly	Met	Lys	Leu	Lys	His	Thr	Val	Arg	Ser	Gln	Glu	Trp	Lys	
			240						245				250			
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Ala	Asn	Ser	Ser	Ala	Ile	Ile	Asp	His	Ile	Phe	Ala	Ser	Lys	Ala	Val	
			255					260					265			
gtg	aat	gcc	gca	att	cca	gcc	tat	cac	cta	aga	gac	ctt	atc	aaa	agc	927
Val	Asn	Ala	Ala	Ile	Pro	Ala	Tyr	His	Leu	Arg	Asp	Leu	Ile	Lys	Ser	
	270					275						280				
atg	ctt	cat	gat	gat	cca	agc	aga	aga	att	cct	gct	gaa	atg	gca	ttg	975
Met	Leu	His	Asp	Asp	Pro	Ser	Arg	Arg	Ile	Pro	Ala	Glu	Met	Ala	Leu	
	285					290					295					
tgc	agc	cca	ttc	ttt	agc	att	cct	ttt	gcc	cct	cat	att	gaa	gat	ctg	1023
Cys	Ser	Pro	Phe	Phe	Ser	Ile	Pro	Phe	Ala	Pro	His	Ile	Glu	Asp	Leu	
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gtc	atg	ctt	ccc	act	cca	gtg	cta	aga	ctg	ctg	aat	gtg	ctg	gat	gat	1071
Val	Met	Leu	Pro	Thr	Pro	Val	Leu	Arg	Leu	Leu	Asn	Val	Leu	Asp	Asp	
			320						325				330			
gat	tat	ctt	gag	aat	gaa	gag	gaa	tat	gaa	gat	gtt	gta	gaa	gat	gta	1119
Asp	Tyr	Leu	Glu	Asn	Glu	Glu	Glu	Tyr	Glu	Asp	Val	Val	Glu	Asp	Val	
			335					340					345			
aaa	gag	gag	tgt	caa	aaa	tat	gga	cca	gtg	gta	tct	cta	ctt	gtt	cca	1167
Lys	Glu	Glu	Cys	Gln	Lys	Tyr	Gly	Pro	Val	Val	Ser	Leu	Leu	Val	Pro	
	350						355					360				
aag	gaa	aat	cct	gg												

380	385	390	395	
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Gly Lys Phe Val Val Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg				
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gga tat ctg tat caa acc ttg ctt taa tcagt aacctaagga ctgtttcctt				1363
Gly Tyr Leu Tyr Gln Thr Leu Leu *				
	415	420		
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gtgagcctat ctaagtcttt gcctactaag gcttcctatg ggagaaaagt catgcttgac				1963
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aaacaaaaca aacaaacaaa aaaaacagcc ggttgcggtg gcacatgctt gcagtcctcg				240
ttactcaaga agcagaagca agaggattgc ttgagcccaa cagtgccttc aaaagacaaa				300
gaacgcctgc aagcc atg atg acc cac ctg cat gtg aag tct aca gaa ccc				351
Met Met Thr His Leu His Val Lys Ser Thr Glu Pro				

	1	5	10	
aaa gcc gcc cct cag ccc ttg aat ctg gta tca agt gtc act ctc tcc				399
Lys Ala Ala Pro Gln Pro Leu Asn Leu Val Ser Ser Val Thr Leu Ser	15	20	25	
aag tcc gca tcg gag gct tct cca cag agc tta cct cat act cca acg				447
Lys Ser Ala Ser Glu Ala Ser Pro Gln Ser Leu Pro His Thr Pro Thr	30	35	40	
acc cca acc gcc ccc ctg act ccc gtc acc caa ggc ccc tct gtc atc				495
Thr Pro Thr Ala Pro Leu Thr Pro Val Thr Gln Gly Pro Ser Val Ile	45	50	55	60
aca acc acc agc atg cac acg gtg gga ccc atc cgc agg cgg tac tca				543
Thr Thr Thr Ser Met His Thr Val Gly Pro Ile Arg Arg Arg Tyr Ser	65	70	75	
gac aaa tac aac gtg ccc att tcg tca gca gat att gcg cag aac caa				591
Asp Lys Tyr Asn Val Pro Ile Ser Ser Ala Asp Ile Ala Gln Asn Gln	80	85	90	
gaa ttt tat aag aac gca gaa gtt aga cca cca ttt aca tat gca tct				639
Glu Phe Tyr Lys Asn Ala Glu Val Arg Pro Pro Phe Thr Tyr Ala Ser	95	100	105	
tta att agg cag gcc att ctc gaa tct cca gaa aag cag cta aca cta				687
Leu Ile Arg Gln Ala Ile Leu Glu Ser Pro Glu Lys Gln Leu Thr Leu	110	115	120	
aat gag atc tat aac tgg ttc aca cga atg ttt gct tac ttc cga cgc				735
Asn Glu Ile Tyr Asn Trp Phe Thr Arg Met Phe Ala Tyr Phe Arg Arg	125	130	135	140
aac gcg gcc acg tgg aag aat gca gtg cgt cat aat ctt agt ctt cac				783
Asn Ala Ala Thr Trp Lys Asn Ala Val Arg His Asn Leu Ser Leu His	145	150	155	
aag tgt ttt gtg cga gta gaa aac gtt aaa ggg gca gta tgg aca gtg				831
Lys Cys Phe Val Arg Val Glu Asn Val Lys Gly Ala Val Trp Thr Val	160	165	170	
gat gaa gta gaa ttc caa aaa cga agg cca caa aag atc agt ggt aac				879
Asp Glu Val Glu Phe Gln Lys Arg Arg Pro Gln Lys Ile Ser Gly Asn	175	180	185	
cct tcc ctt att aaa aac atg cag agc agc cac gcc tac tgc aca cct				927
Pro Ser Leu Ile Lys Asn Met Gln Ser Ser His Ala Tyr Cys Thr Pro	190	195	200	
ctc aat gca gct tta cag gct tca atg gct gag aat agt ata cct cta				975
Leu Asn Ala Ala Leu Gln Ala Ser Met Ala Glu Asn Ser Ile Pro Leu	205	210	215	220
tac act acc gct tcc atg gga aat ccc act ctg ggc aac tta gcc agc				1023
Tyr Thr Thr Ala Ser Met Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser	225	230	235	

gca ata cgg gaa gag ctg aac ggg gca atg gag cat acc aac agc aac 1071  
Ala Ile Arg Glu Glu Leu Asn Gly Ala Met Glu His Thr Asn Ser Asn  
240 245 250

gag agt gac agc agt cca ggc aga tct cct atg caa gcc gtg cat cct 1119  
Glu Ser Asp Ser Ser Pro Gly Arg Ser Pro Met Gln Ala Val His Pro  
255 260 265

gta cac gtc aaa gaa gag ccc ctc gat cca gag gaa gct gaa ggg ccc 1167  
Val His Val Lys Glu Glu Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro  
270 275 280

ctg tcc tta gtg aca aca gcc aac cac agt cca gat ttt gac cat gac 1215  
Leu Ser Leu Val Thr Thr Ala Asn His Ser Pro Asp Phe Asp His Asp  
285 290 295 300

aga gat tac gaa gat gaa cca gta aac gag gac atg gag tga ctatcgg 1264  
Arg Asp Tyr Glu Asp Glu Pro Val Asn Glu Asp Met Glu \*  
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Met Cys Phe Pro Lys Val Leu  
1 5

tct gat gac atg aag aag ctg aag gcc cga atg cac cag gcc ata gaa 159  
Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu  
10 15 20

aga ttt tat gat aaa atg caa aat gca gaa tca gga cgt gga cag gtg 207  
Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val  
25 30 35

atg tcg agc ctg gca gag ctg gag gac gac ttc aaa gag ggc tac ctg 255  
Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu  
40 45 50 55

gag aca gtg gcg gct tat tat gag gag cag cac cca gag ctc act cct 303  
Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro  
60 65 70

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cta ctt gaa aaa gaa aga gat gga tta cgg tgc cga ggc aac aga tcc 351
Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser
      75                      80                      85

cct gtc ccg gat gtt gag gat ccc gca acc gag gag cct ggg gag agc 399
Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser
      90                      95                      100

ttt tgt gac aag gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg 447
Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu
     105                      110                      115

cag acc tgg tgg cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg 495
Gln Thr Trp Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val
    120                      125                      130                      135

gcc ctg gtc cat gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc 543
Ala Leu Val His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe
      140                      145                      150

tgc tgc tct ctg tca gag ctc ttc atg tcc tct ttc cag tcc tac gga 591
Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly
     155                      160                      165

gcc cca cgg ggg gac aag gag gag ctg aca ccc cag aag tgc tct gaa 639
Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu
     170                      175                      180

ccc caa tcc tca aaa tga agatac tgacaccacc ttgcccctcc ccgtcaccgc 693
Pro Gln Ser Ser Lys *
    185

gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg ccctctcccg cacactcagt 753

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gtt tct tca agc tct tct ggc agt gat tct gac agt gag gtt gac aaa 101

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Val	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Asp	Ser	Asp	Ser	Glu	Val	Asp	Lys		
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Lys	Leu	Lys	Arg	Lys	Lys	Gln	Val	Ala	Pro	Glu	Lys	Pro	Val	Lys	Lys		
	25					30					35						
caa	aag	aca	ggt	gag	act	tcg	aga	gcc	ctg	tca	tct	tct	aaa	cag	agc		197
Gln	Lys	Thr	Gly	Glu	Thr	Ser	Arg	Ala	Leu	Ser	Ser	Ser	Lys	Gln	Ser		
	40				45					50					55		
agc	agc	agc	aga	gat	gat	aac	atg	ttt	cag	att	ggg	aaa	atg	agg	tac		245
Ser	Ser	Ser	Arg	Asp	Asp	Asn	Met	Phe	Gln	Ile	Gly	Lys	Met	Arg	Tyr		
				60					65					70			
gtt	agt	gtt	cgc	gat	ttt	aaa	ggc	aaa	gtg	cta	att	gat	att	aga	gaa		293
Val	Ser	Val	Arg	Asp	Phe	Lys	Gly	Lys	Val	Leu	Ile	Asp	Ile	Arg	Glu		
			75					80					85				
tat	tgg	atg	gat	cct	gaa	ggt	gaa	atg	aaa	cca	gga	aga	aaa	ggt	att		341
Tyr	Trp	Met	Asp	Pro	Glu	Gly	Glu	Met	Lys	Pro	Gly	Arg	Lys	Gly	Ile		
		90					95					100					
tct	tta	aat	cca	gaa	caa	tgg	atc	cag	tcc	agc	aga	aaa	gat	atg	atg		389
Ser	Leu	Asn	Pro	Glu	Gln	Trp	Ile	Gln	Ser	Ser	Arg	Lys	Asp	Met	Met		
	105					110						115					
aca	ttg	atg	aag	cac	gtg	agc	ggt	ctg	taa	t	aatg	cgagcc	agatta	at	at		440
Thr	Leu	Met	Lys	His	Val	Ser	Gly	Leu	*								
	120				125												
atcctgtact	gtagatttg	gggtaatctg	tcttatcaca	aaggatgttg	acttctagat												500
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gtaataaatt	agacatctct	tcattttaga	gagaag	atg	gaa	aca	aca	ttg	ctt								174
				Met	Glu	Thr	Thr	Leu	Leu								
				1				5									
ttc	ttt	tct	caa	ata	aat	atg	tgt	gaa	tca	aaa	gaa	aaa	act	ttt	ttc		222

Phe	Phe	Ser	Gln	Ile	Asn	Met	Cys	Glu	Ser	Lys	Glu	Lys	Thr	Phe	Phe		
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Lys	Leu	Ile	His	Gly	Ser	Gly	Lys	Glu	Glu	Thr	Ser	Lys	Glu	Ala	Lys		
		25					30					35					
atc	aga	gct	aag	gaa	aaa	aga	aat	aga	cta	agt	ctt	ctt	gtg	cag	aaa	318	
Ile	Arg	Ala	Lys	Glu	Lys	Arg	Asn	Arg	Leu	Ser	Leu	Leu	Val	Gln	Lys		
	40					45					50						
cct	gag	ttt	cat	gaa	gac	acc	cgc	tcc	agt	aga	tct	ggg	cac	ttg	gcc	366	
Pro	Glu	Phe	His	Glu	Asp	Thr	Arg	Ser	Ser	Arg	Ser	Gly	His	Leu	Ala		
	55				60					65					70		
aaa	gaa	aca	aga	gtc	tcc	cct	gaa	gag	gca	gtg	aaa	tgg	ggg	gaa	tca	414	
Lys	Glu	Thr	Arg	Val	Ser	Pro	Glu	Glu	Ala	Val	Lys	Trp	Gly	Glu	Ser		
			75						80					85			
ttt	gac	aaa	ctg	ctt	tcc	cat	aga	gat	gga	cta	gag	gct	ttt	acc	aga	462	
Phe	Asp	Lys	Leu	Leu	Ser	His	Arg	Asp	Gly	Leu	Glu	Ala	Phe	Thr	Arg		
			90					95					100				
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Phe	Leu	Lys	Thr	Glu	Phe	Ser	Glu	Glu	Asn	Ile	Glu	Phe	Trp	Ile	Ala		
		105					110					115					
tgt	gaa	gat	ttc	aag	aaa	agc	aag	gga	cct	caa	caa	att	cac	ctt	aaa	558	
Cys	Glu	Asp	Phe	Lys	Lys	Ser	Lys	Gly	Pro	Gln	Gln	Ile	His	Leu	Lys		
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gca	aaa	gca	ata	tat	gag	aaa	ttt	ata	cag	act	gat	gcc	cca	aaa	gag	606	
Ala	Lys	Ala	Ile	Tyr	Glu	Lys	Phe	Ile	Gln	Thr	Asp	Ala	Pro	Lys	Glu		
	135				140				145						150		
gtt	aac	ctt	gat	ttt	cac	aca	aaa	gaa	gtc	att	aca	aac	agc	atc	act	654	
Val	Asn	Leu	Asp	Phe	His	Thr	Lys	Glu	Val	Ile	Thr	Asn	Ser	Ile	Thr		
			155					160						165			
caa	cct	acc	ctc	cac	agt	ttt	gat	gct	gca	caa	agc	aga	gtg	tat	cag	702	
Gln	Pro	Thr	Leu	His	Ser	Phe	Asp	Ala	Ala	Gln	Ser	Arg	Val	Tyr	Gln		
			170					175					180				
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Leu	Met	Glu	Gln	Asp	Ser	Tyr	Thr	Arg	Phe	Leu	Lys	Ser	Asp	Ile	Tyr		
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Leu	Asp	Leu	Met	Glu	Gly	Arg	Pro	Gln	Arg	Pro	Thr	Asn	Leu	Arg	Arg		
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Arg	Ser	Arg	Ser	Phe	Thr	Cys	Asn	Glu	Phe	Gln	Asp	Val	Gln	Ser	Asp		
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Val	Ala	Ile	Trp	Leu	*												

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Met Asp Gly Arg Glu Ser Ala Phe  
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cca aaa ctc aag tac ctg gga cag gac aac tcg cta gca gct cag tca 939  
Pro Lys Leu Lys Tyr Leu Gly Gln Asp Asn Ser Leu Ala Ala Gln Ser  
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Pro Pro Trp Arg Thr Gln Ile Arg Met Leu Arg Pro Glu Asn Gln Arg  
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Leu Gly Pro Arg Pro Gln Pro Ser Gln His Asp Thr Asp Ala Ser Leu  
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Gly Glu Gln Gly Leu Ser Ala Ser Ser Gly Val Val Cys Ile Leu Leu  
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Tyr Leu Met Leu \*  
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1601

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		Met	Lys	Leu	Pro	Ser	Ile	Ser	Cys	Pro	His	Glu	Cys				
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Phe	Glu	Ala	Ile	Leu	Ser	Leu	Asp	Thr	Gly	Tyr	Arg	Ala	Pro	Val	Thr		
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ctg	gtg	cgg	aag	ggc	tgc	tgg	acc	ggg	cct	cct	gcg	ggc	cag	acg	caa	325	
Leu	Val	Arg	Lys	Gly	Cys	Trp	Thr	Gly	Pro	Pro	Ala	Gly	Gln	Thr	Gln		
	30					35					40						
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Ser	Asn	Pro	Asp	Ala	Leu	Pro	Pro	Asp	Tyr	Ser	Val	Val	Arg	Gly	Cys		
	45				50					55					60		
aca	act	gac	aaa	tgc	aac	gcc	cac	ctc	atg	act	cat	gac	gcc	ctc	ccc	421	
Thr	Thr	Asp	Lys	Cys	Asn	Ala	His	Leu	Met	Thr	His	Asp	Ala	Leu	Pro		
			65				70					75					
aac	ctg	agc	caa	gca	ccc	gac	ccg	ccg	acg	ctc	agc	ggc	gcc	gag	tgc	469	
Asn	Leu	Ser	Gln	Ala	Pro	Asp	Pro	Pro	Thr	Leu	Ser	Gly	Ala	Glu	Cys		
			80				85					90					
tac	gcc	tgt	atc	ggg	gtc	cac	cag	gat	gac	tgc	gct	atc	ggc	agg	tcc	517	
Tyr	Ala	Cys	Ile	Gly	Val	His	Gln	Asp	Asp	Cys	Ala	Ile	Gly	Arg	Ser		
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cga	cga	gtc	cag	tgt	cac	cag	gac	cag	acc	gcc	tgc	ttc	cag	ggc	aat	565	
Arg	Arg	Val	Gln	Cys	His	Gln	Asp	Gln	Thr	Ala	Cys	Phe	Gln	Gly	Asn		
	110					115					120						
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Gly	Arg	Met	Thr	Val	Gly	Asn	Phe	Ser	Val	Pro	Val	Tyr	Ile	Arg	Thr		
	125				130					135					140		

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Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr Ser Pro Trp Thr	
145 150 155	
gcc atc gac ctc cag ggc tcc tgc tgt gag ggg tac ctc tgc aac agg	709
Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly Tyr Leu Cys Asn Arg	
160 165 170	
aaa tcc atg acc cag ccc ttc acc agt gct tca gcc acc acc cct ccc	757
Lys Ser Met Thr Gln Pro Phe Thr Ser Ala Ser Ala Thr Thr Pro Pro	
175 180 185	
cga gca cta cag gtc ctg gcc ctg ctc ctc cca gtc ctc ctg ctg gtg	805
Arg Ala Leu Gln Val Leu Ala Leu Leu Leu Pro Val Leu Leu Leu Val	
190 195 200	
ggg ctc tca gca tag accgccccctc caggatgctg gggacagggc tcacacacct	860
Gly Leu Ser Ala *	
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atg gtc aac gtc ttg aaa gga gtg ctt ata gaa tgt gat cct gcc atg	167
Met Val Asn Val Leu Lys Gly Val Leu Ile Glu Cys Asp Pro Ala Met	
1 5 10 15	
aag cag ttt ctg ctg tac ttg gat gag tcc aat gcc ctg ggg aag aag	215
Lys Gln Phe Leu Leu Tyr Leu Asp Glu Ser Asn Ala Leu Gly Lys Lys	
20 25 30	
ttc atc att caa gac att gat gac act cac gtc ttt gta ata gca gaa	263
Phe Ile Ile Gln Asp Ile Asp Asp Thr His Val Phe Val Ile Ala Glu	
35 40 45	
ttg gtt aat gtc ctc cag gag cga gtg ggt gaa tta atg gac caa aat	311
Leu Val Asn Val Leu Gln Glu Arg Val Gly Glu Leu Met Asp Gln Asn	
50 55 60	

gct ttt tcc ctt acc cag aaa tga aaatactcaa tatggaccat ttaggaatta 365  
 Ala Phe Ser Leu Thr Gln Lys \*  
 65 70

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 45 50 55

gct cta agg agc agc cag cac ccc ttt ctc atc aga cac ccc cac atc 244  
 Ala Leu Arg Ser Ser Gln His Pro Phe Leu Ile Arg His Pro His Ile  
 60 65 70

cag gag gac aat gac atc ccg ttg tac ctg aag ggc ggc atc gtt gac 292  
 Gln Glu Asp Asn Asp Ile Pro Leu Tyr Leu Lys Gly Gly Ile Val Asp  
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 Asn Ile Leu Tyr Arg Val Thr Met Thr Leu Cys Leu Gly Gly Thr Val  
 95 100 105

tac agc ttg tac tcc ctt ggc tgg gcc tcc ttc ccc agg aat taa gac 388  
 Tyr Ser Leu Tyr Ser Leu Gly Trp Ala Ser Phe Pro Arg Asn \*  
 110 115 120

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Parameter	Unit	Value
Initial concentration	mg/L	100
Initial pH		7.0
Temperature	°C	25
Time	h	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 228359

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					Met Asp												
					1												

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Ile	Arg	Pro	Asn	His	Thr	Ile	Tyr	Ile	Asn	Asn	Met	Asn	Asp	Lys	Ile	
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Gly	His	Val	Val	Asp	Ile	Val	Ala	Leu	Lys	Thr	Met	Lys	Met	Arg	Gly	
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Gln	Ala	Phe	Val	Ile	Phe	Lys	Glu	Leu	Gly	Ser	Ser	Thr	Asn	Ala	Leu	
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Arg	Gln	Leu	Gln	Gly	Phe	Pro	Phe	Tyr	Gly	Lys	Pro	Met	Arg	Ile	Gln	
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Tyr	Ala	Lys	Thr	Asp	Ser	Asp	Ile	Ile	Ser	Lys	Met	Arg	Gly	Thr	Phe	
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Ala	Asp	Lys	Glu	Lys	Lys	Lys	Glu	Lys	Lys	Lys	Ala	Lys	Thr	Val	Glu	
		100				105					110					

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 Gln Thr Ala Thr Thr Asn Lys Lys Pro Gly Phe Lys Glu Val Arg  
 115 120 125 130

ctg gta cca ggg agg cat gac att gct ttt gtt gaa ttt gaa aat gat 609  
 Leu Val Pro Gly Arg His Asp Ile Ala Phe Val Glu Phe Glu Asn Asp  
 135 140 145

ggg cag gct gga gct gcc agg gat gct tta cag gga ttt aag atc aca 657  
 Gly Gln Ala Gly Ala Ala Arg Asp Ala Leu Gln Gly Phe Lys Ile Thr  
 150 155 160

ccg tcc cat gct atg aag atc acc tat gcc aag aaa taa catttgggat 706  
 Pro Ser His Ala Met Lys Ile Thr Tyr Ala Lys Lys \*  
 165 170 175

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 Met Glu Leu Asp Ser Ala Leu Glu Ala Pro  
 1 5 10

tcg cag gaa gac tct aat ttg tcc gag gag ttg tct cac tcc gcc ttt 218  
 Ser Gln Glu Asp Ser Asn Leu Ser Glu Glu Leu Ser His Ser Ala Phe  
 15 20 25

gga cag gcc ttc tcc aag att tta cac tgt ctt gcc cgc ccg gag gca 266  
 Gly Gln Ala Phe Ser Lys Ile Leu His Cys Leu Ala Arg Pro Glu Ala  
 30 35 40

cga cga ggc aat gta aaa gat gca gtt ctt aaa gac ctc ggt gat cta 314  
 Arg Arg Gly Asn Val Lys Asp Ala Val Leu Lys Asp Leu Gly Asp Leu  
 45 50 55

ata gaa gcc aca gaa ttt gat agg tta ttt gag ggg act ggt gca cgg	362
Ile Glu Ala Thr Glu Phe Asp Arg Leu Phe Glu Gly Thr Gly Ala Arg	
60 65 70	
ctc cgc gga atg ccg gag aca ctg ggg cag gta gca aaa gcc ctg gag	410
Leu Arg Gly Met Pro Glu Thr Leu Gly Gln Val Ala Lys Ala Leu Glu	
75 80 85 90	
aag tat gca gcc ccc tcc aag gag gag gaa ggt gga ggt gat ggg cac	458
Lys Tyr Ala Ala Pro Ser Lys Glu Glu Glu Gly Gly Gly Asp Gly His	
95 100 105	
tcc gaa gcg gcc gag aaa gca gcc caa gtt ggg tta ctg ttt ctt aaa	506
Ser Glu Ala Ala Glu Lys Ala Ala Gln Val Gly Leu Leu Phe Leu Lys	
110 115 120	
ctg tta ggg aaa gtt gag act gct aag aat tcc ctg gtc ggc cct gca	554
Leu Leu Gly Lys Val Glu Thr Ala Lys Asn Ser Leu Val Gly Pro Ala	
125 130 135	
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Trp Gln Thr Gly Leu His His Leu Ala Gly Pro Val Tyr Ile Phe Ala	
140 145 150	
atc aca cac agc ttg gag caa cca tgg acc act ccg aga tct cgg gaa	650
Ile Thr His Ser Leu Glu Gln Pro Trp Thr Thr Pro Arg Ser Arg Glu	
155 160 165 170	
gtt gct agg gag gtg ctc acc tca ctg ctt caa gtt act gaa tgc ggt	698
Val Ala Arg Glu Val Leu Thr Ser Leu Leu Gln Val Thr Glu Cys Gly	
175 180 185	
tct gtg gca gga ttc cta cat gga gaa aat gaa gat gag aaa ggg aga	746
Ser Val Ala Gly Phe Leu His Gly Glu Asn Glu Asp Glu Lys Gly Arg	
190 195 200	
ctt tcg gtg ata cta ggg ctt ctc aaa ccc gac ttg tat aag gaa tcc	794
Leu Ser Val Ile Leu Gly Leu Leu Lys Pro Asp Leu Tyr Lys Glu Ser	
205 210 215	
tgg aag aat aac cct gcc atc aaa cat gtt ttc tca tgg act ctg caa	842
Trp Lys Asn Asn Pro Ala Ile Lys His Val Phe Ser Trp Thr Leu Gln	
220 225 230	
cag gtc act cgg ccc tgg ctg agc cag cat ctg gaa agg gta ctt ccc	890
Gln Val Thr Arg Pro Trp Leu Ser Gln His Leu Glu Arg Val Leu Pro	
235 240 245 250	
gca tca ttg gtc att tca gat gac tat cag act gag aac aaa atc ctg	938
Ala Ser Leu Val Ile Ser Asp Asp Tyr Gln Thr Glu Asn Lys Ile Leu	
255 260 265	
ggt gta cac tgt ctc cat cac att gtg ctt aat gtg cca gct gct gat	986
Gly Val His Cys Leu His His Ile Val Leu Asn Val Pro Ala Ala Asp	
270 275 280	

ttg ctc cag tat aac aga gcc cag gtc cta tac cat gcc att tcc aac	1034
Leu Leu Gln Tyr Asn Arg Ala Gln Val Leu Tyr His Ala Ile Ser Asn	
285 290 295	
cac ctg tac aca cca gag cac cac ctc att cag gct gtg ctc ctg tgt	1082
His Leu Tyr Thr Pro Glu His His Leu Ile Gln Ala Val Leu Leu Cys	
300 305 310	
ctg ctg gat tta ttc ccc atc ctg gag aaa acc ctg cac tgg aaa gga	1130
Leu Leu Asp Leu Phe Pro Ile Leu Glu Lys Thr Leu His Trp Lys Gly	
315 320 325 330	
gat gga gct cga ccc acc acc cat tgt gat gag gtc ctg cgg ctg atc	1178
Asp Gly Ala Arg Pro Thr Thr His Cys Asp Glu Val Leu Arg Leu Ile	
335 340 345	
ctg acc cac atg gag cca gag cac cgc ctt ctt tta cgc agg acc tac	1226
Leu Thr His Met Glu Pro Glu His Arg Leu Leu Leu Arg Arg Thr Tyr	
350 355 360	
gca aga aac ctg ccg gct ttc gtg aac agg ttg ggg atc cta act gtc	1274
Ala Arg Asn Leu Pro Ala Phe Val Asn Arg Leu Gly Ile Leu Thr Val	
365 370 375	
cgg cac tta aag agg ctg gag aga gtc atc att ggt tat ctg gag gtt	1322
Arg His Leu Lys Arg Leu Glu Arg Val Ile Ile Gly Tyr Leu Glu Val	
380 385 390	
tat gat gga cct gag gag gaa gct aga ctg aag ata ttg gaa acc cta	1370
Tyr Asp Gly Pro Glu Glu Glu Ala Arg Leu Lys Ile Leu Glu Thr Leu	
395 400 405 410	
aaa ctt ctc atg caa cat act tgg ccc aga gtt tcc tgc aga ctt gtg	1418
Lys Leu Leu Met Gln His Thr Trp Pro Arg Val Ser Cys Arg Leu Val	
415 420 425	
gtc tta ctg aag gcc ctc ttg aaa ctg att tgt gat gta gca agg gat	1466
Val Leu Leu Lys Ala Leu Leu Lys Leu Ile Cys Asp Val Ala Arg Asp	
430 435 440	
cca aac ctt aca cct gag tct gtt aag agc gcc ctg cta cag gag gcc	1514
Pro Asn Leu Thr Pro Glu Ser Val Lys Ser Ala Leu Leu Gln Glu Ala	
445 450 455	
aca gac tgc ctg att ctc ctg gac cgc tgt tct caa gga cgg gta aag	1562
Thr Asp Cys Leu Ile Leu Leu Asp Arg Cys Ser Gln Gly Arg Val Lys	
460 465 470	
ggt ctc ctg gcc aaa att ccc caa agc tgt gaa gac aga aaa gtg gtg	1610
Gly Leu Leu Ala Lys Ile Pro Gln Ser Cys Glu Asp Arg Lys Val Val	
475 480 485 490	
aac tat atc aga aaa gtg cag cag gtt tct gaa ggc gca ccc tac aat	1658
Asn Tyr Ile Arg Lys Val Gln Gln Val Ser Glu Gly Ala Pro Tyr Asn	
495 500 505	
gga act taa gacttgt attactttcc caagaggaaa ggattttctt cccatcccaa	1714

Gly Thr \*

tttgtatgaa tggagttatt taagaaaaaa agatatTTTT acacgaaaaa aaaaaaaaa 1773

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<213> Homo sapiens

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atccgaccac atttcactct caccgctgta ggaatccag atg cag gcc aag tac 114  
Met Gln Ala Lys Tyr  
1 5

agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc 162  
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser  
10 15 20

ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc 210  
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg  
25 30 35

aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc 258  
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr  
40 45 50

ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg 306  
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly  
55 60 65

ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc 354  
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr  
70 75 80 85

att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa 402  
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln  
90 95 100

tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg 450  
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val  
105 110 115

gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga gca cac agg Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg 120 125 130	498
tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 135 140 145	546
cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys 150 155 160 165	594
ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 170 175 180	642
gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 185 190 195	690
aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 200 205 210	738
gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc acc Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 215 220 225	786
agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 230 235 240 245	834
tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 250 255 260	882
gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 265 270 275	930
gaa ggt gac tga ttc gccctctgca actacaaata gcagagtgcg ccaggcggtg Glu Gly Asp * 280	985
ccaaagcaag ggctagtgtga gacattggga aatggaacat aatcaggaaa gactatctct	1045
ctgactagta caaaatgggt tctcgtgttt cctgttcagg atcaccagca tttctgagct	1105
tgggttttatg cacgtattta acagtcacaa gaagtcttat ttacatgccca ccaaccaacc	1165
tcagaaaccc ataatgtcat ctgccttctt ggcttagaga taacttttag ctctctttct	1225
tctcaatgtc taatatcacc tcctgtttt catgtcttcc ttacacttgg tggaataaga	1285
aactttttga agtagaggaa atacattgag gtaacatcct tttctctgac agtcaagtag	1345
tccatcagaa attggcagtc acttccaga ttgtaccagc aaatacacaa ggaattcttt	1405



ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc	210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg	
25 30 35	
aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc	258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr	
40 45 50	
ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg	306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly	
55 60 65	
ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc	354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr	
70 75 80 85	
att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa	402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln	
90 95 100	
tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg	450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val	
105 110 115	
gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc tat aca	498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly Tyr Thr	
120 125 130	
aga aac atg gtg cca gca tct gct tct tct gag agc ctc agg cag ctt	546
Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg Gln Leu	
135 140 145	
cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct tgt aca	594
Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro Cys Thr	
150 155 160 165	
gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac	642
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp	
170 175 180	
agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct	690
Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser	
185 190 195	
acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct	738
Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser	
200 205 210	
cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc	786
Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg	
215 220 225	
cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act	834
Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr	
230 235 240 245	
tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga	882



Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg	
250 255 260	
gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa	930
Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys	
265 270 275	
gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca	978
Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro	
280 285 290	
gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac tga ttc	1026
Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp *	
295 300 305	
gccctctgca actacaaata gcagagtgag ccaggcgggtg ccaaagcaag ggctagttga	1086
gacattggga aatggaacat aatcaggaaa gactatctct ctgactagta caaaatgggt	1146
tctcgtgttt cctgttcagg atcaccagca tttctgagct tgggtttatg cacgtattta	1206
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ctgccttctt ggcttagaga taacttttag ctctctttct tctcaatgtc taatatcacc	1326
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tatccccatc tccgtttcat atcagaacta ccgccccga tattcccttc agagagatta	1746
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aaatgctttt caaaatatga tagcgggtcat tattttgatt gtgccttact gaaagttttt	1986
ggggaattta caagagtact gattacatga ttatctggag aaaataagat gtctttgaaa	2046
tacatgttgg cttcaagaaa acagttttaa cgttttccta aaatgaaatc ttttgagggtg	2106
agcttatggc atcaacacat gggtgatgag gaagctgagt tgcattagtg cacatgattt	2166
ccagtcaggt catgggaaat gaacagagac agtgacatct ttgtagctgc tcctttgtga	2226
ggcacttctt tcttgagatg actccatgca caaatataac agggatcatt gggaaatgaca	2286

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2323

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<213> Homo sapiens

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<400> 143

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Met Leu Thr Gly Val Gly Cys Leu Val Ser Ser Glu Ser	
1 5 10	
ctg agc tgc gtg cag tgt aat tca tgg gaa aaa tcc tgt gtc aac agc	158
Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser	
15 20 25	
att gcc tct gaa tgt ccc tca cat gcc aac acc agc tgt atc agc tcc	206
Ile Ala Ser Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser	
30 35 40 45	
tca gcc agc tcc tct cta gag aca cca gtc aga tta tac cag aat atg	254
Ser Ala Ser Ser Ser Leu Glu Thr Pro Val Arg Leu Tyr Gln Asn Met	
50 55 60	
ttc tgc tca gcg gag aac tgc agt gag gag aca cac att aca gcc ttc	302
Phe Cys Ser Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe	
65 70 75	
act gtc cac gtg tct gct gaa gaa cac ttt cat ttt gta agc cag tgc	350
Thr Val His Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys	
80 85 90	
tgc caa gga aag gaa tgc agc aac acc agc gat gcc ctg gac cct ccc	398
Cys Gln Gly Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro	
95 100 105	
ctg aag aac gtg tcc agc aac gca gag tgc cct gct tgt tat gaa tct	446
Leu Lys Asn Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser	
110 115 120 125	
aat gga act tcc tgt cgt ggg aag ccc tgg aaa tgc tat gaa gaa gaa	494
Asn Gly Thr Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu	
130 135 140	
cag tgt gtc ttt cta gtt gca gaa ctt aag aat gac att gag tct aag	542
Gln Cys Val Phe Leu Val Ala Glu Lys Asn Asp Ile Glu Ser Lys	
145 150 155	

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agt ctc gtg ctg aaa ggc tgt tcc aac gtc agt aac gcc acc tgt cag      590
Ser Leu Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln
      160                      165                      170

ttc ctg tct ggt gaa aac aag act ctt gga gga gtc atc ttt cga aag      638
Phe Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
      175                      180                      185

ttt gag tgt gca aat gta aac agc tta acc ccc acg tct gca cca acc      686
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr
      190                      195                      200                      205

act tcc cac aac gtg ggc tcc aaa gct tcc ctc tac ctc ttg gcc ctt      734
Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu
      210                      215                      220

gcc agc ctc ctt ctt cgg gga ctg ctg ccc tga ggtcctgg ggctgcactt      785
Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro *
      225                      230

tgcccagcac cccatttctg cttctctgag gtccagagca cccctgcgg tgctgacacc      845

ctctttccct gctctgcccc gtttaactgc ccagtaagtg ggagtcacag gtctccaggc      905

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<212> DNA
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<223> n = a,t,c or g

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ggcgtttgtgc gcagagctgg aaagcatggc tgttataaat gaattctgat tttggggagc      180

agatgccaac ttagagcctc gtaccaatct ctctgtcttt aaaagatgag gtgacttggt      240

gatttttctg gaaaattata ggtgcccagc taagacctga atgccatcac cctccccagg      300

gctctgcagt tttctcgtgg tgaacccttg atggatttgt tgttgcttga gaa atg      356

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gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg				1076
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr	230	235	240	
tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat				1124
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp	245	250	255	
gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc				1172
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile	260	265	270	
cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag				1220
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys	275	280	285	
ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac				1268
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His	290	295	300	305
agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc				1316
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val	310	315	320	
cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg gta				1364
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Val	325	330	335	
ccg tga aagtttattt ttgtctgaaa gctttcataa gtatttaaata caacacagta				1420
Pro *				
atcaactatt taattgctgc aatcgggtcaa aatttataaaa agccacacac aaatttctct				1480
ccttctacac gtagctccat aactgcccc ttgccaaaaca cccttcgggg aaccaatcag				1540
catgacattc ctgggcagtt aatgtgagaa gcgagggcag ggcaccgtcc nagtggactt				1600
tatccttcag ggaggggagcgt atcctctctc ttacactctg tgtgtgggtta aatttctaaa				1660
gaacaccatt taatccatag ctatatcag				1689

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 <213> Homo sapiens  
  
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 <221> CDS  
 <222> (104)..(298)  
  
 <400> 145



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Val Leu Ala Leu Lys Ser Asn Phe Glu Phe Ser Lys Asp Val Cys Ile  
40 45 50

gct cat gca aat gaa cta agc gtt cat tgg aat gac acc atc acc acc 367  
Ala His Ala Asn Glu Leu Ser Val His Trp Asn Asp Thr Ile Thr Thr  
55 60 65 70

caa atg aaa aga act ggc tgg aat att cat cag cct act aat gtc atc 415  
Gln Met Lys Arg Thr Gly Trp Asn Ile His Gln Pro Thr Asn Val Ile  
75 80 85

tcc caa ccc act ctc caa act cca tcc caa aaa agc atc cag ttc aga 463  
Ser Gln Pro Thr Leu Gln Thr Pro Ser Gln Lys Ser Ile Gln Phe Arg  
90 95 100

att gcc cac tgt tgg caa aga aag aat gtc act aat tta ttt aca ggg 511  
Ile Ala His Cys Trp Gln Arg Lys Asn Val Thr Asn Leu Phe Thr Gly  
105 110 115

agc aga tag cagggactta cagatgaacc aggcctgcg atttttg 557  
Ser Arg \*  
120

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<211> 1190  
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<213> Homo sapiens  
  
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<222> (172)..(1071)

<400> 147  
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gtccgggggct acacagccag gtgtcagatg tgtctctgct gatctgagtc tgcctgtggc 120  
atggacctgc atcttccttg aagcatctcc agggctgaaa aatcactgac c atg gca 177  
Met Ala  
1

cca tgg tct cat cca tct gca cag ctg cag cca gtg gga gga gac gcc 225  
Pro Trp Ser His Pro Ser Ala Gln Leu Gln Pro Val Gly Gly Asp Ala  
5 10 15

gtg agc cct gcc ctc atg gtt ctg ctc tgc ctc ggg ctg agt ctg ggc 273  
Val Ser Pro Ala Leu Met Val Leu Leu Cys Leu Gly Leu Ser Leu Gly  
20 25 30

ccc agg acc cac gtg cag gca ggg aac ctc tcc aaa gcc acc ctc tgg 321  
Pro Arg Thr His Val Gln Ala Gly Asn Leu Ser Lys Ala Thr Leu Trp  
35 40 45 50

gct gag cca ggc tct gtg atc agc cgg ggg aac tct gtg acc atc cgg	369
Ala Glu Pro Gly Ser Val Ile Ser Arg Gly Asn Ser Val Thr Ile Arg	
55 60 65	
tgt cag ggg acc ctg gag gcc cag gaa tac cgt ctg gtt aaa gag gga	417
Cys Gln Gly Thr Leu Glu Ala Gln Glu Tyr Arg Leu Val Lys Glu Gly	
70 75 80	
agc cca gaa ccc tgg gac aca cag aac cca ctg gag ccc aag aac aag	465
Ser Pro Glu Pro Trp Asp Thr Gln Asn Pro Leu Glu Pro Lys Asn Lys	
85 90 95	
gcc aga ttc tcc atc cca tcc atg aca gag cac cat gca ggg aga tac	513
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr	
100 105 110	
cgc tgt tac tac tac agc cct gca ggc tgg tca gag ccc agc gac ccc	561
Arg Cys Tyr Tyr Tyr Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro	
115 120 125 130	
ctg gag ctg gtg gtg aca gga ttc tac aac aaa ccc acc ctc tca gcc	609
Leu Glu Leu Val Val Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala	
135 140 145	
ctg ccc agt cct gtg gtg acc tca gga gag aac gtg acc ctc cag tgt	657
Leu Pro Ser Pro Val Val Thr Ser Gly Glu Asn Val Thr Leu Gln Cys	
150 155 160	
ggc tca cgg ctg aga ttc gac agg ttc att ctg act gag gaa gga gac	705
Gly Ser Arg Leu Arg Phe Asp Arg Phe Ile Leu Thr Glu Glu Gly Asp	
165 170 175	
cac aag ctc tcc tgg acc ttg gac tca cag ctg acc ccc agt ggg cag	753
His Lys Leu Ser Trp Thr Leu Asp Ser Gln Leu Thr Pro Ser Gly Gln	
180 185 190	
ttc cag gcc ctg ttc cct gtg ggc cct gtg acc ccc agc cac agg tgg	801
Phe Gln Ala Leu Phe Pro Val Gly Pro Val Thr Pro Ser His Arg Trp	
195 200 205 210	
atg ctc aga tgc tat ggc tct cgc agg cat atc ctg cag gta tgg tca	849
Met Leu Arg Cys Tyr Gly Ser Arg Arg His Ile Leu Gln Val Trp Ser	
215 220 225	
gaa ccc agt gac ctc ctg gag att ccg gtc tca gga gca gct gat aac	897
Glu Pro Ser Asp Leu Leu Glu Ile Pro Val Ser Gly Ala Ala Asp Asn	
230 235 240	
ctc agt ccg tca caa aac aag tct gac tct ggg act gcc tca cac ctt	945
Leu Ser Pro Ser Gln Asn Lys Ser Asp Ser Gly Thr Ala Ser His Leu	
245 250 255	
cag gat tac gca gta gag aat ctc atc cgc atg ggc atg gcc ggc ttg	993
Gln Asp Tyr Ala Val Glu Asn Leu Ile Arg Met Gly Met Ala Gly Leu	
260 265 270	



atc ctg gtg gtc ctt ggg att ctg ata ttt cag gat tgg cac agc cag 1041  
 Ile Leu Val Val Leu Gly Ile Leu Ile Phe Gln Asp Trp His Ser Gln  
 275 280 285 290

aga agc ccc caa gct gca gct gga agg tga a cagaagagag aacaatgcac 1092  
 Arg Ser Pro Gln Ala Ala Ala Gly Arg \*  
 295 300

cattgaatgc tggagccttg gaagcgaatc tgatggctct aggaggttcg ggaagaccat 1152

ctgaggccta tgccatctgg actgtctgct ggcaattt 1190

<210> 148  
 <211> 1260  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (156)..(626)

<400> 148  
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 gaattccagc accccggagg tactccagca gcttgtctcc aatccaagct cccaatcacc 120  
 caccgccgca gccccctacg caggccacgc cactg atg cac acc aaa ccc aat 173  
 Met His Thr Lys Pro Asn  
 1 5

agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga ctt 221  
 Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu  
 10 15 20

gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt act 269  
 Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr  
 25 30 35

ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc ctg 317  
 Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu  
 40 45 50

gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta ccg 365  
 Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro  
 55 60 65 70

aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc cca 413  
 Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro  
 75 80 85

ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc acc 461  
 Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr  
 90 95 100





Thr Thr Ser Ser Gly Gly Leu Thr Ile Ser Ser Leu Leu Lys Glu Lys	
220 225 230	
gag ggc tca gaa gta gcc aag ttc act ctg gag gag ctc tgc ctc atc	951
Glu Gly Ser Glu Val Ala Lys Phe Thr Leu Glu Glu Leu Cys Leu Ile	
235 240 245	
tgt aac atc ctg agc acg gca gag tac tgt ctg gcc acc acc cag cag	999
Cys Asn Ile Leu Ser Thr Ala Glu Tyr Cys Leu Ala Thr Thr Gln Gln	
250 255 260	
cta gaa gaa aaa ctc aaa gaa aaa gtg gat gta agt ctg att gaa cga	1047
Leu Glu Glu Lys Leu Lys Glu Lys Val Asp Val Ser Leu Ile Glu Arg	
265 270 275 280	
atc aat ctg act gga gag atg gac acg ttc agc acc gtc atc tcc agc	1095
Ile Asn Leu Thr Gly Glu Met Asp Thr Phe Ser Thr Val Ile Ser Ser	
285 290 295	
agt att cag ctg ctg gtt cag gat ctg gat gct gcc tgt gat cct gcc	1143
Ser Ile Gln Leu Leu Val Gln Asp Leu Asp Ala Ala Cys Asp Pro Ala	
300 305 310	
ctg act gcc atg agc aag atg cag tgg cag aac gtg gag cac gtt ggt	1191
Leu Thr Ala Met Ser Lys Met Gln Trp Gln Asn Val Glu His Val Gly	
315 320 325	
gac cag agc ccc tac gtc acc tct gtc att ctg cac atc aag cag aac	1239
Asp Gln Ser Pro Tyr Val Thr Ser Val Ile Leu His Ile Lys Gln Asn	
330 335 340	
gtc ccc atc atc cgt gac aac ctg gct tcc aca cgc aag tac ttc act	1287
Val Pro Ile Ile Arg Asp Asn Leu Ala Ser Thr Arg Lys Tyr Phe Thr	
345 350 355 360	
cag ttc tgc gtt aaa ttt gca aac tcc ttc att ccc aaa ttc atc acc	1335
Gln Phe Cys Val Lys Phe Ala Asn Ser Phe Ile Pro Lys Phe Ile Thr	
365 370 375	
cac ctc ttc aag tgc aag cca att agc atg gtg gga gca gaa cag gtg	1383
His Leu Phe Lys Cys Lys Pro Ile Ser Met Val Gly Ala Glu Gln Val	
380 385 390	
aga tgg acg tag tat caggcatttg cctgggcagct tttgtttag atcaagcaca	1438
Arg Trp Thr *	
395	
tattcttcta gtccagatct acttggcagg aataaaattg atgatgtccc ctgtttgggg	1498
acagtataat gactcaccgc gaaggtttct taattcggtc ttccatttat ttttaaaaat	1558
tttgtttgaa cgcctactaa gttctgggtg cagggtataa cacagcaagc accatggaaa	1618
ggtccttgct cctagtgtc acactccaat aagaagaagt ggctgggccg ggcacagcgg	1678
ctcacgtgt aacccagca tttcgggagg cctgggcagg cagatcacct ggggtaagga	1738

atttgagagc agcctggcca acatggtgaa atcccatctc tactaaaaat acaaaaatta 1798  
gctgggcatg ggggcaggct accggggagg ctgaggcagg agaatcactt gaacccggga 1858  
ggtggagggtt gcagtgagcc gatatcacac cactgcactc cagcctgggt gacaaagtga 1918  
gactccatct c 1929

<210> 150  
<211> 1230  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> CDS  
<222> (70)..(555)

<400> 150  
aaaaaagttg gtgtatcatc ctccatcctc caaggtctct ggatctctta tagcacagaa 60  
ggtcttttcc atg gca ctg gcg tct tta cga aat ctc tac act cca aat 108  
Met Ala Leu Ala Ser Leu Arg Asn Leu Tyr Thr Pro Asn  
1 5 10  
ata aag gtc agc cga ctg ctg att ttg gga ggt gcc aat att aat tac 156  
Ile Lys Val Ser Arg Leu Leu Ile Leu Gly Gly Ala Asn Ile Asn Tyr  
15 20 25  
cgg aca gag gtt tta aat aat gct cca att cta tgt gtt cag tcc cat 204  
Arg Thr Glu Val Leu Asn Asn Ala Pro Ile Leu Cys Val Gln Ser His  
30 35 40 45  
ctt ggt tac aca gaa atg gta gcc ctg ctg ctg gag ttc ggg gcc aac 252  
Leu Gly Tyr Thr Glu Met Val Ala Leu Leu Leu Glu Phe Gly Ala Asn  
50 55 60  
gtg gat gcc tct tct gaa agt ggc ctg act ccc ctg gga tat gct gca 300  
Val Asp Ala Ser Ser Glu Ser Gly Leu Thr Pro Leu Gly Tyr Ala Ala  
65 70 75  
gca gca ggg tac ctg agc att gtg gtg ctg ctg tgc aag aaa cgg gcc 348  
Ala Ala Gly Tyr Leu Ser Ile Val Val Leu Leu Cys Lys Lys Arg Ala  
80 85 90  
aag gtg gat cat ttg gat aag aac ggg cag tgt gct ttg gtt cat gct 396  
Lys Val Asp His Leu Asp Lys Asn Gly Gln Cys Ala Leu Val His Ala  
95 100 105  
gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac 444  
Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp  
110 115 120 125  
tgg acg atg gcc ggc cag cag caa gga gta ttt aag aag agc cat gcc 492  
Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala

130	135	140	
atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta			540
Ile Gln Gln Ala Leu Ile Ala Ala Ser Met Gly Tyr Thr Glu Val			
145	150	155	
aga agt agg caa tag gattgttttt tcaagctctg tattgaagga cccaggaaac			595
Arg Ser Arg Gln *			
160			
caggagaaaa gattgcacga agacaaaatt gccaaccaaa ttaatgtgaa ttcgtgatcg			655
ctgctctgaa taataaggag attaaactcc atgaagcact ttactcaaat gccaaagtcc			715
ctcaaattat aggtatagaa aggtgctgagt tggaaaggac cgtggaaatg atataattat			775
tctccatggt ttcctccctg tttaacagac agtggcacca aggctcaaag agatgaatta			835
ttgaggtgta gtcacatggt tagataatgt ggcacaggaa cagcataaca tttagaatct			895
cagaaggacc agatttgagt cccagcctcg ctattcatta actctagccc ttgaacaatt			955
tacctatctc ttagaagttt agtttcccat cagcaaagtg aagctaataa actcctttat			1015
acaaggctgt tgtaagggat gcttggtaaa ctgttaaaca ttatacagtt tatttattaa			1075
tgataataac aataatagtg gcaaagttag ggaattggta gtgtgctagg aaatgtttaa			1135
caaccaactg tgaagagggg tgtgggggtg aacaggggtg tgtgtttgtg tgtgcatacg			1195
tttattataa attttactga tagaatgtgt tgccg			1230

<210> 151  
 <211> 1335  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (91)..(1257)

<400> 151		
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gagggagccc gagccaggcc atctccaacc	atg ttc gac gag gcc tcg gcc	111
	Met Phe Asp Glu Ala Ser Ala	
	1 5	
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc		159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu		
10 15 20		
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc		207
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly		

25	30	35	
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc			255
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg			
40	45	50	55
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct			303
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser			
	60	65	70
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca			351
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser			
	75	80	85
tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta gat gat			399
Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu Asp Asp			
	90	95	100
cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc tgc agt			447
Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val Cys Ser			
	105	110	115
gat gtc tct tct tct att agc act tac tgg gat tgg tca gat agc gag			495
Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp Ser Glu			
	120	125	130
ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt gat gta			543
Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser Asp Val			
	140	145	150
ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg ctt cct			591
Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu Leu Pro			
	155	160	165
aaa aag aaa aac aag cac cgg aat tta gat gaa ctc cct tgg agt gca			639
Lys Lys Lys Asn Lys His Arg Asn Leu Asp Glu Leu Pro Trp Ser Ala			
	170	175	180
atg aca aat gat gag cag gtg gaa tat att gag tat ctg agt cgg aaa			687
Met Thr Asn Asp Glu Gln Val Glu Tyr Ile Glu Tyr Leu Ser Arg Lys			
	185	190	195
gtg agt act gag atg ggt ctt cgg gag caa ctt gat att att aag atc			735
Val Ser Thr Glu Met Gly Leu Arg Glu Gln Leu Asp Ile Ile Lys Ile			
	200	205	210
att gat cct tct gct cag atc tcc cct aca gac agg gag ttt att att			783
Ile Asp Pro Ser Ala Gln Ile Ser Pro Thr Asp Arg Glu Phe Ile Ile			
	220	225	230
gaa ctt aac tgt ctc aca gat gaa aaa ctg aag cag gtc aga aac tat			831
Glu Leu Asn Cys Leu Thr Asp Glu Lys Leu Lys Gln Val Arg Asn Tyr			
	235	240	245
atc aag gaa cat agc cct cgc caa cgg cct gca aga gag gcc tgg aag			879
Ile Lys Glu His Ser Pro Arg Gln Arg Pro Ala Arg Glu Ala Trp Lys			
	250	255	260

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aga agc aac ttt agt tgt gca agc acc agt gga gtg agc ggt gcc agt      927
Arg Ser Asn Phe Ser Cys Ala Ser Thr Ser Gly Val Ser Gly Ala Ser
    265                      270                      275

gcc agc gcc agc agc agc agt gcc agc atg gtc agt tct gca agc agc      975
Ala Ser Ala Ser Ser Ser Ser Ala Ser Met Val Ser Ser Ala Ser Ser
    280                      285                      290                      295

agt ggg tcc agt gtt gga aac tct gct tca aac tcc agt gcc aac atg      1023
Ser Gly Ser Ser Val Gly Asn Ser Ala Ser Asn Ser Ser Ala Asn Met
    300                      305                      310

agt cga gca cac agt gac agc aac ctg tct gca agt gca gca gag cgg      1071
Ser Arg Ala His Ser Asp Ser Asn Leu Ser Ala Ser Ala Ala Glu Arg
    315                      320                      325

att cgg gat tca aaa aag cga tcc aag cag cgg aag tta cag cag aag      1119
Ile Arg Asp Ser Lys Lys Arg Ser Lys Gln Arg Lys Leu Gln Gln Lys
    330                      335                      340

gcc ttc cgc aag agg cag ctg aag gag cag agg cag gcc cgg aag gag      1167
Ala Phe Arg Lys Arg Gln Leu Lys Glu Gln Arg Gln Ala Arg Lys Glu
    345                      350                      355

agg ctc agt ggg ctc ttc ctt aac gaa gag gtg ctg tcc ttg aaa gtg      1215
Arg Leu Ser Gly Leu Phe Leu Asn Glu Glu Val Leu Ser Leu Lys Val
    360                      365                      370                      375

act gag gaa gac cat gaa gca gat gtt gat gtt ttg atg taa taagggt      1264
Thr Glu Glu Asp His Glu Ala Asp Val Asp Val Leu Met *
    380                      385

gaatttatca acgttctttg tgagcattaa aatactccat ccttatgggt ttacatgcaa      1324

aaaaaaaaa a                                                                1335

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<210> 152  
 <211> 2251  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (203)..(1582)

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<400> 152
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tggcgctgga cgcttccctc ttggaagcgc ctctccctca ggtctcaaga actgttttga      120

gatgcaggaa ttcatctaatt ttacttgcc gggcgaggtg tgagagccct agcatctgaa      180

agtggtcgac ttgcgagttg tt atg gag aaa act tgt ata gat gca ctt cct      232

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220	225	230	
aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata aca Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr 235 240 245 250			952
gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct gcc Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala Ala 255 260 265			1000
att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac tgg Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp 270 275 280			1048
ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct ctg Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala Leu 285 290 295			1096
gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att cga Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile Arg 300 305 310			1144
tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca ata Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala Ile 315 320 325 330			1192
ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt gat Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp 335 340 345			1240
tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc ttg Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu Leu 350 355 360			1288
gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga gag Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg Glu 365 370 375			1336
ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg tgt Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys 380 385 390			1384
aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct tca Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser 395 400 405 410			1432
aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc att Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile 415 420 425			1480
cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt gta Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys Val 430 435 440			1528
gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca aaa Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys 445 450 455			1576

```

cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct      1632
His *
    460

ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag ttaggaaagt      1692
ttttttctta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt gactgacata      1752
ctggaagaga acaccatttt atctcagggt agtgaagaat cagtgcaggt ccctgactct      1812
tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc aactaaaga      1872
gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaatccaa tagaagtatt      1932
gcagcttcct tctctggctc aagggtgag ttaagtgaaa ggaaaaacag cacaatgggtg      1992
accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga aatgtaaaaa      2052
gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt accatgatga      2112
attctagtga aatgaccctt tgactttgct tttcttaata cagatattta ctgagaggaa      2172
ctatttttat aacacaagaa aaatttacia ttgattaaaa gtatccatgt cttggataca      2232
tacgtaaaaa aaaaaaaaaa                                         2251
    
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<210> 153
<211> 2310
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (306)..(2174)
    
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<400> 153
aaaactccag gaggcggagg aggctagtgg cagtacctgg gcaccctgac cctccccaca      60
ggccagagcc caccctcctg ctcatgaggg cagacaggcc tttccaggga cacagtccct      120
cttctcccca ggaccccagg gccaactccc cctgccggcc ctctgccatc aaattggcag      180
tggtccagg ggagtcacct ggggatgggg gaccactgtt ggggacctct ctgcgtgcac      240
ccctgtagtt ggggaagcag gacagggggc tggggagacg gaagggcgcc aggggttgag      300
agagg      atg gtg gac gtt gtt gga ctt gaa agg gaa aca ggc cct cgg      347
            Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg
            1             5             10

gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg      395
Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala
15             20             25             30
    
```







ttcccagggt tcacgccaca ctctaggaag tgcctgagct agtgagctgg ccaacgagct	120
ccgcgggctg ggacc atg ggc tgc ttc ttc tcc aag aga cgg aag gct gac	171
Met Gly Cys Phe Phe Ser Lys Arg Arg Lys Ala Asp	
1 5 10	
aag gag tgc cgg ccc gag aac gag gag gag cgg cca aag cag tac agc	219
Lys Glu Ser Arg Pro Glu Asn Glu Glu Glu Arg Pro Lys Gln Tyr Ser	
15 20 25	
tgg gat cag cgc gag aag gtt gat cca aaa gac tac atg ttc agt gga	267
Trp Asp Gln Arg Glu Lys Val Asp Pro Lys Asp Tyr Met Phe Ser Gly	
30 35 40	
ctg aag gat gaa aca gta ggt cgc tta cct ggg acg gta gca gga caa	315
Leu Lys Asp Glu Thr Val Gly Arg Leu Pro Gly Thr Val Ala Gly Gln	
45 50 55 60	
cag ttt ctc att caa gac tgt gag aac tgt aac atc tat att ttt gat	363
Gln Phe Leu Ile Gln Asp Cys Glu Asn Cys Asn Ile Tyr Ile Phe Asp	
65 70 75	
cac tct gct aca gtt acc att gat gac tgt act aac tgc ata att ttt	411
His Ser Ala Thr Val Thr Ile Asp Asp Cys Thr Asn Cys Ile Ile Phe	
80 85 90	
ctg gga ccc gtg aaa ggc agc gtg ttt ttc cgg aat tgc aga gat tgc	459
Leu Gly Pro Val Lys Gly Ser Val Phe Phe Arg Asn Cys Arg Asp Cys	
95 100 105	
aag tgc aca tta gcc tgc caa caa ttt cgt gtg cga gat tgt aga aag	507
Lys Cys Thr Leu Ala Cys Gln Gln Phe Arg Val Arg Asp Cys Arg Lys	
110 115 120	
ctg gaa gtc ttt ttg tgt tgt gcc act caa ccc atc att gag tct tcc	555
Leu Glu Val Phe Leu Cys Cys Ala Thr Gln Pro Ile Ile Glu Ser Ser	
125 130 135 140	
tca aat atc aaa ttt gga tgt ttt caa tgg tac tat cct gaa tta gct	603
Ser Asn Ile Lys Phe Gly Cys Phe Gln Trp Tyr Tyr Pro Glu Leu Ala	
145 150 155	
ttc cag ttc aaa gat gca ggg cta agt atc ttc gac aat aca tgg agt	651
Phe Gln Phe Lys Asp Ala Gly Leu Ser Ile Phe Asp Asn Thr Trp Ser	
160 165 170	
aac att cat gac ttt aca cct gtg tca gga gaa ctc aac tgg agc ctt	699
Asn Ile His Asp Phe Thr Pro Val Ser Gly Glu Leu Asn Trp Ser Leu	
175 180 185	
ctt cca gaa gat gct gtg gtt cag gac tat gtt cct ata cct act acc	747
Leu Pro Glu Asp Ala Val Val Gln Asp Tyr Val Pro Ile Pro Thr Thr	
190 195 200	
gaa gag ctc aaa gct gtt cgt gtt tcc aca gaa gcc aat aga agc att	795
Glu Glu Leu Lys Ala Val Arg Val Ser Thr Glu Ala Asn Arg Ser Ile	

205	210	215	220	
gtt cca ata tcc cgg ggt cag aga cag aag agc agc gat gaa tca tgc				843
Val Pro Ile Ser Arg Gly Gln Arg Gln Lys Ser Ser Asp Glu Ser Cys	225	230	235	
tta gtg gta tta ttt gct ggt gat tac act att gca aat gcc aga aaa				891
Leu Val Val Leu Phe Ala Gly Asp Tyr Thr Ile Ala Asn Ala Arg Lys	240	245	250	
cta att gat gag atg gtt ggt aaa ggc ttt ttc cta gtt cag aca aag				939
Leu Ile Asp Glu Met Val Gly Lys Gly Phe Phe Leu Val Gln Thr Lys	255	260	265	
gaa gtg tcc atg aaa gct gag gat gct caa agg gtt ttt cgg gaa aaa				987
Glu Val Ser Met Lys Ala Glu Asp Ala Gln Arg Val Phe Arg Glu Lys	270	275	280	
gca cct gac ttc ctt cct ctt ctg aac aaa ggt cct gtt att gcc ttg				1035
Ala Pro Asp Phe Leu Pro Leu Leu Asn Lys Gly Pro Val Ile Ala Leu	285	290	300	
gag ttt aat ggg gat ggt gct gta gaa gta tgt caa ctt att gta aac				1083
Glu Phe Asn Gly Asp Gly Ala Val Glu Val Cys Gln Leu Ile Val Asn	305	310	315	
gag ata ttc aat ggg acc aag atg ttt gta tct gaa agc aag gag aca				1131
Glu Ile Phe Asn Gly Thr Lys Met Phe Val Ser Glu Ser Lys Glu Thr	320	325	330	
ggt ttc tgg aga tgt aga cac gct cta aca ctt ggc tga tatacagatg				1180
Gly Phe Trp Arg Cys Arg His Ala Leu Thr Leu Gly *	335	340	345	
ggaatatgaa gtgcaatgtg gaaccggac ttggtataag acctttccca ctt				1233

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 <213> Homo sapiens  
 <220>  
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 <222> (256)..(873)

gcacgagcta aactctggga ctggcgggcg gtcaggcggc acagggggaa tcccgggggc	60
ctaaggaggt tgtctcagtt tttgtcagca tctccacccc gaggtggttt gaactttgag	120
cctttttagt tctgatgaa taatttcatt ttctcaagt ttatgacact cggaacgtca	180
agaactggag gtttgtgcaa tttgagaccg gtcggcactg tgcagagatc agagtactaa	240





aaataataaaa ttacatctaa aaattaaaaa aaaaaaaa

1021

<210> 156  
 <211> 1581  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(819)

<400> 156

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 Met Glu Ala Glu Glu Ser Glu Lys Ala Ala Thr Glu Gln Glu Pro Leu  
 1 5 10 15

gaa ggg aca gaa cag aca cta gat gcg gag gag gag cag gag gaa tcc 96  
 Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser  
 20 25 30

gaa gaa gcg gcc tgt ggc agc aag aag cgg gta gtg cca ggt att gtg 144  
 Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val  
 35 40 45

tac ctg ggc cat atc ccg ccg cgc ttc cgg ccc ctg cac gtc cgc aac 192  
 Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn  
 50 55 60

ctt ctc agc gcc tat ggc gag gtc gga cgc gtc ttc ttt cag gct gag 240  
 Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu  
 65 70 75 80

gac cgg ttc gtg aga cgc aag aag aag gca gca gca gct gcc gga gga 288  
 Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly  
 85 90 95

aaa aag cgg tcc tac acc aag gac tac acc gag gga tgg gtg gag ttc 336  
 Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe  
 100 105 110

cgt gac aag cgc ata gcc aag cgc gtg gcg gcc agt cta cac aac acg 384  
 Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr  
 115 120 125

cct atg ggt gcc cgc agg cgc agc ccc ttc cgt tat gat ctt tgg aac 432  
 Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn  
 130 135 140

ctc aag tac ttg cac cgt ttc acc tgg tcc cac ctc agc gag cac ctc 480  
 Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu  
 145 150 155 160

gcc ttt gag cgc cag gtg cgc agg cag cgc ttg aga gcg gag gtt gct 528

Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala	
165 170 175	
caa gcc aag cgt gag acc gac ttc tat ctt caa agt gtg gaa cgg gga	576
Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly	
180 185 190	
caa cgc ttt ctt gcg gcc gat ggg gac cct gct cgc cca gat ggc tcc	624
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser	
195 200 205	
tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa	672
Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys	
210 215 220	
gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag	720
Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln	
225 230 235 240	
gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc	768
Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala	
245 250 255	
ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc	816
Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser	
260 265 270	
tga gggc ctgggtggcc ccttccattt cctggccctg ctctgcttcc tgtctacctc	873
*	
atactagaat gatcgtgact acccgggcag acatttttact gtgttttctca gaccaagtgt	933
ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg	993
tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc	1053
atatgcttgt tttgtttgac tcttggctgc ctacgtctgt aggggtcccct gaaaatccca	1113
cttctgccc ccagaaaggc cttttatttc caactaggag gataatgcct agtccaggca	1173
atctttctct gtttagcagt cacagggtgag ggtggtatta gcatcttttt tatgtagaaa	1233
aaattgagtt aatgggggtgg actggggttg gaagaaatac atttcctaata gtatttatag	1293
aaaataaaaa tatttttatg tgccttttta tttttgttgg tggggagggtc attggacaag	1353
ttccaacttt catcttgtgt tcccttcacc ttcataacct gatcttagag cccccctccc	1413
cctggcaccc accttactgt ttaacctgga tttttttttc tatttaattt ttgtctaata	1473
tattagccca gtttatcaat cagttatctt aagtcagcat tttctaagcc attgtttgag	1533
ggaacagtga caatagggaa taacaccact tagtattaag ggtttttc	1581

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 <211> 1642  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (228)..(911)

<400> 157

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aaggatcctt aattaaatta atcccccccc cccccccgag tagcggcagc ggcgacgacg      60
gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag      120
cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca      180
ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag  atg gga ggc      236
                                     Met Gly Gly
                                     1

aag ctc agc aag aag aag aag ggc tac aat gtg aac gac gag aaa gcc      284
Lys Leu Ser Lys Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala
      5                                10                                15

aag gag aaa gac aag aag gcc gag ggc gcg gcg acg gaa gag gag ggg      332
Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Glu Gly
      20                                25                                30                                35

acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc      380
Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Ala Glu Pro Ala Glu Ala
                                40                                45                                50

aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag      428
Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu
                                55                                60                                65

gag aag gag ggc gag aag gac gcg gcg gct gcc aag gag gag gcc ccg      476
Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Lys Glu Glu Ala Pro
      70                                75                                80

aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag      524
Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu
      85                                90                                95

ccc ccg aag gcg ccc gag cag gag cag gcg gcc ccc ggc ccc gct gcg      572
Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala
      100                                105                                110                                115

ggc ggc gag gcc ccc aaa gct gct gag gcc gcc gcg gcc ccg gcc gag      620
Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu
                                120                                125                                130

agc gcg gcc cct gcc gcc ggg gag gag ccc agc aag gag gaa ggg gaa      668
Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu
                                135                                140                                145

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ccc aaa aag act gag gcg ccc gca gct cct gcc gcc cag gag acc aaa      716
Pro Lys Lys Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Glu Thr Lys
      150                      155                      160

agt gac ggg gcc cca gct tca gac tca aaa ccc ggc agc tcg gag gct      764
Ser Asp Gly Ala Pro Ala Ser Asp Ser Lys Pro Gly Ser Ser Glu Ala
      165                      170                      175

gcc ccc tct tcc aag gag acc ccc gca gcc acg gaa gcg cct agt tcc      812
Ala Pro Ser Ser Lys Glu Thr Pro Ala Ala Thr Glu Ala Pro Ser Ser
      180                      185                      190                      195

aca ccc aag gcc cag ggc ccc gca gcc tct gca gaa gag ccc aag ccg      860
Thr Pro Lys Ala Gln Gly Pro Ala Ala Ser Ala Glu Glu Pro Lys Pro
      200                      205                      210

gtg gag gcc ccg gca gct aat tcc gac caa acc gta acc gtg aaa gag      908
Val Glu Ala Pro Ala Ala Asn Ser Asp Gln Thr Val Thr Val Lys Glu
      215                      220                      225

tga caag gacagcctat aggaaaaaca ataccactta aaacaatctc ctctctctct      965
*

ctctctctct ctctatctct ctctctatct cctctctctc tctcctctcc tatctctcct      1025

ctctctctct cctatactaa cttgtttcaa attggaagta atgatatgta ttgccaagg      1085

aaaaatacag gatgttgtcc catcaaggga gggagggggg gggagaatcc aaatagtatt      1145

tttgtgggga aatatctaata ataccttcag tcaactttac caagaagtcc tggatttcca      1205

agatccgcgt ctgaaagtgc agtacatcgt ttgtacctga aactgccgcc acatgcactc      1265

ctccaccgct gagagttgaa tagcttttct tctgcaatgg gagttgggag tgatgcgttt      1325

gattctgccc acagggcctg tgccaaggca atcagatctt tatgagagca gtattttctg      1385

tgttttcttt ttaatttaca gcctttctta ttttgatatt tttttaatgt tgtggatgaa      1445

tgccagcttt cagacagagc ccacttagct tgtccacatg gatctcaatg ccaatcctcc      1505

attcttcctc tccagatatt tttgggagtg acaaacattc tctcatccta cttagcctac      1565

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attggtcagt ggaaatg                                             1642

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<210> 158  
 <211> 1521  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>

<221> CDS  
 <222> (417)..(1403)

<400> 158

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cgaggagtcg cgccgaggac ggaggccacg atacctgcgt ggctggggct gcgggctccg      120
gggtcaccac cctggggcgac cgggaggtgg cgctccgcc ggccgcagct ggagaggagc      180
gtgtcccaa gccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctcccgag cctggcggtgg ggttcttctg cggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
          20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
          35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
          50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
          65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
          85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
          100             105             110

gaa agg tta ttt gtc aat gaa gaa aat gtt aat gag ttt ctt gaa gag      800
Glu Arg Leu Phe Val Asn Glu Glu Asn Val Asn Glu Phe Leu Glu Glu
          115             120             125

gtc ctg agc tct cca ttc aaa cag tct atg tcc ttg acc cca cca tta      848
Val Leu Ser Ser Pro Phe Lys Gln Ser Met Ser Leu Thr Pro Pro Leu
          130             135             140

att gaa gtt ctt caa gtt act gat aat aag att caa att aat gca aag      896
Ile Glu Val Leu Gln Val Thr Asp Asn Lys Ile Gln Ile Asn Ala Lys
          145             150             155             160

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ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga	944
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg	
165 170 175	
gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt	992
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys	
180 185 190	
aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta	1040
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu	
195 200 205	
caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt	1088
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu	
210 215 220	
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa	1136
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys	
225 230 235 240	
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag	1184
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu	
245 250 255	
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca	1232
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr	
260 265 270	
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat	1280
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn	
275 280 285	
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt	1328
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser	
290 295 300	
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag	1376
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln	
305 310 315 320	
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gactttttaa	1428
Asn Ser Leu Leu Tyr Asp Leu Asp *	
325	
tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact	1488
aaagggtatta aagtataaaa ttaaaatttg caa	1521

<210> 159  
 <211> 1377  
 <212> DNA  
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<220>

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<400> 159

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gggtcaccac cctggggcgac cgggaggtgg cgctccgcc ggccgcagct ggagaggagc      180
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tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctccccgag cctggcggtgg ggttcttctg cgggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
             20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
             35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
             50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
             65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
             85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
             100             105             110

ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga      800
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg
             115             120             125

gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt      848
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys
             130             135             140

aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta      896
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu
             145             150             155             160

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caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt	944
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu	
165 170 175	
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa	992
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys	
180 185 190	
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag	1040
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu	
195 200 205	
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca	1088
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr	
210 215 220	
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat	1136
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn	
225 230 235 240	
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt	1184
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser	
245 250 255	
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag	1232
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln	
260 265 270	
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gactttttaa	1284
Asn Ser Leu Leu Tyr Asp Leu Asp *	
275 280	
tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact	1344
aaagggtatta aagtataaaa ttaaaatttg caa	1377

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 <211> 1611  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (510)..(1112)

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tcgagcccgcc agcgagagtg accagcatgg tccttgccgg cagctcgggg ccggagggtt	120
ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg	180
gctgctgcag caccgcgctg gacatgagcg ctccgccc aa cccgacggcg tcagctggcg	240

cgcgcgcccg cgaccgacgt ggcgaggcgc ccacggggccg cgcagccgcc attgctctcc	300
tgccacggag gggagcgctt ggtggcagtc cgcgggcccg gacggaaggc tgaggcgacg	360
cctcgacgac agcggaccgg agctgcaggg gcaacacatt cagggcgggg tgccccattt	420
aggcctggct gaccggagta agaaactaca acccccgaag tgccttgcg ctaagggtta	480
cggaggcagt gaccacccac cctggagcc atg gtc cac gcc ttc ctc att cac	533
Met Val His Ala Phe Leu Ile His	
1 5	
acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg	581
Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu	
10 15 20	
tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg	629
Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro	
25 30 35 40	
cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct	677
His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala	
45 50 55	
gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct	725
Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser	
60 65 70	
ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg	773
Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val	
75 80 85	
ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac	821
Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn	
90 95 100	
cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta	869
Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu	
105 110 115 120	
ggc ttt gcc ctg gtg ctg gat gcc cat gag aac ctg cta ctg gct gag	917
Gly Phe Ala Leu Val Leu Asp Ala His Glu Asn Leu Leu Leu Ala Glu	
125 130 135	
ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg	965
Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu	
140 145 150	
ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc	1013
Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly	
155 160 165	
atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac	1061
Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Phe Leu Asn Asp	
170 175 180	
cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc	1109

Gln	Phe	Val	Gln	Gly	Leu	Glu	Lys	Glu	Phe	Ser	Ala	Ala	Trp	Pro	Arg
185					190					195					200

tga ttcc tcgttgggat ggtgcttctg agggcaggca gagggtagac acacagccag 1166  
\*

atgaagcttg gcatctccct cctaccacgc agctctgatg tgctgctata ccaggacaag 1226  
tgggtgacac aagcctgcag aaagggggct gggcagaggg tggaggaggt cctgcctgtc 1286  
ctcaggtttag tggaaccaca gaacttcctg agcctagagc tgctgtgtta cttagaccgc 1346  
tgccgtgcgg cagccacgct tgtccttgaa cccaccttcc tccatccctg ccagccgata 1406  
gtgctagggt gaggagctgc ctggagctca ccccgctctt cttccaaacc cacagccacc 1466  
atgcctggcc tcaatctttt cttttaaaca attattccta tattttattg taatgcagtt 1526  
aaccgtgttt gtcagattca atactctgtg acccgtaac caagtctctg tatgtttatt 1586  
actgcaattc aagtggccct gtatt 1611

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<211> 568  
<212> DNA  
<213> Homo sapiens

<220>  
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tacgtaagct tggatcctct agagcggccg cctactacta ctaaattcgc ggccgcgctcg 120  
accgccgccg agtcgcgcgg aggcggaggc ttgggtgcgt tcaagattca gcttcacccg 180  
taaccacccg cc atg gcc gag gaa ggc att gct gct gga ggt gta atg 228  
Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met  
1 5 10  
gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac 276  
Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His  
15 20 25  
gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag 324  
Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys  
30 35 40  
cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg 372  
Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met  
45 50 55 60

tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta	420
Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu	
65 70 75	
att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt	468
Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys	
80 85 90	
aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc	516
Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser	
95 100 105	
tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa	565
Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu *	
110 115 120	
att	568

<210> 162  
 <211> 1837  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (784)..(1473)

<400> 162	
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cttggtaaaa actggttctt aagaacccca agttcgccaa aagaagggttc aagctaataa	120
aggaaacttc tggttaccaa ttccatctgc ctctttctca gtgactcctg acgagctgct	180
catttacaca cacctgctcc cccccccacc ccacagtctg gattgcgaaa cctaccgcac	240
cccccccca gtgcaggaag aaggtgacct tggctctgggg tggggacaga gagtctggga	300
gggggtggtg gctggcagtc tcggtggctg gcgacgcctc ttccgctctt ccttctctggg	360
aggaggcggg caaggcgaag cctctccgct cagtcgatgg ttcccttcag gacgtctcat	420
agaggtgtgg gtgagatccc aggtctgggc cgcaatttct agccacgctg cccaaccttc	480
aggcaagcag tcaggttcca cagctacccc accacactct cagagtcgag gggaacaaga	540
agagggagtg gtctgtaaata gcgtcgggac aagagtgtccc tcttaactcc acctggagct	600
ggcgtcaggg cgatctctgg atgccagcc cataagcctg gcctgtctgt gaggaggctg	660
cgtctggctc ccgctctcac agccattgca gtacattgag ctccatagag acagcgccgg	720
ggcaagtgag agccggacgg gcactgggag actctgtgcc tcgctgagga aaaataacta	780

aac atg ggc aaa gga gat cct aag aag ccg aga ggc aaa atg tca tca	828
Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser	
1 5 10 15	
tat gca ttt ttt gtg caa act tgt cgg gag gag cat aag aag aag cac	876
Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His	
20 25 30	
cca gat gct tca gtc aac ttc tca gag ttt tct aag aag tgc tca gag	924
Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu	
35 40 45	
agg tgg aag acc atg tct gct aaa gag aaa gga aaa ttt gaa gat atg	972
Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met	
50 55 60	
gca aag gcg gac aag gcc cgt tat gaa aga gaa atg aaa acc tat atc	1020
Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile	
65 70 75	
cct ccc aaa ggg gag aca aaa aag aag ttc aag gat ccc aat gca ccc	1068
Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro	
80 85 90 95	
aag agg cct cct tgc gcc ttc ttc ctc ttc tgc tct gag tat cgc cca	1116
Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro	
100 105 110	
aaa atc aaa gga gaa cat cct ggc ctg tcc att ggt gat gtt gcg aag	1164
Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys	
115 120 125	
aaa ctg gga gag atg tgg aat aac act gct gca gat gac aag cag cct	1212
Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro	
130 135 140	
tat gaa aag aag gct gcg aag ctg aag gaa aaa tac gaa aag gat att	1260
Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile	
145 150 155	
gct gca tat cga gct aaa gga aag cct gat gca gca aaa aag gga gtt	1308
Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val	
160 165 170 175	
gtc aag gct gaa aaa agc aaa aaa aag aag gaa gag gag gaa gat gag	1356
Val Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu	
180 185 190	
gaa gat gaa gag gat gag gag gag gag gaa gat gaa gaa gat gaa gat	1404
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp	
195 200 205	
gaa gaa gaa gaa gat gat gat atg atg aat aag ttg gtt cta gcg cag	1452
Glu Glu Glu Glu Asp Asp Asp Met Met Asn Lys Leu Val Leu Ala Gln	
210 215 220	

ttt ttt ttt tct tgt cta taa ag catttaaccc ccctgttaca caactcactc 1505  
Phe Phe Phe Ser Cys Leu \*  
225 230

cttttaaaga aaaaaattga aatgtaaggc tgtgtaagat ttgttttttaa actgtacagt 1565  
gtctttttttt gtatagttaa cacactaccg aatgtgtctt tagatagccc tgtcctgggtg 1625  
gtatttttcaa tagccactaa ccttgcctgg tacagtatgg gggttgtaaa ttggcatgga 1685  
aatttaaagc aggttcttgt tgggtgcacag cacaaattag ttatatatgg ggatggtagt 1745  
tttttcatct tcagttgtct ctgatgcagc ttatacgaaa taattgttgt tctgttaact 1805  
gaataccact ctgtaattgc aaaaaaaaaa aa 1837

<210> 163  
<211> 1454  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (269)..(718)

<400> 163  
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caaccggttac cccgcccacg ccagcagcca cgggtcgcca gcgccacgca gcggaggcgg 120  
gcggcatggc tggcccaagg tgcgcaggcg cactagccct gggggtgctt ccgtgtctgc 180  
gccctgagac atttttggcg ccggccccag cctgagcggg gacggcggcc gggagggcgc 240  
ggcccggggtt cccgttcccc gcggagcc atg cgg tac aac gag aag gag ctg 292  
Met Arg Tyr Asn Glu Lys Glu Leu  
1 5

cag gct ctg tcc cgg cag ccg gcc gag atg gcg gcc gag ctg ggc atg 340  
Gln Ala Leu Ser Arg Gln Pro Ala Glu Met Ala Ala Glu Leu Gly Met  
10 15 20

agg ggc ccc aag aag ggc agc gtg ctg aag cgg cgg ctg gtg aag ctg 388  
Arg Gly Pro Lys Lys Gly Ser Val Leu Lys Arg Arg Leu Val Lys Leu  
25 30 35 40

gtg gtg aat ttc ctc ttc tac ttt cgg aca gac gag gcc gag ccc gtc 436  
Val Val Asn Phe Leu Phe Tyr Phe Arg Thr Asp Glu Ala Glu Pro Val  
45 50 55

gga gcc ctg ctg ctg gag cgc tgc aga gtc gtc cgg gaa gag ccc ggc 484  
Gly Ala Leu Leu Leu Glu Arg Cys Arg Val Val Arg Glu Glu Pro Gly  
60 65 70



<400> 164  
acggcgcg atg gcg gcg gct gcc gcc gag acc ccc gaa gtc ctt cgg gaa 50  
Met Ala Ala Ala Ala Ala Glu Thr Pro Glu Val Leu Arg Glu  
1 5 10

tgc ggt tgc aag ggc atc cgg acc tgt ctg atc tgc gag cgg cag cgc 98  
Cys Gly Cys Lys Gly Ile Arg Thr Cys Leu Ile Cys Glu Arg Gln Arg  
15 20 25 30

ggc agt gac ccg ccc tgg gag ctg ccc cca gcg aaa aca tac cgt ttc 146  
Gly Ser Asp Pro Pro Trp Glu Leu Pro Pro Ala Lys Thr Tyr Arg Phe  
35 40 45

att tac tgc tcc gac acc ggc tgg gcc gtg ggc aca gag gag tct gac 194  
Ile Tyr Cys Ser Asp Thr Gly Trp Ala Val Gly Thr Glu Glu Ser Asp  
50 55 60

ttt gag ggc tgg gcc ttc ccc ttc cca gga gtg atg ctg atc gag gac 242  
Phe Glu Gly Trp Ala Phe Pro Phe Pro Gly Val Met Leu Ile Glu Asp  
65 70 75

ttt gtg acc cgg gag gaa gaa gcc gag ttg gtg cgg ctc atg gac cgt 290  
Phe Val Thr Arg Glu Glu Glu Ala Glu Leu Val Arg Leu Met Asp Arg  
80 85 90

gac ccc tgg aag ctc tcc cag tct gga cgg agg aag cag gac tat ggc 338  
Asp Pro Trp Lys Leu Ser Gln Ser Gly Arg Arg Lys Gln Asp Tyr Gly  
95 100 105 110

ccc aaa gtc aac ttt cgg aaa cag aag cta aag acc gag ggc ttc tgc 386  
Pro Lys Val Asn Phe Arg Lys Gln Lys Leu Lys Thr Glu Gly Phe Cys  
115 120 125

ggc ctc ccc agc ttc agc cgg gag gtg gtg cgg agg atg ggc ctc tac 434  
Gly Leu Pro Ser Phe Ser Arg Glu Val Val Arg Arg Met Gly Leu Tyr  
130 135 140

ccg ggg ctg gag ggc ttc cgg ccc gtc gag cag tgc aac ctg gac tac 482  
Pro Gly Leu Glu Gly Phe Arg Pro Val Glu Gln Cys Asn Leu Asp Tyr  
145 150 155

tgc ccc gag cgg ggc tct gcc att gac ccc cac ctg gac gac gcc tgg 530  
Cys Pro Glu Arg Gly Ser Ala Ile Asp Pro His Leu Asp Asp Ala Trp  
160 165 170

ctg tgg ggg gag cgg ctg gtc agc ctc aac ctc ctg tcc ccc acc gtg 578  
Leu Trp Gly Glu Arg Leu Val Ser Leu Asn Leu Leu Ser Pro Thr Val  
175 180 185 190

ctg tcc atg tgt cgg gag gcg ccc ggg agc ctg ctc ctc tgc tgc gcc 626  
Leu Ser Met Cys Arg Glu Ala Pro Gly Ser Leu Leu Leu Cys Ser Ala  
195 200 205

ccg tgc gct gcc ccg gag gcc ttg gtg gac agc gtg ata gca ccc agc 674  
Pro Ser Ala Ala Pro Glu Ala Leu Val Asp Ser Val Ile Ala Pro Ser  
210 215 220



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cgg tcg gtg cta tgc cag gag gtg gag gtg gcc atc ccc tta ccc gcc      722
Arg Ser Val Leu Cys Gln Glu Val Glu Val Ala Ile Pro Leu Pro Ala
      225                      230                      235

cgc tcc ctg ctg gtc ctc acc ggg gcg gca cgg cac cag tgg aag cat      770
Arg Ser Leu Leu Val Leu Thr Gly Ala Ala Arg His Gln Trp Lys His
      240                      245                      250

gcc atc cac cgc aga cac atc gag gcc cgc cgc gtc tgc gtc act ttc      818
Ala Ile His Arg Arg His Ile Glu Ala Arg Arg Val Cys Val Thr Phe
      255                      260                      265                      270

cgg gag ctg tcg gct gag ttt ggc cct gga ggg agg cag caa gag ctg      866
Arg Glu Leu Ser Ala Glu Phe Gly Pro Gly Gly Arg Gln Gln Glu Leu
      275                      280                      285

ggc cag gaa ctg ctg cgg atc gcc ctc tcc ttc cag gga aga ccc gtg      914
Gly Gln Glu Leu Leu Arg Ile Ala Leu Ser Phe Gln Gly Arg Pro Val
      290                      295                      300

tga accg cctccttggc tccagacttg actgatcccg ggattgaaat gaggagcaca      971
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gaacaggggcc tcctgcaact cacgggggttt caagagaaga tggctgaccc ctgatgctgt      1031

gagcagtgtg agccctgccc aggagcaggt tttgatggga acgtacctcc aggcagcccc      1091

cttcacactg gaccgtggcc acactttttt ggttatttag tttgtcacag tcttggggac      1151

atgggatcat t                                                              1162

<210> 165
<211> 1018
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40)..(747)

<400> 165
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                                   Met Ala Ala Ala Asn
                                   1                      5

ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc      102
Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
      10                      15                      20

cac ttc ata gct tcg ggg atg gtc aat cag gag atg tta aac atg tct      150
His Phe Ile Ala Ser Gly Met Val Asn Gln Glu Met Leu Asn Met Ser
      25                      30                      35

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aag aaa aca gtt tct tgt ttt gtg aac ttc acc aga cta cag cag atc	198
Lys Lys Thr Val Ser Cys Phe Val Asn Phe Thr Arg Leu Gln Gln Ile	
40 45 50	
aca aat att caa gct gaa atc tac cag aaa aac ctg gaa att gaa ctc	246
Thr Asn Ile Gln Ala Glu Ile Tyr Gln Lys Asn Leu Glu Ile Glu Leu	
55 60 65	
ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt ttg	294
Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe Leu	
70 75 80 85	
gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa gca	342
Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu Ala	
90 95 100	
gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc atg	390
Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro Met	
105 110 115	
tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg gta	438
Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met Val	
120 125 130	
cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc cac	486
His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr His	
135 140 145	
ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag aaa	534
Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys Lys	
150 155 160 165	
atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca gaa	582
Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr Glu	
170 175 180	
gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa gtt	630
Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu Val	
185 190 195	
tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat aaa	678
Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr Lys	
200 205 210	
cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat gtc	726
His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His Val	
215 220 225	
caa act att aat gcc aag tag tc atcaacttta tttttgctta attatgtgta	779
Gln Thr Ile Asn Ala Lys *	
230 235	
gtcatatgaa gtctatttct agttgactgt aacatgggta ttaatagtct ttgctgctgg	839
taatactgaa agaacctgct ttatatggga gtatcaagat ctcagggttca ttaagaccaa	899

actgactttt cctttgtttt tcatatatatt ttattctacc tttcagtaaa actagagaag 959  
 ctaaaaaata gccatgacaa tttattaata taagtgaatt aaccattaaa aaaaaaaaaa 1018

<210> 166  
 <211> 925  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (40)..(654)

<400> 166  
 gctcactctt ggcgcttctg cggaaggtgc gtccgagcc atg gcc gct gcc aac 54  
 Met Ala Ala Ala Asn  
 1 5  
 ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc 102  
 Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly  
 10 15 20  
 cac ttc ata gct tcg ggg atg gtc aat cag aaa aac ctg gaa att gaa 150  
 His Phe Ile Ala Ser Gly Met Val Asn Gln Lys Asn Leu Glu Ile Glu  
 25 30 35  
 ctc ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt 198  
 Leu Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe  
 40 45 50  
 ttg gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa 246  
 Leu Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu  
 55 60 65  
 gca gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc 294  
 Ala Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro  
 70 75 80 85  
 atg tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg 342  
 Met Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met  
 90 95 100  
 gta cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc 390  
 Val His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr  
 105 110 115  
 cac ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag 438  
 His Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys  
 120 125 130  
 aaa atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca 486  
 Lys Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr  
 135 140 145

gaa gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa 534  
 Glu Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu  
 150 155 160 165

gtt tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat 582  
 Val Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr  
 170 175 180

aaa cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat 630  
 Lys His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His  
 185 190 195

gtc caa act att aat gcc aag tag tcatcaactt tatttttgct taattatgtg 684  
 Val Gln Thr Ile Asn Ala Lys \*  
 200 205

tagtcatatg aagtctatatt ctagttgact gtaacatggg tattaatagt ctttgctgct 744

ggtaataactg aaagaacctg ctttatattg gagtatcaag atctcagggt cattaagacc 804

aaactgactt ttcctttggt tttcatatat ttttattcta ccttttcagta aaactagaga 864

agctaaaaaa tagccatgac aatttattaa tataagttaa ttaaccatta aaaaaaaaaa 924

a 925

<210> 167  
 <211> 1058  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (190)..(828)

<400> 167  
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ctgagtttgc gaccgtagct gtcgctttcc ggccaacaca gaggtgcctg aaggctgggt 120

gggggtggtga ggcccagggc agctcttggt cagcttctgag aatttctgag cagccctcgt 180

cagtacaag atg gac ccc gta gtc ttg agt tac atg gac agt cta ctg 228  
 Met Asp Pro Val Val Leu Ser Tyr Met Asp Ser Leu Leu  
 1 5 10

cgg caa tca gat gtc tca cta ttg gat ccg cca agc tgg ctc aat gac 276  
 Arg Gln Ser Asp Val Ser Leu Leu Asp Pro Pro Ser Trp Leu Asn Asp  
 15 20 25

cat att att ggg ttt gcg ttt gag tac ttt gcc aac agt cag ttt cat 324  
 His Ile Ile Gly Phe Ala Phe Glu Tyr Phe Ala Asn Ser Gln Phe His  
 30 35 40 45

gac tgc tct gat cac gtc agt ttc atc agc cct gaa gtc acc cag ttc 372  
 Asp Cys Ser Asp His Val Ser Phe Ile Ser Pro Glu Val Thr Gln Phe  
                     50                    55                    60

atc aag tgc act agc aac cca gca gag att gcc atg ttc ctt gaa cca 420  
 Ile Lys Cys Thr Ser Asn Pro Ala Glu Ile Ala Met Phe Leu Glu Pro  
                     65                    70                    75

ctg gac ctc ccc aac aag aga gtt gta ttt tta gcc atc aat gat aac 468  
 Leu Asp Leu Pro Asn Lys Arg Val Val Phe Leu Ala Ile Asn Asp Asn  
                     80                    85                    90

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 Ser Asn Gln Ala Ala Gly Gly Thr His Trp Ser Leu Leu Val Tyr Leu  
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caa gat aaa aat agc ttt ttt cat tat gat tcc cat agc agg agc aac 564  
 Gln Asp Lys Asn Ser Phe Phe His Tyr Asp Ser His Ser Arg Ser Asn  
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tca gtt cac gca aag cag gta gca gag aaa ctg gag gct ttc tta ggc 612  
 Ser Val His Ala Lys Gln Val Ala Glu Lys Leu Glu Ala Phe Leu Gly  
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aga aaa gga gac aaa ctg gcc ttt gtg gaa gag aaa gcc cct gcc caa 660  
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                                         Met Lys Pro Val Leu
                                         1      5

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Gln Ser Leu Tyr His Arg Val Leu Leu Tyr Pro Pro Pro Gln His Arg
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Val Glu Ala Ile Lys Ile Met Lys Glu Ile Leu Gly Ser Pro Gln Arg
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Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp Leu Leu Lys Leu Ile
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Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly Gly Ile Glu Ala Cys
              70              75              80              85

tat gca gcc gtg tcc tgt gtc tgc acc ttg ctg ggt gcc ctg gat gag      401
Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu Gly Ala Leu Asp Glu
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Leu Ser Gln Gly Lys Gly Leu Ser Glu Gly Gln Val Gln Leu Leu Leu
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tcagaccaat atttcagggt gatatttcta agtattacta gaaaatacgt ttgaaagcct 6896  
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 aaataaggat ttaaaggggt atttgtaaac tttgccctcc ttgagaaata tggaactacc 7136  
 ttagagggtta agaggaaggc agtgttctga cttcttttagg tgatctgaaa aaaacaccct 7196  
 tatcatccag tgtaccatct agagatcacc acagaatcca tttttttccc agttccacaa 7256  
 aacactctgt ttgccttcag tttttactca ctagacaata attcaagttt agaaacaggt 7316  
 aatcagctat ttgatcttaa aaggcaatga attgttgga tatcagtga ctatgttgta 7376  
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 cagttcttct ttgtgaacct gtgagtactc cacagtttac tgggggaaaa ggcttcagta 7556  
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 <213> Homo sapiens

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 tgccctgaat aattaagagt ttgctttttt cccatgtctt tgcaatagga taatataaag 180  
 aatagtatta aaagtcagag gctttactaa tctacctata tgtattccat ggctaacaaa 240  
 ccttggtccc ttacat atg agc tct gga ggt tgc cct ggc tgc ctc agg 290  
 Met Ser Ser Gly Gly Ser Pro Gly Cys Leu Arg  
 1 5 10  
 ctt gca gaa ggc tgc ccc aat cac aga gcc tgg gta agg tgg aac agg 338  
 Leu Ala Glu Gly Cys Pro Asn His Arg Ala Trp Val Arg Trp Asn Arg  
 15 20 25

agg cag ccc cac tcg gct ttt ctg att gca tcc cac ctg ttt ctg agt	386
Arg Gln Pro His Ser Ala Phe Leu Ile Ala Ser His Leu Phe Leu Ser	
30 35 40	
gtg ttg gtt tgg ttt aat tct ttt caa ggg ttg gag ttg gaa agt gaa	434
Val Leu Val Trp Phe Asn Ser Phe Gln Gly Leu Glu Leu Glu Ser Glu	
45 50 55	
aac cct aga cac ttg ctg tgg aat gtt tgc ctg gtt gta ttg gtg tgt	482
Asn Pro Arg His Leu Leu Trp Asn Val Cys Leu Val Val Leu Val Cys	
60 65 70 75	
ccc tct tct tca ctg gca tgt cgc ttt caa gtg tac caa agg aca ttt	530
Pro Ser Ser Ser Leu Ala Cys Arg Phe Gln Val Tyr Gln Arg Thr Phe	
80 85 90	
tgt tct gtt gaa agc cac agg acc aaa agg aaa ata ttg caa cta ttt	578
Cys Ser Val Glu Ser His Arg Thr Lys Arg Lys Ile Leu Gln Leu Phe	
95 100 105	
gca aac ata ctt ccc tac cta tac aag cag cca tat act aaa aag cac	626
Ala Asn Ile Leu Pro Tyr Leu Tyr Lys Gln Pro Tyr Thr Lys Lys His	
110 115 120	
taa acaa gcacaaatga acactaaata gccttatacc aaaaagcatt cttgtaactg	683
*	
tcagggcatg gtatgaattc cttcctcttt aagcagcaac ttaccacagg cttggtggct	743
ttaagtaata tagcattaag caaatgggtca gttatttttt aatggtgaaa acttccaagt	803
gtgaataata cggacatagt ttactacctt ttgcttttaa tatacctgggt tatctatttc	863
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ctcagactta actctcccca attaaaatag tttttttttc ccttcccatt tttttgtttt	983
taagagatag ggtcttgctg tgttgcccag gctagagtgc agcagtgaca tgatcatagc	1043
tactgcagc ctggaactcc tgggctcagg atccttctgc ttcggcctcc tgagtagcta	1103
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ggacttgcta tgttgcccag actgggtctcg aactcctggc ctcaagccac caacctctca	1223
aattgctaga attacaagca tgagccacca cacctggcct gttattcctt ctttatctaa	1283
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gccctacaac tatcttctgt ttttagaatt tgtagtcact gttcttagtg ccactggaaa	1463
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taataatagc tcagttttta aaggagggga acaatacccc atgagttcaa attaattttc 1823
tctactttga ggtatacctt cctaattata ttttacatag gctgtttttt ttaagtttaa 1883
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tcataaatat gtcaatttta gaaactcaa ctctttccca tcttttgtat ggataaagtt 2063
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agaaggtgag aatgtgttta tactgtatat ggaaaccta tgccctcttt ctaaagcttt 2483
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<212> DNA
<213> Homo sapiens

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<220>
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<222> (451)..(846)

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ctgaatcaac ctttgatcgt acctttgaac cacattctgt accagtttgt gagccagttt 180
cctgtaatat tgacaatata gaaccaagta gcaataaaga tgatgatttt cttgaaaaaa 240
atggagctga tgaaaaatta gagcaaattt cagagtaaag actcattgga tgagaaaaat 300

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aaagctgata ataattattga tgctaattgaa gaaactctag aaacagatta tacaactatt 360  
 tgttcagatc gacctctctga aaatgaaaag aaggttagagg aagatattat cacagagctt 420  
 gctcttggag aagatgctat atctagcagt atg gaa att gac caa ggt gaa 471  
 Met Glu Ile Asp Gln Gly Glu  
 1 5  
 aag aat gaa gat gaa act tct gca gat ctt gta gaa acg att aat gaa 519  
 Lys Asn Glu Asp Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu  
 10 15 20  
 aat gtt att gaa gat aac aaa agt gag aat atc tta gaa aat aca gac 567  
 Asn Val Ile Glu Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp  
 25 30 35  
 tct atg gag aca gat gaa atc att cct att ttg gaa aag ctt gca cct 615  
 Ser Met Glu Thr Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro  
 40 45 50 55  
 tct gag gat gaa ctt act tgc ttt tct aaa aca tct ctc ctt cca atc 663  
 Ser Glu Asp Glu Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile  
 60 65 70  
 gat gag aca aat cca gat ttg gaa gag aaa atg gaa agt tct ttt ggt 711  
 Asp Glu Thr Asn Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly  
 75 80 85  
 tca cca tct aaa caa gaa agt agt gag agt ttg cca aaa gaa gcc ttt 759  
 Ser Pro Ser Lys Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe  
 90 95 100  
 ctg gtc ctc tct gat gaa gag gat att tcg ggt gaa aaa gat gag tct 807  
 Leu Val Leu Ser Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser  
 105 110 115  
 gaa gtt ata tcg caa aat gaa acg tgc tct cca ggt tag catataactt 856  
 Glu Val Ile Ser Gln Asn Glu Thr Cys Ser Pro Gly \*  
 120 125 130  
 aaatgttaaa gattttttat tgactttgat gaactgttta ataaaacatt atcataatgt 916  
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 cttaacttca tagaattcag aattagtgtg tgtactctgt gagtagcatt gtactaaata 1036  
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 gcagttcttt cttgctatca cttagcgaac aaataactta gaactaaaag cctaatagtt 1216  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (141)..(401)

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 cccaacgtag aggttgagca tcagcggcag catggccgac ccttcgga agtgcagcca 120  
 ttgcacgtat tcgtcatagg atg ctg tgg ccc ggc gca gga ttg gag gga 170  
 Met Leu Trp Pro Gly Ala Gly Leu Glu Gly  
 1 5 10  
 cat aga cct ggt gga agg cgt ggg gct gcc ctg acc cag gga ttt ggc 218  
 His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly  
 15 20 25  
 tcc tgt agc gct gct ggg cag agg tcc gca gga gct gca ggt act tct 266  
 Ser Cys Ser Ala Ala Gly Gln Arg Ser Ala Gly Ala Ala Gly Thr Ser  
 30 35 40

tgg cca act cta gct gct gct tct tgc act gct tcc ggc ggg gtg agg	314
Trp Pro Thr Leu Ala Ala Ala Ser Cys Thr Ala Ser Gly Gly Val Arg	
45 50 55	
acc cac agc tct gat gtg ggc gct tca ggc cat ggt gga gct gag att	362
Thr His Ser Ser Asp Val Gly Ala Ser Gly His Gly Gly Ala Glu Ile	
60 65 70	
cag gtt ggc ttt tcc cct cag ctc cca gct ggc tgg tga acccatcatc	411
Gln Val Gly Phe Ser Pro Gln Leu Pro Ala Gly Trp *	
75 80 85	
atagccaaaa gtactcagca gcagcacctc caggtccaga ggcacctcca gctgcatgca	471
cacacaatga atgaaagact gccaggtgtc cgaaccctgg acatgcagct tgttgagttg	531
caggatgact ctctgttcag ggtccaaggt ctcgttcctg gaatccaggt ccgtgttgagg	591
gaggaagaac ttcattcttg cggttcagcca ttctgggtct ttggtgagca gcctcacaag	651
acagctccac aggttcttgt tgccgagctg gaggccaacg ggggtccatga ggagccagcc	711
ttggtctcct cggtcatgat aggtgctcta ggggtcccccac ggagaggggtc tcatgggtgt	771
ctgggctatg tgtgccttga gctggattga caggttgttt ccatagtgca gactccctca	831
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Met Ala Lys Gly Lys Ser Thr Thr Leu Thr Gln Asp	
1 5 10	
atg agc acc agc ctc cag gaa ggc cag gag gac ggg ccg gca gga tgg	98
Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp	
15 20 25	
aga gcg aat ctg aag ccc gtg gac agg aga agc cca gct gag agg act	146
Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr	
30 35 40	
ctg aag ccc aag gaa cca cgg gcc ctg gca gag ccg agg gcg ggg gag	194
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu	
45 50 55 60	

gcc ccc agg aag gtc tca ggc agc ttt gct ggg agt gtc cac atc acc	242
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr	
65 70 75	
ctg acc ccc gtg agg cct gac agg acc cca cgc cca gcc agc cca gga	290
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly	
80 85 90	
ccc agc ctc cca gcc agg tcc ccc tcc cca ccc cgc cgc agg aga ctg	338
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Arg Leu	
95 100 105	
gcc gtc cct gcc agc ctc gac gtt tgt gac aac tgg ctt cgg ccg gag	386
Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu	
110 115 120	
ccc cct ggc cag gaa gcc cga gtg cag agc tgg aag gag gag gag aag	434
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys	
125 130 135 140	
aaa cct cac ctt cag ggc aaa cca ggg aga ccc ttg tcc ccg gcc aat	482
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn	
145 150 155	
gtc cct gct ctg cct ggc gag acg gtg acc tcc cca gtc agg ctg cac	530
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His	
160 165 170	
ccc gac tac ctc tcc ccg gag gag ata cag agg cag ctg cag gac atc	578
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile	
175 180 185	
gag agg cgg ctg gac gcc ctg gag ctc cgc ggc gtg gag ctg gag aag	626
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys	
190 195 200	
cga ctg cgg gcg gcc gag gga gat gac gct gag gat agc ctc atg gtg	674
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val	
205 210 215 220	
gac tgg ttc tgg ctc att cac gag aag cag ctt ctg ctg aga cag gag	722
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu	
225 230 235	
tca gag ctg atg tac aag tcc aag gcc cag cgt ctg gag gag cag cag	770
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln	
240 245 250	
ctg gac atc gag ggc gag ctg cgc cgg ctc atg gcc aag ccc gag gct	818
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala	
255 260 265	
ctg aag tca ctg cag gag cgg cgg cgg gag cag gag ctg ctg gag cag	866
Leu Lys Ser Leu Gln Glu Arg Arg Arg Glu Gln Glu Leu Leu Glu Gln	
270 275 280	

tac gtg agc acc gtg aac gac cgc agt gac atc gtg gac tcg ctg gac	914
Tyr Val Ser Thr Val Asn Asp Arg Ser Asp Ile Val Asp Ser Leu Asp	
285 290 295 300	
gag gac cgg ctc cgg gaa caa gag gag gat cag atg ctg cgg gac atg	962
Glu Asp Arg Leu Arg Glu Gln Glu Glu Asp Gln Met Leu Arg Asp Met	
305 310 315	
att gag aag ctg ggc ctc cag agg aag aag tcc aag ttc cgc ttg tcc	1010
Ile Glu Lys Leu Gly Leu Gln Arg Lys Lys Ser Lys Phe Arg Leu Ser	
320 325 330	
aag atc tgg tca cca aaa agc aaa agc agc ccc tcc cag tag tagccag	1059
Lys Ile Trp Ser Pro Lys Ser Lys Ser Ser Pro Ser Gln *	
335 340 345	
tagggccgtg ggctcggccc ggacctggca tccggacttg gactcggggc catgggcttg	1119
gccccgaccc ggaaccgga cttgtactcg gggccgtggg ctcggccccg acccggcatt	1179
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ttcggctttg atg acc tta atc cag gca aat cct aaa tcc tat cca gtc	169
Met Thr Leu Ile Gln Ala Asn Pro Lys Ser Tyr Pro Val	
1 5 10	
ggc agc atc cag atg aac cac aac tcc ttc ctc agc gca acc agg cca	217
Gly Ser Ile Gln Met Asn His Asn Ser Phe Leu Ser Ala Thr Arg Pro	
15 20 25	
agg gag tgc tcc atc ccc tgc ctc gca gtt act gat tct cca agc cgg	265
Arg Glu Cys Ser Ile Pro Cys Leu Ala Val Thr Asp Ser Pro Ser Arg	
30 35 40 45	
gcg ccg ccc agt cct ggc ggg gct tcc ccc acc cct ctc cgc gcc ggg	313
Ala Pro Pro Ser Pro Gly Gly Ala Ser Pro Thr Pro Leu Arg Ala Gly	
50 55 60	

caa tcg cgc gtt ctt tct tta ctt gtg ctc cac tgg tgg gca gca tgt	361
Gln Ser Arg Val Leu Ser Leu Leu Val Leu His Trp Trp Ala Ala Cys	
65 70 75	
gct ccc gcg tcc aca gct ctg ttt cgc ctt ccg gtc ccc gta gct ctg	409
Ala Pro Ala Ser Thr Ala Leu Phe Arg Leu Pro Val Pro Val Ala Leu	
80 85 90	
cag ggg aac ggg atc tct gcc gcc tcc tcg gcc gct aag cga ccc ggg	457
Gln Gly Asn Gly Ile Ser Ala Ala Ser Ser Ala Ala Lys Arg Pro Gly	
95 100 105	
gct gcc cga cct agc gag tgc gca cga ccg ccc agc gag ggg tag ccg	505
Ala Ala Arg Pro Ser Glu Cys Ala Arg Pro Pro Ser Glu Gly *	
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agtcgaggca gcacggttcc caaggcagcc aaggctgcgc c	546

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (50)..(793)

<400> 174

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gag cag ccc cag atg caa gac gcc gac gag ccc gcg gac tcc gga ggg	103	
Glu Gln Pro Gln Met Gln Asp Ala Asp Glu Pro Ala Asp Ser Gly Gly		
5 10 15		
gaa ggc cgg gca ggc ggg cca ccg cag gtc gcc ggc gcc cag gcg gcg	151	
Glu Gly Arg Ala Gly Gly Pro Pro Gln Val Ala Gly Ala Gln Ala Ala		
20 25 30		
tgc agc gag gac cgc atg acc ctg ctc ctc agg ctg aga gca cag aca	199	
Cys Ser Glu Asp Arg Met Thr Leu Leu Leu Arg Leu Arg Ala Gln Thr		
35 40 45 50		
aaa caa caa ctc tta gaa tat aaa tca atg gtt gat gca agt gaa gaa	247	
Lys Gln Gln Leu Leu Glu Tyr Lys Ser Met Val Asp Ala Ser Glu Glu		
55 60 65		
aaa act cca gaa caa att atg caa gaa aag caa atc gaa gct aaa att	295	
Lys Thr Pro Glu Gln Ile Met Gln Glu Lys Gln Ile Glu Ala Lys Ile		
70 75 80		
gaa gac ctg gaa aat gaa att gaa gag gta aaa gtt gct ttt gag ata	343	
Glu Asp Leu Glu Asn Glu Ile Glu Glu Val Lys Val Ala Phe Glu Ile		

85	90	95	
aaa aag ctt gca tta gac agg atg aga ctt tca act gca ctt aaa aaa			391
Lys Lys Leu Ala Leu Asp Arg Met Arg Leu Ser Thr Ala Leu Lys Lys			
100	105	110	
aac ctg gag aaa att agc aga cag tct agt gtg ctc atg gat aac atg			439
Asn Leu Glu Lys Ile Ser Arg Gln Ser Ser Val Leu Met Asp Asn Met			
115	120	125	130
aaa cac cta tta gag cta aat aaa tta ata atg aaa tca cag cag gaa			487
Lys His Leu Leu Glu Leu Asn Lys Leu Ile Met Lys Ser Gln Gln Glu			
135	140	145	
tct tgg gat tta gag gaa aaa ctg ctt gat att aga aag aag aga ttg			535
Ser Trp Asp Leu Glu Glu Lys Leu Leu Asp Ile Arg Lys Lys Arg Leu			
150	155	160	
caa tta aaa caa gct tca gaa agt aag ctt tta gaa ata cag act gaa			583
Gln Leu Lys Gln Ala Ser Glu Ser Lys Leu Leu Glu Ile Gln Thr Glu			
165	170	175	
aag aac aaa cag aag att gat ttg gac agt atg gaa aac tca gag agg			631
Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg			
180	185	190	
ata aag atc ata cga caa aac cta cag atg gag ata aaa att act act			679
Ile Lys Ile Ile Arg Gln Asn Leu Gln Met Glu Ile Lys Ile Thr Thr			
195	200	205	210
gtt att caa cat gtg ttc cag aac ctt att ttg ggg agt aaa gtc aat			727
Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn			
215	220	225	
tgg gca gag gat cct gcc ctt aag gaa att gtt ctg cag ctt gag aag			775
Trp Ala Glu Asp Pro Ala Leu Lys Glu Ile Val Leu Gln Leu Glu Lys			
230	235	240	
aat gtt gac atg atg taa taagaa ttcatttctg acatatttta catttctggc			829
Asn Val Asp Met Met *			
245			
aatctcaact cttatttgga atacttctgt gcatttgtct gtccaccgta attttagaaa			889
agcatatcca taacgtttac agttgtagta cagttgtggt tagttatttg tagtgggatt			949
gaaagtaatt tttttctttt tatatttcta tattcagggtt ggtttttttg tgccgttcgc			1009

<210> 175  
 <211> 834  
 <212> DNA  
 <213> Homo sapiens  
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<221> CDS  
 <222> (12)..(833)

<400> 175

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Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu	
1 5 10	
cag ctg gac ttg gtg aat gga gag aat gtg gag cag cat cct tca acc	98
Gln Leu Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr	
15 20 25	
ctg agt gtc cag gag gga gac agc gct gtt atc aag tgt act tat tca	146
Leu Ser Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser	
30 35 40 45	
gac agt gcc tca aac tac ttc cct tgg tat aag caa gaa ctt gga aaa	194
Asp Ser Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys	
50 55 60	
aga cct cag ctt att ata gac att cgt tca aat gtg ggc gaa aag aaa	242
Arg Pro Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys	
65 70 75	
gac caa cga att gct gtt aca ttg aac aag aca gcc aaa cat ttc tcc	290
Asp Gln Arg Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser	
80 85 90	
ctg cac atc aca gag acc caa cct gaa gac tcg gct gtc tac ttc tgt	338
Leu His Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys	
95 100 105	
gca gca agt aac ggc cag gca gga act gct ctg atc ttt ggg aag gga	386
Ala Ala Ser Asn Gly Gln Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly	
110 115 120 125	
acc acc tta tca gtg agt tcc aat atc cag aac cct gac cct gcc gtg	434
Thr Thr Leu Ser Val Ser Ser Asn Ile Gln Asn Pro Asp Pro Ala Val	
130 135 140	
tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc cta ttc	482
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe	
145 150 155	
acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat tct gat	530
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp	
160 165 170	
gtg tat atc aca gac aaa act gtg cta gac atg agg tct atg gac ttc	578
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe	
175 180 185	
aag agc aac agt gct gtg gcc tgg agc aac aaa tct gac ttt gca tgt	626
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys	
190 195 200 205	
gca aac gcc ttc aac aac agc att att cca gaa gac acc ttc ttc ccc	674

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro	
210 215 220	
agc cca gaa agt tcc tgt gat gtc aag ctg gtc gag aaa agc ttt gaa	722
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu	
225 230 235	
aca gat acg aac cta aac ttt caa aac ctg tca gtg att ggg ttc cga	770
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg	
240 245 250	
atc ctc ctc ctg aaa gtg gcc ggg ttt aat ctg ctc atg acg ctg cgg	818
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg	
255 260 265	
ctg tgg tcc agc tga g	834
Leu Trp Ser Ser *	
270	

<210> 176  
 <211> 778  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (34)..(576)  
 <220>  
 <221> misc\_feature  
 <222> (1)...(778)  
 <223> n = a,t,c or g

<400> 176	
tttcgtagac ctctctgtct tgtagcatct gcc atg aga atc agg ctc ctg tgc	54
Met Arg Ile Arg Leu Leu Cys	
1 5	
tgt gtg gcc ttt tct ctc ctg tgg gca ggt cca gtg att gct ggg atc	102
Cys Val Ala Phe Ser Leu Leu Trp Ala Gly Pro Val Ile Ala Gly Ile	
10 15 20	
acc cag gca cca aca tct cag atc ctg gca gca gga cgg cgc atg aca	150
Thr Gln Ala Pro Thr Ser Gln Ile Leu Ala Ala Gly Arg Arg Met Thr	
25 30 35	
ctg aga tgt acc cag gat atg aga cat aat gcc atg tac tgg tat aga	198
Leu Arg Cys Thr Gln Asp Met Arg His Asn Ala Met Tyr Trp Tyr Arg	
40 45 50 55	
caa gat cta gga ctg ggg cta agg ctc atc cat tat tca aat act gca	246
Gln Asp Leu Gly Leu Gly Leu Arg Leu Ile His Tyr Ser Asn Thr Ala	
60 65 70	

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ggt acc act ggc aaa gga gaa gtc cct gat ggt tat agt gtc tcc aga      294
Gly Thr Thr Gly Lys Gly Glu Val Pro Asp Gly Tyr Ser Val Ser Arg
      75                      80                      85

gca aac aca gat gat ttc ccc ctc acg ttg gcg tct gct gta ccc tct      342
Ala Asn Thr Asp Asp Phe Pro Leu Thr Leu Ala Ser Ala Val Pro Ser
      90                      95                      100

cag aca tct gtg tac ttc tgt gcc agc agt gac ggg gct agc ggg agt      390
Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly Ala Ser Gly Ser
      105                      110                      115

ccc cac acc ggg gag ctg ttt ttt gga gaa ggc tct agg ctg acc gta      438
Pro His Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val
      120                      125                      130                      135

ctg gag gac ctg aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag      486
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
      140                      145                      150

cca tca gaa gca gag atc tcc cac acc caa aag gcc aca ctg gtg tgc      534
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
      155                      160                      165

ctg gcc aca ggc ttc tac ccc gac cac gtg gag ctg agc tga ttttttc      583
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser *
      170                      175                      180

atagactatg agcttctaaa aaatcatccc catattcgtc attacattct tgggatcaaa      643

tatactgcat gaaaaaagat gctcagaaaa gtctatgtta agttaatgta gaatatatga      703

atgagtgaag gaaagtgttt tgaaaccatc ataggaata taataagata anattacact      763

agaataaaat gaaac                                                    778

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<210> 177  
 <211> 708  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (176)..(493)

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<400> 177
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caggcgctct ggggcatgag cagggaatac taaccagcc ctgggggctc aatctctccc      120

cacccttgca ggagaggctt ggggtgagtt ttgggaataa ggaccatcca gccac atg      178
Met
1

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acg aag ggg aag gaa aat ccc cat caa ggc aaa aac aca gtc caa ggc 226
Thr Lys Gly Lys Glu Asn Pro His Gln Gly Lys Asn Thr Val Gln Gly
      5              10              15

tct gag gcc caa att ccg ggg aga ggg gtg aag gtt gtt tgt cgc acc 274
Ser Glu Ala Gln Ile Pro Gly Arg Gly Val Lys Val Val Cys Arg Thr
      20              25              30

tgg gtt aaa ggg tgg ggg tgg aga gta gga gaa gag gct aca cag gtg 322
Trp Val Lys Gly Trp Gly Trp Arg Val Gly Glu Glu Ala Thr Gln Val
      35              40              45

aga agg tgt cag atc aca aag ggc ctt gta tgc caa act aag aag act 370
Arg Arg Cys Gln Ile Thr Lys Gly Leu Val Cys Gln Thr Lys Lys Thr
      50              55              60              65

gaa ctt gac cat gaa gtt agg cag acc ctc tgg aga gtt tta aag caa 418
Glu Leu Asp His Glu Val Arg Gln Thr Leu Trp Arg Val Leu Lys Gln
      70              75              80

gga gtc gtg tgg atg aac aaa cct gtg atg ggc tgg ggt tac caa gga 466
Gly Val Val Trp Met Asn Lys Pro Val Met Gly Trp Gly Tyr Gln Gly
      85              90              95

ggg ctt cct gga gga ggt cag act tga gctga gggaaggata ggatttggag 518
Gly Leu Pro Gly Gly Gly Gln Thr *
      100              105

agctgacatt ctgatgagcg gcttcggtta aagctcacia aaacccttcc ctcccccatg 578

ccctttgaaa tcatttgaat caaagattgc gtgtgttaaa gacatgtttg tctgttatct 638

gaaagctgtg gtttctcttt aacagattca gggcctcatc ctttgactcg gaccaagaag 698

gaattatgag 708

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<210> 178  
 <211> 1463  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (120)..(1175)

<220>  
 <221> misc\_feature  
 <222> (1)...(1463)  
 <223> n = a,t,c or g

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<400> 178
tttcgtgcaa agaaaactgt gagagagaga atttttaaaa agcagctggg gcctgaggtt 60

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tctccccag	taccctgggt	cacctcagcc	cagagctggc	ggcaggccccc	cagcccctc		119
atg tca gag ccc cct gtg tac tgt aac ctg gtg gac ctt cgc cgc tgt							167
Met Ser Glu Pro Pro Val Tyr Cys Asn Leu Val Asp Leu Arg Arg Cys							
1	5					10	15
cct cgg tcc cca ccc cca ggc cct gca tgc ccc ctg ctg cag agg ctg							215
Pro Arg Ser Pro Pro Pro Gly Pro Ala Cys Pro Leu Leu Gln Arg Leu							
	20					25	30
gat gcc tgg gag cag cac ctg gac ccc aac tct gga cgc tgc ttc tac							263
Asp Ala Trp Glu Gln His Leu Asp Pro Asn Ser Gly Arg Cys Phe Tyr							
	35					40	45
ata aat tca ctg act ggc tgc aag tcc tgg aag ccc ccg cgc cgc agt							311
Ile Asn Ser Leu Thr Gly Cys Lys Ser Trp Lys Pro Pro Arg Arg Ser							
	50					55	60
cgc agc gag acg aac cct ggc tcc atg gag ggg aca cag acc ctg aag							359
Arg Ser Glu Thr Asn Pro Gly Ser Met Glu Gly Thr Gln Thr Leu Lys							
65					70		75
agg aac aat gat gtc ctg caa cct cag gca aag ggc ttc aga tct gac							407
Arg Asn Asn Asp Val Leu Gln Pro Gln Ala Lys Gly Phe Arg Ser Asp							
	85					90	95
aca ggg acc cca gaa ccg ctt gac cca cag ggt tca ctc agc ctc agc							455
Thr Gly Thr Pro Glu Pro Leu Asp Pro Gln Gly Ser Leu Ser Leu Ser							
	100					105	110
caa cgc acc tcg cag ctt gac cct cca gcc ttg cag gcc cct cga cct							503
Gln Arg Thr Ser Gln Leu Asp Pro Pro Ala Leu Gln Ala Pro Arg Pro							
	115					120	125
ctg ccg cag ctc ctg gac gac ccc cat gag gtg gaa aag tcg ggt ctg							551
Leu Pro Gln Leu Leu Asp Asp Pro His Glu Val Glu Lys Ser Gly Leu							
	130					135	140
ctc aac atg acc aag att gcc caa ggg ggg cgc aag ctc agg aag aac							599
Leu Asn Met Thr Lys Ile Ala Gln Gly Gly Arg Lys Leu Arg Lys Asn							
145					150		155
tgg ggc ccg tct tgg gtg gtg tta acg ggt aac agc ctg gtg ttc tac							647
Trp Gly Pro Ser Trp Val Val Leu Thr Gly Asn Ser Leu Val Phe Tyr							
	165					170	175
cga gag cca ccg ccg aca gcg ccc tcc tca ggc tgg gga cca gcg ggt							695
Arg Glu Pro Pro Pro Thr Ala Pro Ser Ser Ser Gly Trp Gly Pro Ala Gly							
	180					185	190
agc cgg ccc gaa agt agc gtg gac ctg cgc ggg gcg gcc ctg gcg cac							743
Ser Arg Pro Glu Ser Ser Val Asp Leu Arg Gly Ala Ala Leu Ala His							
	195					200	205
ggc cgc cac ctg tcc agc cgc cgc aac gtc ctg cac atc cgc acg atc							791
Gly Arg His Leu Ser Ser Arg Arg Asn Val Leu His Ile Arg Thr Ile							
	210					215	220



caagtcgcgaa aagggtact agtgttctag gtgtctttcc agaaagatta tgcgcataata 120

a atg tgc aca ctt gca tgt gtg cac aca cat aca cac act ctc ata 166  
Met Cys Thr Leu Ala Cys Val His Thr His Thr His Thr Leu Ile  
1 5 10 15

tac cta aaa tac gaa tgg gag cac atg aca cac aca ttc tgc ctg ctg 214  
Tyr Leu Lys Tyr Glu Trp Glu His Met Thr His Thr Phe Cys Leu Leu  
20 25 30

ctt tgt ctg tgc ata att tta tct tcc agg tca tct gtg ctg gtg tct 262  
Leu Cys Leu Cys Ile Ile Leu Ser Ser Arg Ser Ser Val Leu Val Ser  
35 40 45

atc agt ctg cta gtc ttt ccc cgc cat gtg gcc att gtt cca gtc ccc 310  
Ile Ser Leu Leu Val Phe Pro Arg His Val Ala Ile Val Pro Val Pro  
50 55 60

tcc tat gca cac cca ggt ttc tct agg acc atg tta tcc cag agc cag 358  
Ser Tyr Ala His Pro Gly Phe Ser Arg Thr Met Leu Ser Gln Ser Gln  
65 70 75

gtg gac agg aca caa agg gct agg ggt caa tgg ggg tgt tct cgc ctc 406  
Val Asp Arg Thr Gln Arg Ala Arg Gly Gln Trp Gly Cys Ser Arg Leu  
80 85 90 95

cag tct gcc ctg cca gcc ccc agt cgt ggg tgg acc tgc cat cag ctt 454  
Gln Ser Ala Leu Pro Ala Pro Ser Arg Gly Trp Thr Cys His Gln Leu  
100 105 110

gct ctg ccc act ccc cag gcc tga gctgctggcg aaacaggcaa gtgactgcac 508  
Ala Leu Pro Thr Pro Gln Ala \*

115

tgcccatggc cggtcaccag cctcaggtga acccaggag gggttcctac ctagcactca 568

tcatttcttc aacttcacta ctgtgtcgcc ctgtgggaca gggaagtcca agtcggggaa 628

aaagcctgtg gggaggggtt ggtgggagat ggggagccca tatggcccag 678

<210> 180  
<211> 599  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (189)..(512)

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cctttccaaa tttgtaattc tctgactata agaaatctgg ctctgtctct ttccctgtctg 120





ccg gcc atc aag gcc ctg atg cgg cca gac ccg cgc ctc aag tgg gcg Pro Ala Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala 35 40 45	205
gtg ctg gtg ctg gtg ctg gtg cag atg ctg gcc tgc tgg ctg gtg cgc Val Leu Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg 50 55 60	253
ggg ctg gcc tgg cgc tgg ctg ctg ttc tgg gcc tac gcc ttt ggt ggc Gly Leu Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly 65 70 75	301
tgc gtg aac cac tcg ctg acg ctg gcc atc cac gac atc tcg cac aac Cys Val Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn 80 85 90	349
gcg gcc ttc ggc acg ggc cgt gcg gca cgc aac cgc tgg ctg gcc gtg Ala Ala Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val 95 100 105 110	397
ttc gcc aac ctg ccc gtg ggt gtg ccc tac gcc gcc tcc ttc aag aag Phe Ala Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys 115 120 125	445
tac cac gtg gac cac cac cgc tac ctg ggc ggc gac ggg ctg gac gtg Tyr His Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val 130 135 140	493
gac gtg ccc acg cgt ctg gag ggc tgg ttc ttc tgc acg ccc gcc cgc Asp Val Pro Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg 145 150 155	541
aag ctg ctc tgg ctg gtg ctg cag ccc ttc ttc tac tca cta cgg ccg Lys Leu Leu Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro 160 165 170	589
ctc tgc gtc cac ccc aag gcc gtg acc cgc atg gag gtg ctc aac acg Leu Cys Val His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr 175 180 185 190	637
ctg gtg cag ctg gcg gcc gac ctg gcc atc ttt gcc ctt tgg ggg ctc Leu Val Gln Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu 195 200 205	685
aag ccc gtg gtc tac ctg ctg gcc agc tcc ttc ctg ggc ctg ggc ctg Lys Pro Val Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu 210 215 220	733
cac ccc atc tcg ggc cac ttc gtg gcc gag cac tac atg ttc ctc aag His Pro Ile Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys 225 230 235	781
ggc cac gag acc tac tcc tac tat ggg cct ctc aac tgg atc acc ttc Gly His Glu Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe 240 245 250	829
aat gtg ggc tac cac gtg gag cac cac gac ttc ccc agc atc ccg ggc	877

Asn Val Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly	
255 260 265 270	
tac aac ctg ccg ctg gtg cgg aag atc gcg ccc gag tac tac gac cac	925
Tyr Asn Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His	
275 280 285	
ctg ccg cag cac cac tcc tgg gtg aag gtg ctc tgg gat ttt gtg ttt	973
Leu Pro Gln His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe	
290 295 300	
gag gac tcc ctg ggg ccc tat gcc agg gtg aag cgg gtg tac agg ctg	1021
Glu Asp Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu	
305 310 315	
gca aaa gat ggt ctg tga gcccgg gctgcctcct ggtggtggcc attgtcccc	1075
Ala Lys Asp Gly Leu *	
320	
atcgccccct cagccttgca cccagcact gagaagctac atttccttcc tgtgctctgg	1135
actgctgccc ttgtccccga ggagtgtccc gcgcagccac acctggcaac agcagtgtgg	1195
gctgcagggc tccgtctgca cgtggacttg ccctggacct tgagtgtggc cctccctttc	1255
tgggcctccc caggtgagggc ctggccctgc cccaccatga cctgggtgct ctgagcccac	1315
ggttcccaag gagctgactt ctccgggggtg cctgtgcctt acattaaacc cggcgtttgt	1375
ttcacagcca aaaaaaaaaa a	1396

<210> 182  
 <211> 2728  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (22)..(2688)

<400> 182	
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gag ctg tgg acc ttc gcg ggt tcc cgg gac ccg agc gca ccg cgg cta	99
Glu Leu Trp Thr Phe Ala Gly Ser Arg Asp Pro Ser Ala Pro Arg Leu	
15 20 25	
gcc tac ggc tac ggc ccg ggc agc ctg cgc gag ctg cgg gcg cgc gag	147
Ala Tyr Gly Tyr Gly Pro Gly Ser Leu Arg Glu Leu Arg Ala Arg Glu	
30 35 40	
ttc agc cgc ctg gca gga act gtc tat ctt gac cat gca ggt gcc acc	195

Phe	Ser	Arg	Leu	Ala	Gly	Thr	Val	Tyr	Leu	Asp	His	Ala	Gly	Ala	Thr		
		45					50					55					
ttg	ttc	tcc	cag	agc	cag	ctc	gaa	agc	ttc	act	agt	gat	ctc	atg	gaa	243	
Leu	Phe	Ser	Gln	Ser	Gln	Leu	Glu	Ser	Phe	Thr	Ser	Asp	Leu	Met	Glu		
	60					65				70							
aac	act	tat	ggg	aat	cct	cac	agc	cag	aac	atc	agc	agc	aag	ctc	acc	291	
Asn	Thr	Tyr	Gly	Asn	Pro	His	Ser	Gln	Asn	Ile	Ser	Ser	Lys	Leu	Thr		
	75				80				85					90			
cat	gac	act	gtg	gag	cag	gtg	cgc	tac	aga	atc	ctg	gcg	cac	ttc	cac	339	
His	Asp	Thr	Val	Glu	Gln	Val	Arg	Tyr	Arg	Ile	Leu	Ala	His	Phe	His		
			95					100						105			
acc	acc	gca	gaa	gac	tac	act	gtg	atc	ttc	act	gcc	ggg	agc	acg	gct	387	
Thr	Thr	Ala	Glu	Asp	Tyr	Thr	Val	Ile	Phe	Thr	Ala	Gly	Ser	Thr	Ala		
		110					115					120					
gct	ctc	aaa	ctg	gtg	gca	gag	gcc	ttt	cca	tgg	gtg	tcc	cag	ggc	cca	435	
Ala	Leu	Lys	Leu	Val	Ala	Glu	Ala	Phe	Pro	Trp	Val	Ser	Gln	Gly	Pro		
	125					130					135						
gag	agc	agt	ggg	agt	cgc	ttc	tgt	tac	ctc	acc	gac	agc	cac	acc	tcc	483	
Glu	Ser	Ser	Gly	Ser	Arg	Phe	Cys	Tyr	Leu	Thr	Asp	Ser	His	Thr	Ser		
	140					145				150							
gta	gtg	ggg	atg	agg	aac	gtg	acc	atg	gct	ata	aat	gtc	ata	tcc	atc	531	
Val	Val	Gly	Met	Arg	Asn	Val	Thr	Met	Ala	Ile	Asn	Val	Ile	Ser	Ile		
	155				160				165					170			
ccg	gtc	agg	cca	gag	gac	ctg	tgg	tct	gca	gag	gaa	cgt	ggg	gct	tca	579	
Pro	Val	Arg	Pro	Glu	Asp	Leu	Trp	Ser	Ala	Glu	Glu	Arg	Gly	Ala	Ser		
			175					180						185			
gcc	agc	aac	cca	gac	tgc	cag	ctg	ccg	cat	ctc	ttc	tgc	tac	cca	gct	627	
Ala	Ser	Asn	Pro	Asp	Cys	Gln	Leu	Pro	His	Leu	Phe	Cys	Tyr	Pro	Ala		
		190						195					200				
cag	agt	aac	ttt	tct	gga	gtc	aga	tac	ccc	ctg	tcc	tgg	ata	gaa	gag	675	
Gln	Ser	Asn	Phe	Ser	Gly	Val	Arg	Tyr	Pro	Leu	Ser	Trp	Ile	Glu	Glu		
	205					210						215					
gtc	aag	tct	ggg	cgg	ttg	cgc	cct	gtg	agc	acg	cct	ggg	aag	tgg	ttt	723	
Val	Lys	Ser	Gly	Arg	Leu	Arg	Pro	Val	Ser	Thr	Pro	Gly	Lys	Trp	Phe		
	220					225					230						
gtg	ctg	ctg	gat	gca	gcc	tcc	tac	gtg	agc	acc	tgc	cct	ttg	gac	ctg	771	
Val	Leu	Leu	Asp	Ala	Ala	Ser	Tyr	Val	Ser	Thr	Ser	Pro	Leu	Asp	Leu		
	235				240					245				250			
tca	gct	cac	cag	gcc	gac	ttt	gtc	ccc	atc	tcc	ttc	tat	aag	atc	ttc	819	
Ser	Ala	His	Gln	Ala	Asp	Phe	Val	Pro	Ile	Ser	Phe	Tyr	Lys	Ile	Phe		
			255					260					265				
ggg	ttt	cct	aca	ggc	ctg	ggc	gct	ctg	ctg	gtc	cat	aat	cgt	gcg	gct	867	
Gly	Phe	Pro	Thr	Gly	Leu	Gly	Ala	Leu	Leu	Val	His	Asn	Arg	Ala	Ala		



gag act gga gcc cca tca gca gac agc cag gct gat gtt ata cct gct	1587
Glu Thr Gly Ala Pro Ser Ala Asp Ser Gln Ala Asp Val Ile Pro Ala	
510 515 520	
gtc atg ggc aga cgt agc ctc tcg cct cag gaa gat gcc ctc aca ggc	1635
Val Met Gly Arg Arg Ser Leu Ser Pro Gln Glu Asp Ala Leu Thr Gly	
525 530 535	
tcc agg gtt tgg aac aac tcg tct act gtg aat gct gtg cct gtg gcc	1683
Ser Arg Val Trp Asn Asn Ser Ser Thr Val Asn Ala Val Pro Val Ala	
540 545 550	
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Pro Pro Val Cys Asp Val Ala Arg Thr Gln Pro Thr Pro Ser Glu Lys	
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gct gca gga gtc ctg gag ggg gcc ctt ggg cca cat gtt gtc act aac	1779
Ala Ala Gly Val Leu Glu Gly Ala Leu Gly Pro His Val Val Thr Asn	
575 580 585	
ctt tat ctc tat cca atc aaa tcc tgt gct gca ttt gag gtg acc agg	1827
Leu Tyr Leu Tyr Pro Ile Lys Ser Cys Ala Ala Phe Glu Val Thr Arg	
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Trp Pro Val Gly Asn Gln Gly Leu Leu Tyr Asp Arg Ser Trp Met Val	
605 610 615	
gtg aat cac aat ggt gtt tgc ctg agt cag aag cag gaa ccc cgg ctc	1923
Val Asn His Asn Gly Val Cys Leu Ser Gln Lys Gln Glu Pro Arg Leu	
620 625 630	
tgc ctg atc cag ccc ttc atc gac ttg cgg caa agg atc atg gtc atc	1971
Cys Leu Ile Gln Pro Phe Ile Asp Leu Arg Gln Arg Ile Met Val Ile	
635 640 645 650	
aaa gcc aaa ggg atg gag cct ata gag gtg cct ctt gag gaa aat agt	2019
Lys Ala Lys Gly Met Glu Pro Ile Glu Val Pro Leu Glu Glu Asn Ser	
655 660 665	
gaa cgg act cag att cgc caa agc agg gtc tgt gct gac aga gta agt	2067
Glu Arg Thr Gln Ile Arg Gln Ser Arg Val Cys Ala Asp Arg Val Ser	
670 675 680	
act tat gat tgt gga gaa aaa att tca agc tgg ttg tca aca ttt ttt	2115
Thr Tyr Asp Cys Gly Glu Lys Ile Ser Ser Trp Leu Ser Thr Phe Phe	
685 690 695	
ggc cgt cct tgt aat ttg atc aaa caa agt tca aac tct caa agg aat	2163
Gly Arg Pro Cys Asn Leu Ile Lys Gln Ser Ser Asn Ser Gln Arg Asn	
700 705 710	
gca aag aag aaa cat gga aaa gat caa ctt cct ggt aca atg gcc acc	2211
Ala Lys Lys Lys His Gly Lys Asp Gln Leu Pro Gly Thr Met Ala Thr	
715 720 725 730	

ctt tct ctg gtg aat gag gca cag tat ctg ctg atc aac aca tcc agt	2259
Leu Ser Leu Val Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser	
735 740 745	
att ttg gaa ctt cac cgg caa cta aac acc agt gat gag aat gga aag	2307
Ile Leu Glu Leu His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys	
750 755 760	
gag gaa tta ttc tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat	2355
Glu Glu Leu Phe Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn	
765 770 775	
att att atc aat gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag	2403
Ile Ile Ile Asn Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu	
780 785 790	
att tca att ggc tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga	2451
Ile Ser Ile Gly Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg	
795 800 805 810	
tgc cag atg att tgc atc gac cag caa act ggg caa cga aac cag cat	2499
Cys Gln Met Ile Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His	
815 820 825	
gtt ttc caa aaa ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc	2547
Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly	
830 835 840	
atg tac ctg atg cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg	2595
Met Tyr Leu Met His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu	
845 850 855	
tct gta gga tct cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt	2643
Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly	
860 865 870	
cat gat tta cct gca tct gag aaa cac cag gat gtt acc tcc taa aaa	2691
His Asp Leu Pro Ala Ser Glu Lys His Gln Asp Val Thr Ser *	
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ctgtgaggtg tgcgaagccc cagccgagcg ggtgtgcgcg gcctgcacag tcacttatta 180  
ctggtctggg ccgaatcggt caggctgaag aatatctatt ccaagcccag tggacagtcc 240  
tcaaataaac tgactgtagt aatgccaccc actctttact gcacgcgaat ctgggacttc 300  
tctatatagc taagaaaaac tatgaagagg cccgttatca tctggccaat gatatttatt 360  
ttgccagttg tgcatttgga acagaggaca ttaggacttc aggaggctac ttccacctgg 420  
ctaatatatt ctatgacctt aaaaagttgg acctggcaga cacattgtac accaaggtct 480  
ctgagatctg gcacgcatat ttgaacaatc actatcaagt cctctcacag gctcacatcc 540  
aaciaa atg gat tta ctg ggc aaa cta ttt gag aat gac act ggc ttg 587  
Met Asp Leu Leu Gly Lys Leu Phe Glu Asn Asp Thr Gly Leu  
1 5 10  
gat gaa gcc caa gaa gca gaa gcc att cgc atc ctg act tca atc ttg 635  
Asp Glu Ala Gln Glu Ala Glu Ala Ile Arg Ile Leu Thr Ser Ile Leu  
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aac att cga gaa tct aca tct gac aaa gcc ccc caa aaa acc atc ttt 683  
Asn Ile Arg Glu Ser Thr Ser Asp Lys Ala Pro Gln Lys Thr Ile Phe  
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gtt ctg aag atc ctg gtc atg ctt tac tac ctg atg atg aat tct tca 731  
Val Leu Lys Ile Leu Val Met Leu Tyr Tyr Leu Met Met Asn Ser Ser  
50 55 60  
aag gca cag gaa tat ggc atg agg gcc ctc agt cta gcc aaa gaa caa 779  
Lys Ala Gln Glu Tyr Gly Met Arg Ala Leu Ser Leu Ala Lys Glu Gln  
65 70 75  
cag ctt gat gtc cat gag caa agc acc att caa gag tta tta agt ctc 827  
Gln Leu Asp Val His Glu Gln Ser Thr Ile Gln Glu Leu Leu Ser Leu  
80 85 90  
att tca act gaa gac cat ccc att act tag t gacccatgag ctctgcatca 878  
Ile Ser Thr Glu Asp His Pro Ile Thr \*  
95 100  
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gggtactgtag actgctgaag tttccaccct cttcccctgg gattgcacac atagctgtta 998  
tttttttctt acacagcata ttaagggaat ataaagcttt aggcatagaa atcactaaaa 1058  
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gtagtcagat cactaatatg gtatttgtaa ttaaaactaca aatagtttgt catttcccag 1178  
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aggaataaaa gctatatattg aacaaaaa 1265

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cccagtgaga gcggctttcc aggacggtgc gatgtgctgc gcagcgaaga ggcaggaggc      180
cggtttcctg gggtagcggg acaggcgggc gcttactctg tgcgcttgct tccccaaccc      240
tgcaccggcc  atg cgc ccg gcc ttg gcg gtg ggc ctg gtg ttc gca ggc      289
              Met Arg Pro Ala Leu Ala Val Gly Leu Val Phe Ala Gly
              1              5              10

tgc tgc agt aac gtg atc ttc cta gag ctc ctg gcc cgg aag cat cca      337
Cys Cys Ser Asn Val Ile Phe Leu Glu Leu Leu Ala Arg Lys His Pro
              15              20              25

gga tgt ggg aac att gtg aca ttt gca caa ttt tta ttt att gct gtg      385
Gly Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val
              30              35              40              45

gaa ggc ttc ctc ttt gaa gct gat ttg gga agg aag cca cca gct atc      433
Glu Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile
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cca ata agg tac tat gcc ata atg gtg acc atg ttc ttc acc gtg agc      481
Pro Ile Arg Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser
              65              70              75

gtg gtg aac aac tat gcc ctg aat ctc aac att gcc atg ccc ctg cat      529
Val Val Asn Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His
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atg ata ttt aga tcc ggt tct cta att gcc aac acg att cta gga att      577
Met Ile Phe Arg Ser Gly Ser Leu Ile Ala Asn Thr Ile Leu Gly Ile
              95              100              105

atc att ttg aag aaa aga tac agt ata ttc aaa tat acc tcc att gcc      625
Ile Ile Leu Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala
              110              115              120              125

ctg gtg tct gtg ggg ata ttt att tgc act ttt atg tca gca aag cag      673
Leu Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln
              130              135              140

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Val Thr Ser Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe	
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gtg tgg tgg tta cta ggt att ggg gca ttg act ttt gct ctt ctg atg	769
Val Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met	
160 165 170	
tca gca agg atg ggg ata ttc caa gag act ctc tac aaa cga ttt ggg	817
Ser Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly	
175 180 185	
aaa cac tcc aag gag gct ttg ttt tat aat cac gcc ctt cca ctt ccg	865
Lys His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro	
190 195 200 205	
ggt ttc gtc ttc ttg gct tct gat att tat gac cat gca gtt cta ttc	913
Gly Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe	
210 215 220	
aat aag tct gag tta tat gaa att ccc gtc atc gga gtg acc ctg ccc	961
Asn Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro	
225 230 235	
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Ile Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys	
240 245 250	
atc cgg ggt gtg ttt atc ctc acc aca gaa tgc gcc tcc ctc acc gtc	1057
Ile Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val	
255 260 265	
acg ctc gtc gtg acc cta cgc aaa ttt gtg agc ctc atc ttt tcc atc	1105
Thr Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile	
270 275 280 285	
ttg tac ttc cag aac ccc ttc acc ctg tgg cac tgg ctg ggc acc ttg	1153
Leu Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu	
290 295 300	
ttt gtc ttc att ggg acc tta atg tac aca gag gtg tgg aac aac cta	1201
Phe Val Phe Ile Gly Thr Leu Met Tyr Thr Glu Val Trp Asn Asn Leu	
305 310 315	
ggg acc aca aaa agt gag cct cag aag gac agc aag aag aac tga ggc	1249
Gly Thr Thr Lys Ser Glu Pro Gln Lys Asp Ser Lys Lys Asn *	
320 325 330	
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aggaagaaga cgcagaagca ggacgaccct gaaagattca gcctcttcat cctcaaacag    180
gtcgcttctc gggagttctt ggtgttgaa tattttacag caaagcagtc gaccaggcct    240
cctcttccca cctgtccagc agcatgaaag cagcatgatt ggccgaccgc aggagaagcc    300
cccagaacca ggcccccaac tcagccatct gcggaggcca aggtgtgagc gacgtctcct    360
caccacagtg ctgtgtggtc tatacctcag ccaggagag gatgtgaaac cccccgcct    420
gcacatgagt ggtacaggcc aacaggaaca cctggctcca gccacgttca cagacatgtc    480
agccgtggag tagtgctgac acttttctct cagcttctca gggtttcagt ccttttggg    540
ttggtttatt tacctttttt atggttttgt ggctggacgt tcacaaccaa ggcagacagc    600
atgggtgacc agcaactgta caagaccaac catgtggccc atggtagtga gaaccttttc    660
taccaacagc caccacttgg cgtccacagc gggctgagcc cactgatggc taccaatata    720
cctactccca ggccagcgag atccggaccc agaagcttac cagcgggtgtc ttacacaagc    780

tggaactcttt caccaggtg tttgccaaac aaaacctgcy aattcagggtc aacaat      836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct      884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
   1             5             10            15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca      932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
           20             25             30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac      980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
           35             40             45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag    1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
           50             55             60

cac cct acc caa ggg cac ctg tat tat gac tac cag cag cct ctg gct    1076
His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
           65             70             75             80

cag gtg cca gtg cag gga gga cag cca ctg cag gcc cca cag atg ctg    1124
Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
           85             90             95
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tca cag cac atg caa cag atg cag cag cac cag tat tac cca ccg cag	1172
Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln	
100 105 110	
caa cag cag caa gcc ggg caa cag cgt atc tcc atg caa gaa ata cag	1220
Gln Gln Gln Gln Ala Gly Gln Gln Arg Ile Ser Met Gln Glu Ile Gln	
115 120 125	
acg cag ccg caa caa att cgc cca tca cag cca cag ccg ccg cca cag	1268
Thr Gln Pro Gln Gln Ile Arg Pro Ser Gln Pro Gln Pro Pro Pro Gln	
130 135 140	
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Gln Gln Gln Pro Gln Gln Leu Gln Leu Gln Gln Arg Gln Gly Ser Met	
145 150 155 160	
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Gln Ile Pro Gln Tyr Tyr Gln Pro Gln Pro Met Met Gln His Leu Gln	
165 170 175	
gag cag cag cag caa cag atg cac ctg cag cct cct tct tat cac agg	1412
Glu Gln Gln Gln Gln Gln Met His Leu Gln Pro Pro Ser Tyr His Arg	
180 185 190	
gac cct cac cag tat acc cca gag cag gca cac act gtc cag ctg att	1460
Asp Pro His Gln Tyr Thr Pro Glu Gln Ala His Thr Val Gln Leu Ile	
195 200 205	
ccc ctg ggc tcc atg tcc cag tac tac tac cag gag ccc cag cag ccc	1508
Pro Leu Gly Ser Met Ser Gln Tyr Tyr Tyr Gln Glu Pro Gln Gln Pro	
210 215 220	
tac agc cac ccc ctc tac cag cag agc cac ctg tcc cag cac cag cag	1556
Tyr Ser His Pro Leu Tyr Gln Gln Ser His Leu Ser Gln His Gln Gln	
225 230 235 240	
cgt gag gac agt cag ctg aag acc tac tct agt gac aga cag gcc cag	1604
Arg Glu Asp Ser Gln Leu Lys Thr Tyr Ser Ser Asp Arg Gln Ala Gln	
245 250 255	
gcc atg ctg agc tcc cat ggg gac ctg ggg cct cct gac aca gga atg	1652
Ala Met Leu Ser Ser His Gly Asp Leu Gly Pro Pro Asp Thr Gly Met	
260 265 270	
gga gac cca gcg agc tca gat ctg acc cgg gtc agc agc acc ctc ccc	1700
Gly Asp Pro Ala Ser Ser Asp Leu Thr Arg Val Ser Ser Thr Leu Pro	
275 280 285	
cat cgc ccc ctc cta tcc ccc agt ggg atc cac ctc aac aac atg ggg	1748
His Arg Pro Leu Leu Ser Pro Ser Gly Ile His Leu Asn Asn Met Gly	
290 295 300	
cct cag cat cag cag ctg tct ccc agt gcc atg tgg ccc cag atg cac	1796
Pro Gln His Gln Gln Leu Ser Pro Ser Ala Met Trp Pro Gln Met His	
305 310 315 320	

cta cct gat ggg aga gcc cag cca ggg tcc cct gag tca agt ggc caa	1844
Leu Pro Asp Gly Arg Ala Gln Pro Gly Ser Pro Glu Ser Ser Gly Gln	
325 330 335	
ccc aaa gga gcg ttt ggg gag cag ttt gat gcc aag aac aag ctg aca	1892
Pro Lys Gly Ala Phe Gly Glu Gln Phe Asp Ala Lys Asn Lys Leu Thr	
340 345 350	
tgc tcc atc tgc ctg aag gag ttc aag aac ctg cct gcc ctg aat ggc	1940
Cys Ser Ile Cys Leu Lys Glu Phe Lys Asn Leu Pro Ala Leu Asn Gly	
355 360 365	
cac atg cgg tcc cac ggg gga atg agg gcc tcc ccc aac ctc aaa cag	1988
His Met Arg Ser His Gly Gly Met Arg Ala Ser Pro Asn Leu Lys Gln	
370 375 380	
gaa atc ccc agg aag cat cag ccg agt gtg ccc aaa gcc gag gag ccc	2036
Glu Ile Pro Arg Lys His Gln Pro Ser Val Pro Lys Ala Glu Glu Pro	
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ctc aag acc gtg cag gag aag aaa aag ttc cgg cac cgg tcg gaa cct	2084
Leu Lys Thr Val Gln Glu Lys Lys Lys Phe Arg His Arg Ser Glu Pro	
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ctc ttc atc ccg ccg ccg ccc tcc tac aac ccg aac ccc gct gcc tcc	2132
Leu Phe Ile Pro Pro Pro Pro Ser Tyr Asn Pro Asn Pro Ala Ala Ser	
420 425 430	
tac tcg ggc gcc acc ctg tac cag agc cag ctg cgc tcc ccg cgc gtc	2180
Tyr Ser Gly Ala Thr Leu Tyr Gln Ser Gln Leu Arg Ser Pro Arg Val	
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Leu Gly Asp His Leu Leu Leu Asp Pro Thr His Glu Leu Pro Pro Tyr	
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acg ccc cca ccc atg ctg agc ccg gtg cgc cag ggc tcg ggg ctc ttc	2276
Thr Pro Pro Pro Met Leu Ser Pro Val Arg Gln Gly Ser Gly Leu Phe	
465 470 475 480	
agc aat gtc ctc atc tcc ggc cac ggc cct ggc gcc cac ccg cag ctg	2324
Ser Asn Val Leu Ile Ser Gly His Gly Pro Gly Ala His Pro Gln Leu	
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Pro Leu Thr Pro Leu Thr Pro Thr Pro Arg Val Leu Leu Cys Arg Ser	
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Asn Ser Ile Asp Gly Ser Asn Val Thr Val Thr Pro Gly Pro Gly Glu	
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Gln Thr Val Asp Val Glu Pro Arg Ile Asn Ile Gly Leu Arg Phe Gln	
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gca gaa atc cct gaa ctc caa gat atc tct gcc ctg gcc cag gac aca	2516

Ala Glu Ile Pro Glu Leu Gln Asp Ile Ser Ala Leu Ala Gln Asp Thr	
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His Lys Ala Thr Leu Val Trp Lys Pro Trp Pro Glu Leu Glu Asn His	
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Asp Leu Gln Gln Arg Val Glu Asn Leu Leu Asn Leu Cys Cys Ser Ser	
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gca ttg cca ggt gga ggg acc aat tct gaa ttt gct ttg cac tct ctg	2660
Ala Leu Pro Gly Gly Gly Thr Asn Ser Glu Phe Ala Leu His Ser Leu	
595 600 605	
ttt gag gcc aaa ggt gat gtg atg gtt gct ctg gaa atg ctg cta ctg	2708
Phe Glu Ala Lys Gly Asp Val Met Val Ala Leu Glu Met Leu Leu Leu	
610 615 620	
cgg aag cct gtc agg tta aaa tgt cat cct tta gca aat tac cac tat	2756
Arg Lys Pro Val Arg Leu Lys Cys His Pro Leu Ala Asn Tyr His Tyr	
625 630 635 640	
gcc ggt tgc gac aag tgg acc tcc cta gaa aga aaa ctg ttt aac aaa	2804
Ala Gly Ser Asp Lys Trp Thr Ser Leu Glu Arg Lys Leu Phe Asn Lys	
645 650 655	
gca cta gcc act tac agc aaa gac ttt att ttt gta cag aag atg gtg	2852
Ala Leu Ala Thr Tyr Ser Lys Asp Phe Ile Phe Val Gln Lys Met Val	
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Lys Ser Lys Thr Val Ala Gln Cys Val Glu Tyr Tyr Tyr Thr Trp Lys	
675 680 685	
aag atc atg cgg ctg ggg cgg aaa cac cgg aca cgc ctg gca gaa atc	2948
Lys Ile Met Arg Leu Gly Arg Lys His Arg Thr Arg Leu Ala Glu Ile	
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Ile Asp Asp Cys Val Thr Ser Glu Glu Glu Glu Glu Leu Glu Glu Glu	
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Glu Glu Glu Asp Pro Glu Glu Asp Arg Lys Ser Thr Lys Glu Glu Glu	
725 730 735	
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Ser Glu Val Pro Lys Ser Pro Glu Pro Pro Pro Val Pro Val Leu Ala	
740 745 750	
ccc acg gag ggg ccg ccc ctg cag gcc ctg ggc cag ccc tca ggc tcc	3140
Pro Thr Glu Gly Pro Pro Leu Gln Ala Leu Gly Gln Pro Ser Gly Ser	
755 760 765	
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Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Asp Cys Arg Cys His Val	

770	775	780	
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Thr Pro Phe Leu Pro Gln Val Phe Ser Ser Arg Gln Ala Leu Asn Gly			
785	790	795	800
cat gcc cgc atc cac ggg ggc acc aac cag gtg acc aag gcc cga ggt			3284
His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr Lys Ala Arg Gly			
	805	810	815
gcc atc ccc tct ggg aag cag aag cct ggt ggc acc cag agt ggg tac			3332
Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr Gln Ser Gly Tyr			
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tgt tcg gta aag agc tca ccc tct cac agc acc acc agc ggc gag aca			3380
Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr Ser Gly Glu Thr			
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gac ccc acc acc atc ttc ccc tgc aag gag tgt ggc aaa gtc ttc ttc			3428
Asp Pro Thr Thr Ile Phe Pro Cys Lys Glu Cys Gly Lys Val Phe Phe			
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aag atc aaa agc cga aat gca cac atg aaa act cac atg cag cag gag			3476
Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His Met Gln Gln Glu			
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gaa caa cag agg caa aag gct cag aag gcg gct ttt gca gct gag atg			3524
Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe Ala Ala Glu Met			
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gca gcc acg att gag agg act acg ggg ccc gtg ggg gcg ccg ggg ctg			3572
Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly Ala Pro Gly Leu			
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ctg ccc ctg gac cag ctg agt ctg atc aaa ccc atc aag gat gtg gac			3620
Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile Lys Asp Val Asp			
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atc ctc gac gac gac gtc gtc cag cag ttg gga ggt gtc atg gaa gag			3668
Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly Val Met Glu Glu			
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gct gaa gtt gtg gac acc gat ctt ctc ttg gat gat caa gat tca gtc			3716
Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp Gln Asp Ser Val			
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Leu Leu Gln Gly Asp Ala Glu Leu *			
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tggactcttt caccaggtg tttgccaacc aaaacctgcg aattcagggtc aacaat      836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct      884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
  1             5             10            15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca      932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
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gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac      980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
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Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
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Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu	
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Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln	
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Thr Gln Pro Gln Gln Ile Arg Pro Ser Gln Pro Gln Pro Pro Pro Gln	
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Gln Gln Gln Pro Gln Gln Leu Gln Leu Gln Gln Arg Gln Gly Ser Met	
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Gln Ile Pro Gln Tyr Tyr Gln Pro Gln Pro Met Met Gln His Leu Gln	
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Glu Gln Gln Gln Gln Gln Met His Leu Gln Pro Pro Ser Tyr His Arg	
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Tyr Ser His Pro Leu Tyr Gln Gln Ser His Leu Ser Gln His Gln Gln	
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Arg Glu Asp Ser Gln Leu Lys Thr Tyr Ser Ser Asp Arg Gln Ala Gln	
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Gly Asp Pro Ala Ser Ser Asp Leu Thr Arg Val Ser Ser Thr Leu Pro	
275 280 285	
cat cgc ccc ctc cta tcc ccc agt ggg atc cac ctc aac aac atg ggg	1748



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Pro	Gln	His	Gln	Gln	Leu	Ser	Pro	Ser	Ala	Met	Trp	Pro	Gln	Met	His	
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Leu	Pro	Asp	Gly	Arg	Ala	Gln	Pro	Gly	Ser	Pro	Glu	Ser	Ser	Gly	Gln	
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Pro	Lys	Gly	Ala	Phe	Gly	Glu	Gln	Phe	Asp	Ala	Lys	Asn	Lys	Leu	Thr	
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Cys	Ser	Ile	Cys	Leu	Lys	Glu	Phe	Lys	Asn	Leu	Pro	Ala	Leu	Asn	Gly	
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Glu	Ile	Pro	Arg	Lys	His	Gln	Pro	Ser	Val	Pro	Lys	Ala	Glu	Glu	Pro	
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Leu	Lys	Thr	Val	Gln	Glu	Lys	Lys	Lys	Phe	Arg	His	Arg	Ser	Glu	Pro	
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Leu	Phe	Ile	Pro	Pro	Pro	Pro	Ser	Tyr	Asn	Pro	Asn	Pro	Ala	Ala	Ser	
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Tyr	Ser	Gly	Ala	Thr	Leu	Tyr	Gln	Ser	Gln	Leu	Arg	Ser	Pro	Arg	Val	
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Leu	Gly	Asp	His	Leu	Leu	Leu	Asp	Pro	Thr	His	Glu	Leu	Pro	Pro	Tyr	
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Thr	Pro	Pro	Pro	Met	Leu	Ser	Pro	Val	Arg	Gln	Gly	Ser	Gly	Leu	Phe	
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Pro	Leu	Thr	Pro	Leu	Thr	Pro	Thr	Pro	Arg	Val	Leu	Leu	Cys	Arg	Ser	
			500					505					510			
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Asn	Ser	Ile	Asp	Gly	Ser	Asn	Val	Thr	Val	Thr	Pro	Gly	Pro	Gly	Glu	

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Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Val Phe Ser Ser Arg Gln	
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Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys Gly Lys Tyr Asn Ala	65	70	75	
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Met Val Leu Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asp Leu	80	85	90	
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Cys Asp Arg Thr Phe Thr Leu Lys Thr Val Leu Met Ile Ala Ile Gln	95	100	105	110
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Leu Leu Ser Arg Met Glu Tyr Val His Ser Lys Asn Leu Ile Tyr Arg	115	120	125	
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Asp Val Lys Pro Glu Asn Phe Leu Ile Gly Arg Gln Gly Asn Lys Lys	130	135	140	
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Asp Pro Glu Thr Lys Lys His Ile Pro Tyr Arg Glu His Lys Ser Leu	160	165	170	
act gga act gca aga tat atg tct atc aac acg cat ctt ggc aaa gag				936
Thr Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr His Leu Gly Lys Glu	175	180	185	190
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Gln Ser Arg Arg Asp Asp Leu Glu Ala Leu Gly His Met Phe Met Tyr	195	200	205	
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Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Asp Thr Leu	210	215	220	
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Lys Glu Arg Tyr Gln Lys Ile Gly Asp Thr Lys Arg Asn Thr Pro Ile	225	230	235	
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275 280 285	
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Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro Val Gly Ser	
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Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr	
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His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn Gln Val Val	
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Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val Val Glu Glu	
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Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys Thr Ala Gln	
370 375 380	
cgc cac aag tga cca gtgcctccca ggagtcctca ggccctgggg actctgactc	1567
Arg His Lys *	
385	
aattgtacct gcagctcctg ccattttctca ttggaaggga ctctcttttg ggggaggggtg	1627
gatatccaaa ctaaaaagaa gaaaacagat gccccagaa ggggccagtg cgggcagcca	1687
gggcctagtg ggtcattggc catctccgcc tgcctaaggc tctgagcagg tcccagagct	1747
gctgttcttc cactgcttgc ccatagggct gcttggttga ctctccttcc cattgtttac	1807
agtgaagggtg tcattcacia aaactcaagg actgctattc tccttcttcc ccttagttta	1867
ctcctgggtt ttaccccacc ctcaaccctc tccagcataa aacctagtg gctaaaggct	1927
ttgtctgcag aaggagatca agaggctggg ggtaaggcca agaaggtagg aggaaaatgg	1987
cagacctggg ctggagaaga accttctccg tatcccaggt gtgcctggca gtatggtttc	2047
ctcttctct gtgcctgtgc agcattcatc ccagctggcc ttggggttca ggttcttct	2107
tccctccctc ctgtgaagtt aactgtagg acacaagctg tgagcaatct gcagtctact	2167

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gtccctgtgt gttggcggttc ttagcttttt tgacaaactc ttttctccag gtagtaggac 2227
aatgaaaatt gttttaagca aaggaaagaa aactgacttt gttgcacttt tagttttttt 2287
aaaaaaaaa aaaacaaaaa catgaaaaaa a 2318

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<210> 188
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (505)..(1119)

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cctggctgtg gtggcctgtg gcaatcggct ggaggagacg ctggatcatgc tcaaatacgc 180
tgtgcttttt agccacagga agatccaatt ccacatcttc actgaagact ctctgaagcc 240
cgagtttgat aagcagttac gccatggcct gactcatata caaagaagtt tgagcacaga 300
atctacccca tcacattttc tgttggaac cctcaggagt ggaagaaatt gttcaaacc 360
tgtgctgccc agagactctt tcttccggtg attttaaagg atgtggactc acttctctac 420
gtggacaccg atgtcctctt tctgagacct gttgatgaca tctggaagct tctgaggctg 480
ttaattcca ccagcttgc agcc atg gcc cct gag cac gaa atc ccc aag 531
Met Ala Pro Glu His Glu Ile Pro Lys
1 5
att ggc tgg tac agc cgc ttt gct agg cat cct ttc tat ggc tct gca 579
Ile Gly Trp Tyr Ser Arg Phe Ala Arg His Pro Phe Tyr Gly Ser Ala
10 15 20 25
gga gtt aat tca gga gtc atg tta atg aat tta act cgg ata aga agt 627
Gly Val Asn Ser Gly Val Met Leu Met Asn Leu Thr Arg Ile Arg Ser
30 35 40
acc cag ttc aag aac agc atg att cca aca ggc ctg gct tgg gag gac 675
Thr Gln Phe Lys Asn Ser Met Ile Pro Thr Gly Leu Ala Trp Glu Asp
45 50 55
atg ttg tac cct ctg tac cag aag tac aag aat gcc atc acg tgg gga 723
Met Leu Tyr Pro Leu Tyr Gln Lys Tyr Lys Asn Ala Ile Thr Trp Gly
60 65 70
gac cag gat tta tta aat att att ttt tat ttc aac cca gag tgt ctc 771
Asp Gln Asp Leu Leu Asn Ile Ile Phe Tyr Phe Asn Pro Glu Cys Leu

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75	80	85	
tat gta ttc ccc tgc cag tgg aac tac cgt ccc gat cac tgc atg tac			819
Tyr Val Phe Pro Cys Gln Trp Asn Tyr Arg Pro Asp His Cys Met Tyr			
90	95	100	105
gga agc aac tgc aga gag gct gag cat gaa ggt gtg tct gtt ctg cat			867
Gly Ser Asn Cys Arg Glu Ala Glu His Glu Gly Val Ser Val Leu His			
110	115		120
gga aac cga ggc gtc tac cat gac gat aag caa cca acg ttc aga gca			915
Gly Asn Arg Gly Val Tyr His Asp Asp Lys Gln Pro Thr Phe Arg Ala			
125	130		135
ctc tat gaa gca ata cgg gat ttt ccc ttt caa gac aat ctc ttt caa			963
Leu Tyr Glu Ala Ile Arg Asp Phe Pro Phe Gln Asp Asn Leu Phe Gln			
140	145		150
tcc atg tat tac ccc ctt cag ctg aag ttt ttg gag act gtg cac act			1011
Ser Met Tyr Tyr Pro Leu Gln Leu Lys Phe Leu Glu Thr Val His Thr			
155	160		165
tta tgt gga cga atc ccg caa gtt ttt ctg aag caa att gag aaa aca			1059
Leu Cys Gly Arg Ile Pro Gln Val Phe Leu Lys Gln Ile Glu Lys Thr			
170	175		180
atg aaa agg gct tat gag aaa cac gtc atc atc cat gtt ggc ccc aac			1107
Met Lys Arg Ala Tyr Glu Lys His Val Ile Ile His Val Gly Pro Asn			
190	195		200
cag atg cac tga ata ttttgtcttg ttgcaagtca attaggtgtc ttgtgaacaa			1162
Gln Met His *			
205			
ggaaatacta atctctaagc tgccctgggtc tttttgtgtg aatatttaaat ggtgctccat			1222
gactgttgag ttttaaaaac ctcgttaaata tttgccaaat cagttgcccc caaaagggaa			1282
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 <212> DNA  
 <213> Homo sapiens

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ggacc atg aac gtg ttc cga atc ctc ggc gac ctg agc cac ctc ctg 167  
 Met Asn Val Phe Arg Ile Leu Gly Asp Leu Ser His Leu Leu  
 1 5 10

gcc atg atc ttg ctg ctg ggg aag atc tgg agg tcc aag tgc tgc aag 215  
 Ala Met Ile Leu Leu Gly Lys Ile Trp Arg Ser Lys Cys Cys Lys  
 15 20 25 30

ggc atc tct ggg aag agc cag atc ctg ttt gct ctc gtc ttc acc acc 263  
 Gly Ile Ser Gly Lys Ser Gln Ile Leu Phe Ala Leu Val Phe Thr Thr  
 35 40 45

agg tac ctg gac ctg ttc acc aac ttc atc tcc atc tac aac aca gta 311  
 Arg Tyr Leu Asp Leu Phe Thr Asn Phe Ile Ser Ile Tyr Asn Thr Val  
 50 55 60

atg aag gtg gtt ttt ctc ctc tgt gcc tat gtt aca gtg tac atg ata 359  
 Met Lys Val Val Phe Leu Leu Cys Ala Tyr Val Thr Val Tyr Met Ile  
 65 70 75

tat ggg aaa ttc cgt aaa act ttt gac agt gag aat gac aca ttc cgc 407  
 Tyr Gly Lys Phe Arg Lys Thr Phe Asp Ser Glu Asn Asp Thr Phe Arg  
 80 85 90

ctg gag ttt ctt ctg gtc cca gtc att ggc ctt tcc ttc ctt gaa aac 455  
 Leu Glu Phe Leu Leu Val Pro Val Ile Gly Leu Ser Phe Leu Glu Asn  
 95 100 105 110

tac agt ttc act ctg ctg gag atc ctc tgg act ttc tct atc tat ctg 503  
 Tyr Ser Phe Thr Leu Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu  
 115 120 125

gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag act gga 551  
 Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys Thr Gly  
 130 135 140

gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt ctg tac 599  
 Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly Leu Tyr  
 145 150 155

cgg gca ctc tac ctg gct aac tgg atc agg cgg tac cag act gag aat 647  
 Arg Ala Leu Tyr Leu Ala Asn Trp Ile Arg Arg Tyr Gln Thr Glu Asn  
 160 165 170

ttc tat gac caa att gca gtc gtg tct gga gta gta caa acc atc ttc 695  
 Phe Tyr Asp Gln Ile Ala Val Val Ser Gly Val Val Gln Thr Ile Phe  
 175 180 185 190

tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag gga aag 743  
 Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys Gly Lys  
 195 200 205

aag tta agt ctt cca atg cca atc tga ggacc ttcagagaca gtctacgcct 795  
 Lys Leu Ser Leu Pro Met Pro Ile \*  
 210 215

taacaagcac atgaaggaaa ctattctgaa tgttctcttt ggcaacttat ccataatttg 855

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ggatcaaatg ttaaaaccag aaaagtgttt agtgtggatt tcagcaaac ctgatcatcc 915
caccagaag accttctcat caatagatcg cccttaaaga cccattgtaa ggtcataaaa 975
aacctcggcc aactgcacaa agatgggtgcc tctactgcaac aagaaacctt aaggtgtctt 1035
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gagcaagtca accccaatct ggaacaatgt ccctcctctt agaatgtccc aactaaagac 1155
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taccttaata ccaataacct aatgggtactt aggcgagtac catttgcaca atcactgttt 1455
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tcaatccaat atcccccatc tttgtcttga aacaaaaact gttttaagac gtctacgttg 1635
aattattcag agaattaagc aataaaagct cacaccttat tgtcaaaaaa 1685

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<210> 190
<211> 716
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (151)..(636)

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accgggggcg gagacgtggc agccgccctg cccgccagaa agtttcctag aagtttctg 120
ggcgcggggc cactgactgac tggctggacc      atg aac gtg ttc cga atc ctc 171
                                   Met Asn Val Phe Arg Ile Leu
                                   1                      5

ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ctg ggg aag atc 219
Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Leu Gly Lys Ile
      10                      15                      20

tgg agg tcc aag tgc tgc aag ggc atc tct ggg aag agc cag atc ctg 267
Trp Arg Ser Lys Cys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
      25                      30                      35

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ttt gct ctc gtc ttc acc acc agg tac ctg gac ctg ttc acc aac ttc	315
Phe Ala Leu Val Phe Thr Thr Arg Tyr Leu Asp Leu Phe Thr Asn Phe	
40 45 50 55	
atc tcc atc tac aac aca gta atg aag atc ctc tgg act ttc tct atc	363
Ile Ser Ile Tyr Asn Thr Val Met Lys Ile Leu Trp Thr Phe Ser Ile	
60 65 70	
tat ctg gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag	411
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys	
75 80 85	
act gga gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt	459
Thr Gly Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly	
90 95 100	
ctg tac cgg gca ctc tac ctg gct aac tgg atc aag cgg tac cag act	507
Leu Tyr Arg Ala Leu Tyr Leu Ala Asn Trp Ile Lys Arg Tyr Gln Thr	
105 110 115	
gag aat ttc tat gac caa att gca gtc ggg tct gga gta gta caa acc	555
Glu Asn Phe Tyr Asp Gln Ile Ala Val Gly Ser Gly Val Val Gln Thr	
120 125 130 135	
atc ttc tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag	603
Ile Phe Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys	
140 145 150	
gga aag aag tta agt ctt cca atg cca atc tga ggaccttc agagacagtc	654
Gly Lys Lys Leu Ser Leu Pro Met Pro Ile *	
155 160	
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ta	716

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 <212> DNA  
 <213> Homo sapiens

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ttacaggcac ctgccaccat gccagctaa tttttatatt tttaagagat gggggttcac	180
catgttggcc aggctggtct caaactcctg acctcaggcg atccgcccac cttggcctcc	240



<400> 192  
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Met Val Ala  
1

aaa gac agg cag ctt cct acc tta atg gca cag ccc ccg caa act gta 103  
Lys Asp Arg Gln Leu Pro Thr Leu Met Ala Gln Pro Pro Gln Thr Val  
5 10 15

gta cag gtg ctt gca gtg aaa acc acg cag cag ctc cct aaa ctg cag 151  
Val Gln Val Leu Ala Val Lys Thr Thr Gln Gln Leu Pro Lys Leu Gln  
20 25 30 35

cag gct ccg aac caa cca aaa atc tac gtg caa ccc caa acc ccc cag 199  
Gln Ala Pro Asn Gln Pro Lys Ile Tyr Val Gln Pro Gln Thr Pro Gln  
40 45 50

agc caa atg tcg ctc cca gct tct tca gag aaa cag acg gca agc cag 247  
Ser Gln Met Ser Leu Pro Ala Ser Ser Glu Lys Gln Thr Ala Ser Gln  
55 60 65

gtg gag cag cca att ata acc caa gga tcc tct gtt aca aag ata act 295  
Val Glu Gln Pro Ile Ile Thr Gln Gly Ser Ser Val Thr Lys Ile Thr  
70 75 80

ttt gag ggg cgc cag cct ccc aca gtt aca aag ata act ggt ggc agt 343  
Phe Glu Gly Arg Gln Pro Pro Thr Val Thr Lys Ile Thr Gly Gly Ser  
85 90 95

tct gtg cct aag ctg aca tca cca gtt aca agc ata tct ccc att cag 391  
Ser Val Pro Lys Leu Thr Ser Pro Val Thr Ser Ile Ser Pro Ile Gln  
100 105 110 115

gcc tct gag aag aca gca gtg tct gac att ttg aaa atg tct ttg atg 439  
Ala Ser Glu Lys Thr Ala Val Ser Asp Ile Leu Lys Met Ser Leu Met  
120 125 130

gaa gct cag att gat aca aat gta gaa cat atg ata gtg gat ccc cca 487  
Glu Ala Gln Ile Asp Thr Asn Val Glu His Met Ile Val Asp Pro Pro  
135 140 145

aag aag gct ctt gcc act agc atg ctc act ggt gaa gca gga tca tta 535  
Lys Lys Ala Leu Ala Thr Ser Met Leu Thr Gly Glu Ala Gly Ser Leu  
150 155 160

ccc tcc acc cac atg gtg gtg gca ggg atg gcg aat tcc act ccc cag 583  
Pro Ser Thr His Met Val Val Ala Gly Met Ala Asn Ser Thr Pro Gln  
165 170 175

caa cag aaa tgt aga gag tcc tgt tcg agt cca tcc act gtt ggc tct 631  
Gln Gln Lys Cys Arg Glu Ser Cys Ser Ser Pro Ser Thr Val Gly Ser  
180 185 190 195

tcc cta acg aca agg aaa att gat cca cca gca gtg cct gcg aca ggc 679  
Ser Leu Thr Thr Arg Lys Ile Asp Pro Pro Ala Val Pro Ala Thr Gly  
200 205 210



caa cta gta gag agt caa aat gaa tta cag aat caa ttg gat aaa tgt	326
Gln Leu Val Glu Ser Gln Asn Glu Leu Gln Asn Gln Leu Asp Lys Cys	
30 35 40	
cgt aat gaa atg atg acc atg act gag agt tat gaa caa gaa aaa tat	374
Arg Asn Glu Met Met Thr Met Thr Glu Ser Tyr Glu Gln Glu Lys Tyr	
45 50 55 60	
acc ctt caa aga gaa gtt gaa ctc aag agt cga atg tta gaa agt ttg	422
Thr Leu Gln Arg Glu Val Glu Leu Lys Ser Arg Met Leu Glu Ser Leu	
65 70 75	
agc tgc gaa tgt gaa gct att aaa caa caa caa aaa atg cac ctg gag	470
Ser Cys Glu Cys Glu Ala Ile Lys Gln Gln Gln Lys Met His Leu Glu	
80 85 90	
aaa ttg gaa gaa caa cta agc aga agc cat gga cag gaa gtg aat gaa	518
Lys Leu Glu Glu Gln Leu Ser Arg Ser His Gly Gln Glu Val Asn Glu	
95 100 105	
cta aaa act aag ata gaa aaa ctg aaa gtg gaa tta gat gaa gcc agg	566
Leu Lys Thr Lys Ile Glu Lys Leu Lys Val Glu Leu Asp Glu Ala Arg	
110 115 120	
ctt agt gaa aag cag ctg aag cac caa gta gat cat cag aag gaa ctc	614
Leu Ser Glu Lys Gln Leu Lys His Gln Val Asp His Gln Lys Glu Leu	
125 130 135 140	
ctc tct tgt aaa tca gag gaa ctg cgc gta atg tct gaa cgt gtg cag	662
Leu Ser Cys Lys Ser Glu Glu Leu Arg Val Met Ser Glu Arg Val Gln	
145 150 155	
gaa agc atg tct tca gag atg ctg gct ctt caa att gag ctg aca gaa	710
Glu Ser Met Ser Ser Glu Met Leu Ala Leu Gln Ile Glu Leu Thr Glu	
160 165 170	
atg gag agt atg aag acc acc ctc aaa gaa gaa gtg aat gaa cta caa	758
Met Glu Ser Met Lys Thr Thr Leu Lys Glu Glu Val Asn Glu Leu Gln	
175 180 185	
tac aga caa gaa cag cta gaa ctt ctt att act aac cta atg cgc cag	806
Tyr Arg Gln Glu Gln Leu Glu Leu Leu Ile Thr Asn Leu Met Arg Gln	
190 195 200	
gta gac cgg ctt aaa gag gaa aaa gaa gag cga gag aaa gaa gca gtt	854
Val Asp Arg Leu Lys Glu Glu Lys Glu Glu Arg Glu Lys Glu Ala Val	
205 210 215 220	
tct tac tat aat gcc cta gag aaa gct cgt gta gca aat caa gat ctt	902
Ser Tyr Tyr Asn Ala Leu Glu Lys Ala Arg Val Ala Asn Gln Asp Leu	
225 230 235	
cag gta cag ttg gac cag gca ctc cag caa gcc ttg gat ccc aat agt	950
Gln Val Gln Leu Asp Gln Ala Leu Gln Gln Ala Leu Asp Pro Asn Ser	
240 245 250	
aaa ggc aac tct ttg ttt gca gag gtg gaa gat cga agg gca gca atg	998

Lys Gly Asn Ser Leu Phe Ala Glu Val Glu Asp Arg Arg Ala Ala Met	
255 260 265	
gaa cgt cag ctt atc agt atg aaa gtc aag tat cag tca cta aag aag	1046
Glu Arg Gln Leu Ile Ser Met Lys Val Lys Tyr Gln Ser Leu Lys Lys	
270 275 280	
caa aat gta ttt aac aga gaa cag atg cag aga atg aag tta caa att	1094
Gln Asn Val Phe Asn Arg Glu Gln Met Gln Arg Met Lys Leu Gln Ile	
285 290 295 300	
gcc acg ttg cta cag atg aaa ggg tct caa act gaa ttt gag cag cag	1142
Ala Thr Leu Leu Gln Met Lys Gly Ser Gln Thr Glu Phe Glu Gln Gln	
305 310 315	
gaa cgg ttg ctt gcc atg ttg gag cag aag aat ggt gaa ata aaa cat	1190
Glu Arg Leu Leu Ala Met Leu Glu Gln Lys Asn Gly Glu Ile Lys His	
320 325 330	
ctt tta ggt gaa att aga aat ctg gag aaa ttt aag aat tta tat gac	1238
Leu Leu Gly Glu Ile Arg Asn Leu Glu Lys Phe Lys Asn Leu Tyr Asp	
335 340 345	
agt atg gaa tcc aag cct tca gtc gac tct ggt act ctg gaa gat aac	1286
Ser Met Glu Ser Lys Pro Ser Val Asp Ser Gly Thr Leu Glu Asp Asn	
350 355 360	
acc tat tat aca gat tta ctt cag atg aag ctg gat aac tta aac aaa	1334
Thr Tyr Tyr Thr Asp Leu Leu Gln Met Lys Leu Asp Asn Leu Asn Lys	
365 370 375 380	
gaa att gaa agc act aaa ggt gaa ttg tcc ata cag cga atg aaa gca	1382
Glu Ile Glu Ser Thr Lys Gly Glu Leu Ser Ile Gln Arg Met Lys Ala	
385 390 395	
tta ttt gag agc cag cgg gct cta gat att gag cga aaa ctt ttt tgc	1430
Leu Phe Glu Ser Gln Arg Ala Leu Asp Ile Glu Arg Lys Leu Phe Cys	
400 405 410	
aaa tga aagatgcctc cagctttcag aaagtgaaaa tatgaaactg agagctaaac	1486
Lys *	
tagatgaatt gaaactaaaa tatgaacctg aagagacagt tgaagtgcct gtactgaaaa	1546
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tagtcagtct ctctcctcac aaaaatctgc ccgtggatat gcagctgaag aaggaaaaga	1786
aatgtgtgaa actcatagga gttcccgtg acgctgaggc cttaagtgaa agaagtggaa	1846
acaccccaaa ctctcccagg ttagctgctg aatcaaagct tcaaacagaa gttaaagaag	1906



gaaaagaaac ttcaagcaaa ttggaaaaag aaacttgtaa gaaatcacac cctattctat 1966  
atgtgtcttc taaatctact ccagagaccc agtgcctca acagtaaaga cttttcttta 2026  
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cagagccatg tatttgagaa tgcttcaatc atattttcct atgtactttt ttttataaac 2386  
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atgtggctta aaatatatac attatattgt ttcaggattt tgtcagtgtt taaagaacca 2506  
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<210> 194  
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<212> DNA  
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<221> CDS  
<222> (528)..(953)

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ttatggtata tgcaaagcaa ttaaaacagc tcctgcaaaa gagtaaacac catataaata 180  
ttcattaaat aacatacaaa cataccaggt tgggaaaaat cagtaagcat aggagtcagg 240  
aaattccaag ttggttatca caactcttgg ccacagggc tttaatccag gtgcccttgt 300  
ctcctaccct tgttgccatc ccagtgtctc caggagtaa gtagaaataa agatcctatc 360  
tcacctcttg ggcattttcc cctgccctga aagcgtataa tcgcttagca cagtcgggtgc 420  
ttaaggggcc aggctccaaa gaagattaaa ggaacagttt gtgggggtgca ctgggcagca 480  
gtactctcct ctgagttcaa tcactcttgca ctctaagaat caccacc atg gcc ctt 536  
Met Ala Leu

gtg cca ggg aga agc aag gag gat ggg ctt tgg act aga aat agc cca	584
Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg Asn Ser Pro	
5 10 15	
ggc tcc tcc cag cat cca gaa agt ccc agg ctg ccc aac cct ctc tgg	632
Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn Pro Leu Trp	
20 25 30 35	
gac aga gga aaa att ggc aag gtt gaa ggt cac cag cac att cag gtt	680
Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His Ile Gln Val	
40 45 50	
agt act tcc tca gcc tgt gtc tgg cag ctg gct tac cct cca gtt tgg	728
Ser Thr Ser Ser Ala Cys Val Trp Gln Leu Ala Tyr Pro Pro Val Trp	
55 60 65	
ccc aac ctc cct gct gtc cct att cag gat ttc tct caa aag tcc cat	776
Pro Asn Leu Pro Ala Val Pro Ile Gln Asp Phe Ser Gln Lys Ser His	
70 75 80	
ctg ccg tct att gtg gtg gaa tcc agt gag gtg aat gaa gag agt ggg	824
Leu Pro Ser Ile Val Val Glu Ser Ser Glu Val Asn Glu Glu Ser Gly	
85 90 95	
gat ctc cat ttg ccc cat gag gag ctg ctg ctg ctc act gat ggt gag	872
Asp Leu His Leu Pro His Glu Glu Leu Leu Leu Leu Thr Asp Gly Glu	
100 105 110 115	
gaa gag gat gct gag gcc ttc ttc caa gac caa agt gaa gag cca ggt	920
Glu Glu Asp Ala Glu Ala Phe Phe Gln Asp Gln Ser Glu Glu Pro Gly	
120 125 130	
gag gga ggt ggc tca ttc agg ggg cca ctg tga gctgaatg ttctgggcag	971
Glu Gly Gly Gly Ser Phe Arg Gly Pro Leu *	
135 140	
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 <212> DNA  
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	1 5 10

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Val Leu Asn Leu Val Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu	
15 20 25	
agt ggc tct ggg gac cag cca ctc ttc cgt gga gct gat cga tat gac	145
Ser Gly Ser Gly Asp Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp	
30 35 40	
ttt gcc atc atg ata cct cca gga ggc acg gaa tgc ttt tgg caa ttt	193
Phe Ala Ile Met Ile Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe	
45 50 55	
gcc cac cag act gga tac ttc tat ttc agt tac gag gtt cag cgg aca	241
Ala His Gln Thr Gly Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr	
60 65 70 75	
gtg ggg atg tca cat gac cgg cat gtt gct gcc acg gca cat aac cca	289
Val Gly Met Ser His Asp Arg His Val Ala Ala Thr Ala His Asn Pro	
80 85 90	
cag gga ttt ctc ata gac acc tcc cag ggt gtt cgg ggc cag att aac	337
Gln Gly Phe Leu Ile Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn	
95 100 105	
ttc tct acc caa gag aca ggt ttt tat cag ctt tgt cta agt aat cag	385
Phe Ser Thr Gln Glu Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln	
110 115 120	
cat aat cac ttc ggt tct gtg caa gtg tac ctc aac ttt ggg gtc ttc	433
His Asn His Phe Gly Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe	
125 130 135	
tat gag ggg cct gag act gat cac aaa cag aag gaa aga aaa caa ctg	481
Tyr Glu Gly Pro Glu Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu	
140 145 150 155	
aat gat act ctg gat gca att gag gac ggc aca caa aag gtg cag aac	529
Asn Asp Thr Leu Asp Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn	
160 165 170	
aat atc ttt cac atg tgg cga tac tac aac ttt gcc cgg atg agg aaa	577
Asn Ile Phe His Met Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys	
175 180 185	
atg gct gac ttt ttc ctt atc caa tca aac tat aac tac gtg aac tgg	625
Met Ala Asp Phe Phe Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp	
190 195 200	
tgg tgg aca gcc cag agc ctt gtt att att ctt tct ggg atc ctg caa	673
Trp Ser Thr Ala Gln Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln	
205 210 215	
ctg tat ttc ttg aag cgt ctc ttc aat gtt cca aca act aca gat aca	721
Leu Tyr Phe Leu Lys Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr	
220 225 230 235	
aag aag cca aga tgc taa gctaag gtgactatag caccctggct gttttcttct	775

Lys Lys Pro Arg Cys \*  
240

ggggcttagt cgaatcagct ttgtaatggt atgggacaaa aatcaattat ctcattaatg 835  
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aaaaaaaaa 903

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<212> DNA  
<213> Homo sapiens

<220>  
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1 5 10

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Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu  
15 20 25

att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg 147  
Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala  
30 35 40

act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat 195  
Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn  
45 50 55

gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat 243  
Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp  
60 65 70 75

tgt gcc gcg agg gct cag gtg acc gat gcc tcc tgg ggt gct ttc tca 291  
Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser  
80 85 90

gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa 344  
Gly Lys Glu Trp Gly Arg \*  
95

aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt 404

ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac 464

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg 524

aatgggaaaa tcattttgaa aaatgtaaat tgctgctcaa gtagacatta ttgtgtgaaa 584

tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg 644  
ctagg 649

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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (36)..(275)

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Met Pro Val Ala Val Gly  
1 5  
  
ccc tac gga cag tcc cag cca agc tgc ttc tac cgt gta aaa atg ggc 101  
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Tyr Arg Val Lys Met Gly  
10 15 20  
  
ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc 149  
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly  
25 30 35  
  
acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 197  
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly  
40 45 50  
  
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 245  
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe  
55 60 65 70  
  
atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct 296  
Met Ala Ile Gly Met Gly Ile Arg Cys \*  
75 80  
  
gtcccttccc atcaatccca gcccatgtac taataaaaga aagtctttga gtaaaaaaaaa 356  
aaaa 360

<210> 198  
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<213> Homo sapiens  
  
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<222> (206)..(535)

<400> 198

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ggccatcttt ctggggagga ctctcccagg tagggaaggc cagaggtggc ccagtgcctg 180

gagggttagg gtctctgcct gggat atg caa gag gaa gta gga aag gga ggt 232  
Met Gln Glu Glu Val Gly Lys Gly Gly  
1 5

ctc atg gat gat cct agg ctg cta gaa gtc ctt aag gcc cca tct agt 280  
Leu Met Asp Asp Pro Arg Leu Leu Glu Val Leu Lys Ala Pro Ser Ser  
10 15 20 25

cca ttc cac tcc cta ccc cca ttc cag agc cga gta gta agt tta cag 328  
Pro Phe His Ser Leu Pro Pro Phe Gln Ser Arg Val Val Ser Leu Gln  
30 35 40

atg ttt ccc cca tta cgt acc ccc acc cat ccc tgc tgc agc gag cct 376  
Met Phe Pro Pro Leu Arg Thr Pro Thr His Pro Cys Cys Ser Glu Pro  
45 50 55

gag agc cag gca gag cca ggc aca gct cct cag tct tct cac aca gtc 424  
Glu Ser Gln Ala Glu Pro Gly Thr Ala Pro Gln Ser Ser His Thr Val  
60 65 70

ctg ccg gtg gcc ttc cct cat gac cct tgc ttg gga ggg tgg agc act 472  
Leu Pro Val Ala Phe Pro His Asp Pro Cys Leu Gly Gly Trp Ser Thr  
75 80 85

ggc tcc ttg acc cta aaa ggt agc tgg cag ggg caa gat ggg ggc cag 520  
Gly Ser Leu Thr Leu Lys Gly Ser Trp Gln Gly Gln Asp Gly Gly Gln  
90 95 100 105

cta cct aat gga tga aagccacaag tgaatacagt tcttgtcacc aggggtgccc 575  
Leu Pro Asn Gly \*  
110

tgccctcact cggcagggag ttctgacacc ccagggcccg tgagctacct gcttgagccc 635

ctgtttctgg ggcaccttcg aggaggcgtt gtggagggca tcgccccctg tttattcaca 695

acaccctcag gggcaaacag gcctgggacc cgctgacacc attttgggta gctggatgca 755

cccgacagca gtgggggtcca cacactgagc tccagctggc actgccact caagggctga 815

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aacatgagac ttctgtgac cagtccacc tggctcccag ctgtctgtat cctcctgccc 1115



His Gly Glu Lys Leu Lys Met Phe Cys Lys Glu Asp Val Leu Ile Met	
105 110 115	
tgt gag gcc tgc agc cag tcc cca gag cat gag gcc cac agt gtt gtg	679
Cys Glu Ala Cys Ser Gln Ser Pro Glu His Glu Ala His Ser Val Val	
120 125 130	
cca atg gag gat gtt gcc tgg gag tac aag tgg gaa ctt cat gag gcc	727
Pro Met Glu Asp Val Ala Trp Glu Tyr Lys Trp Glu Leu His Glu Ala	
135 140 145	
ctc gaa cat ctg aag aaa gag caa gaa gag gcc tgg aag ctt gaa gtt	775
Leu Glu His Leu Lys Lys Glu Gln Glu Glu Ala Trp Lys Leu Glu Val	
150 155 160	
ggc gaa agg aaa cga act gcc acc tgg aag ata cag gtg gaa acc cga	823
Gly Glu Arg Lys Arg Thr Ala Thr Trp Lys Ile Gln Val Glu Thr Arg	
165 170 175 180	
aaa cag agt att gta tgg gag ttt gaa aaa tac cag cga tta cta gag	871
Lys Gln Ser Ile Val Trp Glu Phe Glu Lys Tyr Gln Arg Leu Leu Glu	
185 190 195	
aaa aag cag cca cca cat cgg cag ctg ggg gca gag gta gca gca gct	919
Lys Lys Gln Pro Pro His Arg Gln Leu Gly Ala Glu Val Ala Ala Ala	
200 205 210	
ctg gcc agc cta cag cgg gag gca gcg gag acc atg cag aaa ctg gag	967
Leu Ala Ser Leu Gln Arg Glu Ala Ala Glu Thr Met Gln Lys Leu Glu	
215 220 225	
ttg aac cat agc gag ctc atc cag cag agc cag gtc ctg tgg agg atg	1015
Leu Asn His Ser Glu Leu Ile Gln Gln Ser Gln Val Leu Trp Arg Met	
230 235 240	
att gca gag ttg aaa gag agg tcg cag agg cct gtc cgc tgg atg ttg	1063
Ile Ala Glu Leu Lys Glu Arg Ser Gln Arg Pro Val Arg Trp Met Leu	
245 250 255 260	
cag gat att cag gaa gtg tta aac agg agc aaa tct tgg agc ttg cag	1111
Gln Asp Ile Gln Glu Val Leu Asn Arg Ser Lys Ser Trp Ser Leu Gln	
265 270 275	
cag cca gaa cca atc tcc ctg gag ttg aag aca gat tgc cgt gtg ctg	1159
Gln Pro Glu Pro Ile Ser Leu Glu Leu Lys Thr Asp Cys Arg Val Leu	
280 285 290	
ggg cta aga gag atc ctg aag act tat gca gct gat gtg cgc ttg gat	1207
Gly Leu Arg Glu Ile Leu Lys Thr Tyr Ala Ala Asp Val Arg Leu Asp	
295 300 305	
cca gat act gct tac tcc cgt ctc atc gtg tct gag gac aga aaa cgt	1255
Pro Asp Thr Ala Tyr Ser Arg Leu Ile Val Ser Glu Asp Arg Lys Arg	
310 315 320	
gtg cac tat gga gac acc aac cag aaa ctg cca gac aat cct gag aga	1303
Val His Tyr Gly Asp Thr Asn Gln Lys Leu Pro Asp Asn Pro Glu Arg	



325	330	335	340	
ttt tac cgc tat aat atc gtc ctg gga agc cag tgc atc tcc tca ggc				1351
Phe Tyr Arg Tyr Asn Ile Val Leu Gly Ser Gln Cys Ile Ser Ser Gly	345	350	355	
cgg cac tac tgg gag gtg gag gtg gga gac agg tct gag tgg ggc ctg				1399
Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Ser Glu Trp Gly Leu	360	365	370	
gga gta tgt aag caa aat gta gac cgg aag gag gtg gtc tac tta tcc				1447
Gly Val Cys Lys Gln Asn Val Asp Arg Lys Glu Val Val Tyr Leu Ser	375	380	385	
ccc cac tat gga ttc tgg gtg ata agg ctg agg aag gga aat gag tac				1495
Pro His Tyr Gly Phe Trp Val Ile Arg Leu Arg Lys Gly Asn Glu Tyr	390	395	400	
cga gca ggc acc gat gag tac cca atc ctg tcc ttg ccg gtc cct cct				1543
Arg Ala Gly Thr Asp Glu Tyr Pro Ile Leu Ser Leu Pro Val Pro Pro	405	410	415	420
cgc cgg gtg gga atc ttc gtg gat tat gag gcc cat gac att tct ttc				1591
Arg Arg Val Gly Ile Phe Val Asp Tyr Glu Ala His Asp Ile Ser Phe	425	430	435	
tac aat gtg act gac tgt ggc tcc cac atc ttc act ttc ccc cgc tat				1639
Tyr Asn Val Thr Asp Cys Gly Ser His Ile Phe Thr Phe Pro Arg Tyr	440	445	450	
ccc ttc cct ggg cgc ctg ctg ccc tat ttt agt cct tgc tac agc att				1687
Pro Phe Pro Gly Arg Leu Leu Pro Tyr Phe Ser Pro Cys Tyr Ser Ile	455	460	465	
gga acc aac aac act gct cct ctg gcc atc tgc tcc ctg gat ggg gag				1735
Gly Thr Asn Asn Thr Ala Pro Leu Ala Ile Cys Ser Leu Asp Gly Glu	470	475	480	
gac taa gaaagctacc accctaacca cagaggcttg gaattgggcc tggccccat				1791
Asp *				
485				
ggggcttggga ggaccgagcc actgacaggt atcccctgaa actgagctga gcccagtatc				1851
caaggattcc tctgtctgat cctttgggtct ttgctaccag gctgaagtct gtcatgaaac				1911
cacttatttt aaaaagcaga ggcccagtca aatgagcatt gcatcccatg agggaagcac				1971
gacagggctg atgggtgagga tcagagcagt tctaaggatga ctcggtgggg taaggatcag				2031
gactttgtcc atgtagtagc caaccaccct cttccctgat tcccgtccgg tgtcacagtt				2091
cagtcagtga ggatgatgaa gtagatacag tcttcaggac accattagat gggctttccc				2151
aataggccaa aaaaatgctg cgcataccca gagctggttg ttgtgctgag gccagtcaga				2211
ggatgcttcc cctgaggttt gctataacta agcaaccttt atgtgactct caccttctga				2271

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cctcctggca agagaaattc agtgcagcag ggggacacag acctgcccac gccaccccac 2331
tgccgttccc tctctgagca caagctgggc aaatcactgt cccttggact ccagtagacc 2391
agtgtcctag tcttgccttt tttctctaag tggcaggatc agaaaacctg cgagcttttag 2451
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (331)..(1047)

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tctcaccagc agagaacagc tgacggtctt tccataagtg cttctaagag agatgtgtgg 180
taccctgggc taagtagaca gcaactgagc cctccctccc accccagggc tcccagagca 240
acagggagca gggagcatag gacctggccg cagccaggaa tctacactga ccggctcagc 300
ccatgaagta tcttgggctg aagtcacagg      atg aga ctg ttt gta tct gta 351
                                   Met Arg Leu Phe Val Ser Val
                                   1              5

act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc 399
Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
      10              15              20

tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca 447
Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
      25              30              35

gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc 495
Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser
      40              45              50              55

tct ctc tca ggc tgt ggg agc tgg cag ccc cgg aag ctg cca gtc ttc 543
Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe
      60              65              70

aag tcc ctc cgg cac atg agg cag gtc ctg ggt gcc cct tct ttc cgc 591
Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
      75              80              85

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atg ctg gcc tgg cac gtt ctc atg ggg aac cag gtg atc tgg aaa agc	639
Met Leu Ala Trp His Val Leu Met Gly Asn Gln Val Ile Trp Lys Ser	
90 95 100	
aga gac gtg gac ctc gtc cag tca gct ttt gaa gta ctt cgg acc atg	687
Arg Asp Val Asp Leu Val Gln Ser Ala Phe Glu Val Leu Arg Thr Met	
105 110 115	
ctt ccc gtg ggc tgc gtc cgc atc atc cca tac agc agc cag tac gag	735
Leu Pro Val Gly Cys Val Arg Ile Ile Pro Tyr Ser Ser Gln Tyr Glu	
120 125 130 135	
gag gcc tat cgg tgc aac ttc ctg ggg ctc agc ccg cac gtg cag atc	783
Glu Ala Tyr Arg Cys Asn Phe Leu Gly Leu Ser Pro His Val Gln Ile	
140 145 150	
ccc ccc cac gtg ctc tcc tca gag ttt gct gtc atc gtg gag gtc cac	831
Pro Pro His Val Leu Ser Ser Glu Phe Ala Val Ile Val Glu Val His	
155 160 165	
gca gcc gca cgt tcc acc ctc cac cct gtg ggg tgt gag gat gac cag	879
Ala Ala Ala Arg Ser Thr Leu His Pro Val Gly Cys Glu Asp Asp Gln	
170 175 180	
tct ctc agc aag tac gag ttt gtg gtg acc agt ggg agc cct gta gct	927
Ser Leu Ser Lys Tyr Glu Phe Val Val Thr Ser Gly Ser Pro Val Ala	
185 190 195	
gca gac cga gtg ggc ccc acc atc ctg aat aag att gaa gcg gct ctg	975
Ala Asp Arg Val Gly Pro Thr Ile Leu Asn Lys Ile Glu Ala Ala Leu	
200 205 210 215	
acc aac cag aac ctg tct gtg gat gtg gtg gac cag tgc ctc gtc tgc	1023
Thr Asn Gln Asn Leu Ser Val Asp Val Val Asp Gln Cys Leu Val Cys	
220 225 230	
ctc aag gag gag tgg atg aag taa gcaacagtgt gggtgaggcc cctttgcttg	1077
Leu Lys Glu Trp Met Lys *	
235	
cgaccctgga gaaaacctgg agctgtttcc aaaagaggag ctgggccgtg gccactgagg	1137
gaggagctga gagaagaggt tgggggagggt gttccaactc cacgtccgcc actgcaaagc	1197
tcaggtggcc tcgggaggcg gtcattcatgt ctgcctccgg ctccctgcatg gggagggtggg	1257
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(416)

<400> 201

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Met Leu Thr His Pro Leu Gln Gly  
1 5

cct ggc ctt gac tta ggg ctg cac tgt atc ctc agc aac ggc ctt gca 161  
Pro Gly Leu Asp Leu Gly Leu His Cys Ile Leu Ser Asn Gly Leu Ala  
10 15 20

gga gcc cct ttt gga ctg ctt tcc cta ttc agc cca aag ttg ggg tgg 209  
Gly Ala Pro Phe Gly Leu Leu Ser Leu Phe Ser Pro Lys Leu Gly Trp  
25 30 35 40

tgg gag aag agg ggt tgg agt gaa tcc atc tct att caa att cca gct 257  
Trp Glu Lys Arg Gly Trp Ser Glu Ser Ile Ser Ile Gln Ile Pro Ala  
45 50 55

ggg att act cta gga gtc ttc ctg gct tgt ttt ggg ctc aaa ctt agc 305  
Gly Ile Thr Leu Gly Val Phe Leu Ala Cys Phe Gly Leu Lys Leu Ser  
60 65 70

tac att gtt tat tgg ctc cca aag tcg gga ttg aag agt gaa aag atg 353  
Tyr Ile Val Tyr Trp Leu Pro Lys Ser Gly Leu Lys Ser Glu Lys Met  
75 80 85

cag gca atg aat cct tct gca cac tcc tcc ccc cac att cct gac act 401  
Gln Ala Met Asn Pro Ser Ala His Ser Ser Pro His Ile Pro Asp Thr  
90 95 100

agt aag aac caa taa acacttggtg acggaaaaaa aaaaa 441  
Ser Lys Asn Gln \*  
105

<210> 202

<211> 732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(296)

<400> 202

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ggaaaaagta a atg aag ttc cag gaa tgt cat tct gaa gta atg agg cat	110
Met Lys Phe Gln Glu Cys His Ser Glu Val Met Arg His	
1 5 10	
gga cag aaa ata tac ccc tca cat cat cgg att gag atg gca gtc gaa	158
Gly Gln Lys Ile Tyr Pro Ser His His Arg Ile Glu Met Ala Val Glu	
15 20 25	
ata gct tca ttg aag tgt cag cac tca tcc atc aat caa tca ccc aca	206
Ile Ala Ser Leu Lys Cys Gln His Ser Ser Ile Asn Gln Ser Pro Thr	
30 35 40 45	
agg aaa aat agc aac agt aca acg ggg tgg ctt tta tgg gat tta ctc	254
Arg Lys Asn Ser Asn Ser Thr Thr Gly Trp Leu Leu Trp Asp Leu Leu	
50 55 60	
atg ggc ata ggg aat agc ggc tca aat gta gtt ctg aca tga aaagcaa	303
Met Gly Ile Gly Asn Ser Gly Ser Asn Val Val Leu Thr *	
65 70 75	
ggtgctgata ttatttttta tgatgggagg atcataaagt gaattgagaa cagtgaggtc	363
tgtctttgct taacctattc aaccagaaat gaatggagct cgactggaaa ggaacagtct	423
tcagatgggt taagattgaa ggggtggactg gactctactg agcaccgtcc ttcaacaagg	483
aaattctatt aaaggaaaat caatgcatta gtattgggggt tctcgtagct gttaaaaatt	543
gtctgtcca atccagggtt attaggccaa agttacataa ttcagatctc actgcaacca	603
tccaaaagtg gattctcgag cccttgctcc aatgggggga ggagatcaat acaattccca	663
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aaaaaaaa	732

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cagatagcag tagtccaact gggatattag ccacctcaga gtccaaatcc atg cca	116
Met Pro	
1	
gtg ttg ggt tct gta tcc agt gta aca aaa aca gcc ttg aac aag aaa	164
Val Leu Gly Ser Val Ser Ser Val Thr Lys Thr Ala Leu Asn Lys Lys	

5	10	15	
act ctg gag gca gaa ttc aac agc ccg tcc ccc cca aca cct gag cca			212
Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro			
20	25	30	
ggt gaa ggg ccc cgt aaa ttg gaa gga tgc aca agt tcc aag gtt acg			260
Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr			
35	40	45	50
ttt cag cct ccc agt agc att gga tgc agg aaa aaa tac att gac ggt			308
Phe Gln Pro Pro Ser Ser Ile Gly Cys Arg Lys Lys Tyr Ile Asp Gly			
55	60	65	
gaa aaa caa gcc gaa cca gtt gta gtt tta gat cct gtt tct aca cat			356
Glu Lys Gln Ala Glu Pro Val Val Val Leu Asp Pro Val Ser Thr His			
70	75	80	
gaa ccc caa acc aaa gac cag gtt gct gaa aaa gat cca act caa cac			404
Glu Pro Gln Thr Lys Asp Gln Val Ala Glu Lys Asp Pro Thr Gln His			
85	90	95	
aag gag gat gaa ggc gaa att caa cca gaa aac aaa gaa gac agc att			452
Lys Glu Asp Glu Gly Glu Ile Gln Pro Glu Asn Lys Glu Asp Ser Ile			
100	105	110	
gaa aac gtg aga gag aca gac agc tcc aac tgc tga tcca taaaccagaa			502
Glu Asn Val Arg Glu Thr Asp Ser Ser Asn Cys *			
115	120	125	
gcctgacatg ttggaagtc cttttcaata agcacatgat tagtggtggt atattggcaa			562
gggctgtaga cattctgctc tggctactgt attcagaata caggttcttt tctgggtgtca			622
cttttgtaag tagcaactat aaacataagt aagctgttta gcaaaacaca cattcctagt			682
aggttttggt tttttgatct ttataaagat gaggtttttt tcctagttac tgtattaagt			742
atgacttctt ttagaagggtt acaaaaaaat tcagatgttg ataccttttt aggaaatgtg			802
cataccactc atcaaatgga atgctgaaag ttgaggtgc ttgtatataa tcggataaac			862
aaaactgac aacccaatgt gattttaaaa gcccccaaag aagcttctgt tttgggtctg			922
atcctcttga tggagaaact gcagcagcat ggaaattggt gggtagctgt gcatacaagt			982
tattttctac agtagactga gataaactga aaactcagga gctggcatca aactcgtagt			1042
cccatagtca gtgttaatta cacacattgt taactattgg atgaaaaata catgctattg			1102
atttgtgtcca aagcctcccg aggacctccg tggggatgct ctggtagcct gaatacagaa			1162
ctgaggtgaa agtccaaacc ttgaatttta cagtagtaag ttggtaaacc atgtgctctg			1222
tgctatgagt taattatggt ttcccaaata ctaatgtggc acaagtacca tattttatca			1282
gagttcttat gtacagtatg gtgaagataa gtgacaagca cacatttttc ttgcttcact			1342

gctgttctat attacacagg tttgttgttg ttttttttaa aaaagaaatt aagcagtagt 1402  
tagtctctaa aaatacaatg tttcaggcta ccacagtga taaatagaaa tgtaatcagg 1462  
gattaaaaaa aaaa 1476

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<211> 721  
<212> DNA  
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<220>  
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acgcagactg acgtgctttt gggaggggtgt gccgtgaagc ctgcagtacg tgtgccgtga 180  
ggctcatagt tg atg agg gac ttt ccc tgc tcc acc gtc act ccc cca 228  
Met Arg Asp Phe Pro Cys Ser Thr Val Thr Pro Pro  
1 5 10  
act ctg ccc gcc tct gtc ccc gcc tca gtc ccc gcc tcc atc ccc gcc 276  
Thr Leu Pro Ala Ser Val Pro Ala Ser Val Pro Ala Ser Ile Pro Ala  
15 20 25  
tct gtc ccc tgg cct tgg cgg cta ttt ttg cca cct gcc ttg ggt gcc 324  
Ser Val Pro Trp Pro Trp Arg Leu Phe Leu Pro Pro Ala Leu Gly Ala  
30 35 40  
cag gag tcc cct act gct gtg ggc tgg ggt tgg ggg cac agc agc ccc 372  
Gln Glu Ser Pro Thr Ala Val Gly Trp Gly Trp Gly His Ser Ser Pro  
45 50 55 60  
aag cct gag agg ctg gag ccc atg gct agt ggc tca tcc cca ctg cat 420  
Lys Pro Glu Arg Leu Glu Pro Met Ala Ser Gly Ser Ser Pro Leu His  
65 70 75  
tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat 468  
Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn  
80 85 90  
gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg 516  
Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu  
95 100 105  
tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga 564  
Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys \*  
110 115 120

tgaccacacc ccgtccaggc cagacaccac cccccacccc actgtcgtgg tggccccaga 624  
tctctgtaat tttatgtaga gtttgagctg aagccccgta tatttaattt atttttgttaa 684  
acatgaaagt gcacccctttc cctccaaaaa aaaaaaa 721

<210> 205  
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<220>  
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<222> (71)..(2899)

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Met Ala Ser Val Ala Ser Cys Asp Ser Arg Pro Ser Ser  
1 5 10  
gac gag ctc cct gga gac ccc tct tca caa gaa gaa gat gag gac tat 157  
Asp Glu Leu Pro Gly Asp Pro Ser Ser Gln Glu Glu Asp Glu Asp Tyr  
15 20 25  
gat ttt gaa gat cgg gtc agc gac tcg ggt tca tat tcc tca gcg agt 205  
Asp Phe Glu Asp Arg Val Ser Asp Ser Gly Ser Tyr Ser Ser Ala Ser  
30 35 40 45  
agc gat tat gat gat ctt gag cct gaa tgg ctg gac agt gtg cag aaa 253  
Ser Asp Tyr Asp Asp Leu Glu Pro Glu Trp Leu Asp Ser Val Gln Lys  
50 55 60  
aat gga gag ctg ttt tat ttg gaa ttg agt gag gat gaa gaa gaa agc 301  
Asn Gly Glu Leu Phe Tyr Leu Glu Leu Ser Glu Asp Glu Glu Glu Ser  
65 70 75  
ctc ctt cct gag aca cca act gtg aac cat gtc agg ttc agt gaa aat 349  
Leu Leu Pro Glu Thr Pro Thr Val Asn His Val Arg Phe Ser Glu Asn  
80 85 90  
gag att atc att gaa gat gac tac aaa gaa aga aaa aag tat gaa ccc 397  
Glu Ile Ile Ile Glu Asp Asp Tyr Lys Glu Arg Lys Lys Tyr Glu Pro  
95 100 105  
aaa ctc aag cag ttt acc aaa att tta aga agg aaa aga ctt tta ccc 445  
Lys Leu Lys Gln Phe Thr Lys Ile Leu Arg Arg Lys Arg Leu Leu Pro  
110 115 120 125  
aag cgc tgc aat aaa aaa aat agc aat gac aat gga cca gta tcc att 493  
Lys Arg Cys Asn Lys Lys Asn Ser Asn Asp Asn Gly Pro Val Ser Ile  
130 135 140



cta aag cat cag tcc aat cag aag aca gga gtc att gtc caa cag cgg	541
Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg	
145 150 155	
tac aaa gat gtg aat gtt tat gta aac ccc aaa aag cta act gtt atc	589
Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile	
160 165 170	
aaa gcc aaa gag cag ctc aag ctt ctg gaa gtg ctg gtt gga att att	637
Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile	
175 180 185	
cat cag acc aag tgg agc tgg aga aga acc gga aag cag ggt gat gga	685
His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly	
190 195 200 205	
gag agg ctt gtg gtt cat ggc ctg ctg cca ggg gga tct gct atg aag	733
Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys	
210 215 220	
agc ggt cag gta ctc att ggt gat gtc ctt gtt gct gtg aat gat gtc	781
Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val	
225 230 235	
gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga	829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat	925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
270 275 280 285	
tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt	973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser	
290 295 300	
ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac	1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
305 310 315	
tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg	1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca	1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca	1165
Leu Cys Asp Met Leu Glu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	

tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa	1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt	1261
Ser Asp Lys Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
400 405 410	
atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct	1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct	1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	
gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct	1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala	
450 455 460	
tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca	1501
Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr	
465 470 475	
ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg	1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu	
480 485 490	
gag gct gca gat ttt gca gaa ctg tcc gag gat tac tat gac atg agg	1597
Glu Ala Ala Asp Phe Ala Glu Leu Ser Glu Asp Tyr Tyr Asp Met Arg	
495 500 505	
cgg ctg tat aca att ttg ggg tct tct cta ttt tac aag ggt tat ttg	1645
Arg Leu Tyr Thr Ile Leu Gly Ser Ser Leu Phe Tyr Lys Gly Tyr Leu	
510 515 520 525	
ata tgc agt cat ttg ccc aag gat gat ctt att gat att gcc gta tac	1693
Ile Cys Ser His Leu Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr	
530 535 540	
tgt cgc cac tat tgc ctg ctg cct tta gca gca aaa caa aga att ggt	1741
Cys Arg His Tyr Cys Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly	
545 550 555	
cag ttg atc ata tgg aga gaa gtg ttt cct cag cat cac ctc cga cct	1789
Gln Leu Ile Ile Trp Arg Glu Val Phe Pro Gln His His Leu Arg Pro	
560 565 570	
ttg gca gac tca agc act gaa gtc ttt ccg gaa cct gaa gga aga tat	1837
Leu Ala Asp Ser Ser Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr	
575 580 585	
ttt ttg cta gtt gtt ggc ttg aaa cat tat atg cta tgt gta cta tta	1885

Phe	Leu	Leu	Val	Val	Gly	Leu	Lys	His	Tyr	Met	Leu	Cys	Val	Leu	Leu	
590					595					600					605	
gaa	gct	gga	ggt	tgc	gca	tcc	aaa	gct	att	ggg	agt	cct	gga	cca	gac	1933
Glu	Ala	Gly	Gly	Cys	Ala	Ser	Lys	Ala	Ile	Gly	Ser	Pro	Gly	Pro	Asp	
				610					615					620		
tgt	gta	tat	gtg	gat	caa	gtc	aaa	aca	act	ctt	cac	cag	ctg	gat	gga	1981
Cys	Val	Tyr	Val	Asp	Gln	Val	Lys	Thr	Thr	Leu	His	Gln	Leu	Asp	Gly	
			625					630					635			
gta	gat	tct	cgc	ata	gat	gaa	cgg	cta	gca	tct	tct	cca	gtc	ccc	tgt	2029
Val	Asp	Ser	Arg	Ile	Asp	Glu	Arg	Leu	Ala	Ser	Ser	Pro	Val	Pro	Cys	
		640					645					650				
ttg	tct	tgt	gct	gac	tgg	ttc	ctt	act	gga	tca	cgt	gaa	aaa	aca	gat	2077
Leu	Ser	Cys	Ala	Asp	Trp	Phe	Leu	Thr	Gly	Ser	Arg	Glu	Lys	Thr	Asp	
	655					660					665					
agc	ttg	acc	act	tgc	cct	att	ctc	agt	agg	cta	caa	ggt	act	tcc	aaa	2125
Ser	Leu	Thr	Thr	Ser	Pro	Ile	Leu	Ser	Arg	Leu	Gln	Gly	Thr	Ser	Lys	
670					675					680					685	
gta	gca	act	tct	cca	aca	tgc	aga	aga	acg	ctt	ttt	ggt	gac	tat	tcc	2173
Val	Ala	Thr	Ser	Pro	Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser	
				690					695					700		
tta	aag	aca	cgc	aag	cct	agt	cct	tcc	tgt	agt	agt	gga	gga	tct	gac	2221
Leu	Lys	Thr	Arg	Lys	Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp	
			705					710					715			
aat	ggt	tgt	gaa	ggt	gga	gaa	gat	gat	ggc	ttt	agc	ccc	cat	act	aca	2269
Asn	Gly	Cys	Glu	Gly	Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr	
		720					725					730				
ccg	gat	gca	gta	cgg	aag	caa	aga	gaa	tct	cag	ggc	tct	gat	ggt	tta	2317
Pro	Asp	Ala	Val	Arg	Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu	
	735					740					745					
gaa	gaa	agt	ggg	acc	ttg	ctt	aag	gtc	act	aaa	aag	aag	tct	act	ctt	2365
Glu	Glu	Ser	Gly	Thr	Leu	Leu	Lys	Val	Thr	Lys	Lys	Lys	Ser	Thr	Leu	
750					755				760						765	
cca	aat	cca	ttt	cat	ttg	gga	aac	ttg	aaa	aag	gac	ctt	cca	gaa	aaa	2413
Pro	Asn	Pro	Phe	His	Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys	
				770					775					780		
gaa	tta	gaa	ata	tat	aac	aca	gtg	aaa	ctg	aca	tct	ggt	cct	gag	aac	2461
Glu	Leu	Glu	Ile	Tyr	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn	
			785					790					795			
aca	ctt	ttc	cac	tac	gtt	gcc	tta	gaa	aca	gtg	caa	gga	atc	ttt	att	2509
Thr	Leu	Phe	His	Tyr	Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile	
		800					805					810				
act	cct	acc	ctt	gaa	gag	gtg	gca	cag	cta	agt	ggc	tct	atc	cac	cct	2557
Thr	Pro	Thr	Leu	Glu	Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro	





agc	ggg	cag	gta	ctc	att	ggg	gat	gtc	ctt	gtt	gct	gtg	aat	gat	gtc	781	
Ser	Gly	Gln	Val	Leu	Ile	Gly	Asp	Val	Leu	Val	Ala	Val	Asn	Asp	Val		
			225				230						235				
gat	gtt	act	act	gaa	aac	atc	gag	aga	gtt	ctg	tct	tgc	att	cct	gga	829	
Asp	Val	Thr	Thr	Glu	Asn	Ile	Glu	Arg	Val	Leu	Ser	Cys	Ile	Pro	Gly		
			240				245						250				
cct	atg	cag	gtg	aaa	ctg	aca	ttt	gaa	aat	gca	tat	gat	gtg	aaa	agg	877	
Pro	Met	Gln	Val	Lys	Leu	Thr	Phe	Glu	Asn	Ala	Tyr	Asp	Val	Lys	Arg		
			255				260						265				
gag	aca	tcc	cat	cca	aga	cag	aaa	aag	aca	cag	tcc	aac	aca	agt	gat	925	
Glu	Thr	Ser	His	Pro	Arg	Gln	Lys	Lys	Thr	Gln	Ser	Asn	Thr	Ser	Asp		
			270				275						280				
															285		
tta	gtc	aag	ctt	ctc	tgg	gga	gaa	gag	gtt	gaa	ggg	atc	cag	cag	agt	973	
Leu	Val	Lys	Leu	Leu	Trp	Gly	Glu	Glu	Val	Glu	Gly	Ile	Gln	Gln	Ser		
						290									300		
ggc	cta	aac	act	cct	cat	atc	att	atg	tat	ctc	aca	cta	cag	ctc	gac	1021	
Gly	Leu	Asn	Thr	Pro	His	Ile	Ile	Met	Tyr	Leu	Thr	Leu	Gln	Leu	Asp		
						305									310		
															315		
tca	gaa	acc	tca	aag	gaa	gag	cag	gaa	att	ctt	tat	cat	tat	cca	atg	1069	
Ser	Glu	Thr	Ser	Lys	Glu	Glu	Gln	Glu	Ile	Leu	Tyr	His	Tyr	Pro	Met		
						320									325		
															330		
tct	gaa	gca	tct	cag	aaa	ctt	aaa	agt	gtg	aga	ggg	att	ttt	ctc	aca	1117	
Ser	Glu	Ala	Ser	Gln	Lys	Leu	Lys	Ser	Val	Arg	Gly	Ile	Phe	Leu	Thr		
						335									340		
															345		
ctc	tgt	gac	atg	ctg	gaa	aac	gta	act	ggg	aca	caa	gtt	act	agt	tca	1165	
Leu	Cys	Asp	Met	Leu	Glu	Asn	Val	Thr	Gly	Thr	Gln	Val	Thr	Ser	Ser		
						350									355		
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															365		
tcc	ctc	ctt	tta	aat	gga	aaa	caa	att	cat	gtg	gct	tat	tgg	aaa	gaa	1213	
Ser	Leu	Leu	Leu	Asn	Gly	Lys	Gln	Ile	His	Val	Ala	Tyr	Trp	Lys	Glu		
						370									375		
															380		
tct	gac	aag	ttg	ttg	cta	att	ggc	ctg	cct	gct	gaa	gaa	gtt	cct	ctt	1261	
Ser	Asp	Lys	Leu	Leu	Leu	Ile	Gly	Leu	Pro	Ala	Glu	Glu	Val	Pro	Leu		
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cct	cgt	cta	agg	aac	atg	ata	gaa	aat	gtc	atc	caa	acc	tta	aaa	ttt	1309	
Pro	Arg	Leu	Arg	Asn	Met	Ile	Glu	Asn	Val	Ile	Gln	Thr	Leu	Lys	Phe		
						400									405		
															410		
atg	tat	ggg	tct	tta	gat	agt	gcc	ttt	tgc	cag	att	gag	aat	gtt	cct	1357	
Met	Tyr	Gly	Ser	Leu	Asp	Ser	Ala	Phe	Cys	Gln	Ile	Glu	Asn	Val	Pro		
						415									420		
															42		

gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct	1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala	
450 455 460	
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Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr	
465 470 475	
ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg	1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu	
480 485 490	
gag gct gca gat ttt gca gaa ctg ggt tat ttg ata tgc agt cat ttg	1597
Glu Ala Ala Asp Phe Ala Glu Leu Gly Tyr Leu Ile Cys Ser His Leu	
495 500 505	
ccc aag gat gat ctt att gat att gcc gta tac tgt cgc cac tat tgc	1645
Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr Cys Arg His Tyr Cys	
510 515 520 525	
ctg ctg cct tta gca gca aaa caa aga att ggt cag ttg atc ata ttg	1693
Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly Gln Leu Ile Ile Trp	
530 535 540	
aga gaa gtg ttt cct cag cat cac ctc cga cct ttg gca gac tca agc	1741
Arg Glu Val Phe Pro Gln His His Leu Arg Pro Leu Ala Asp Ser Ser	
545 550 555	
act gaa gtc ttt ccg gaa cct gaa gga aga tat ttt ttg cta gtt gtt	1789
Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr Phe Leu Leu Val Val	
560 565 570	
ggc ttg aaa cat tat atg cta tgt gta cta tta gaa gct gga ggt tgc	1837
Gly Leu Lys His Tyr Met Leu Cys Val Leu Leu Glu Ala Gly Gly Cys	
575 580 585	
gca tcc aaa gct att ggg agt cct gga cca gac tgt gta tat gtg gat	1885
Ala Ser Lys Ala Ile Gly Ser Pro Gly Pro Asp Cys Val Tyr Val Asp	
590 595 600 605	
caa gtc aaa aca act ctt cac cag ctg gat gga gta gat tct cgc ata	1933
Gln Val Lys Thr Thr Leu His Gln Leu Asp Gly Val Asp Ser Arg Ile	
610 615 620	
gat gaa cgg cta gca tct tct cca gtc ccc tgt ttg tct tgt gct gac	1981
Asp Glu Arg Leu Ala Ser Ser Pro Val Pro Cys Leu Ser Cys Ala Asp	
625 630 635	
tgg ttc ctt act gga tca cgt gaa aaa aca gat agc ttg acc act tcg	2029
Trp Phe Leu Thr Gly Ser Arg Glu Lys Thr Asp Ser Leu Thr Thr Ser	
640 645 650	
cct att ctc agt agg cta caa ggt act tcc aaa gta gca act tct cca	2077
Pro Ile Leu Ser Arg Leu Gln Gly Thr Ser Lys Val Ala Thr Ser Pro	
655 660 665	
aca tgc aga aga acg ctt ttt ggt gac tat tcc tta aag aca cgc aag	2125

Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser	Leu	Lys	Thr	Arg	Lys	
670					675					680					685	
cct	agt	cct	tcc	tgt	agt	agt	gga	gga	tct	gac	aat	ggg	tgt	gaa	ggg	2173
Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp	Asn	Gly	Cys	Glu	Gly	
				690					695					700		
gga	gaa	gat	gat	ggc	ttt	agc	ccc	cat	act	aca	ccg	gat	gca	gta	cgg	2221
Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr	Pro	Asp	Ala	Val	Arg	
			705					710					715			
aag	caa	aga	gaa	tct	cag	ggc	tct	gat	ggg	tta	gaa	gaa	agt	ggg	acc	2269
Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu	Glu	Glu	Ser	Gly	Thr	
		720					725					730				
ttg	ctt	aag	gtc	act	aaa	aag	aag	tct	act	ctt	cca	aat	cca	ttt	cat	2317
Leu	Leu	Lys	Val	Thr	Lys	Lys	Lys	Ser	Thr	Leu	Pro	Asn	Pro	Phe	His	
	735					740					745					
ttg	gga	aac	ttg	aaa	aag	gac	ctt	cca	gaa	aaa	gaa	tta	gaa	ata	tat	2365
Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys	Glu	Leu	Glu	Ile	Tyr	
750					755				760						765	
aac	aca	gtg	aaa	ctg	aca	tct	ggg	cct	gag	aac	aca	ctt	ttc	cac	tac	2413
Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn	Thr	Leu	Phe	His	Tyr	
			770					775						780		
gtt	gcc	tta	gaa	aca	gtg	caa	gga	atc	ttt	att	act	cct	acc	ctt	gaa	2461
Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile	Thr	Pro	Thr	Leu	Glu	
			785					790					795			
gag	gtg	gca	cag	cta	agt	ggc	tct	atc	cac	cct	cag	cta	ata	aag	aat	2509
Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro	Gln	Leu	Ile	Lys	Asn	
		800					805					810				
ttc	cat	cag	tgt	tgt	ctt	tcc	att	cgt	gca	gtt	ttc	caa	cag	aca	ttg	2557
Phe	His	Gln	Cys	Cys	Leu	Ser	Ile	Arg	Ala	Val	Phe	Gln	Gln	Thr	Leu	
	815					820					825					
gtg	gaa	gag	aaa	aag	aaa	gga	cta	aat	agt	gga	gac	cat	tca	gat	tct	2605
Val	Glu	Glu	Lys	Lys	Lys	Gly	Leu	Asn	Ser	Gly	Asp	His	Ser	Asp	Ser	
830					835					840					845	
gca	aag	tca	gtg	tct	tct	ctt	aac	cct	gtt	aaa	gaa	cat	ggg	gtg	ttg	2653
Ala	Lys	Ser	Val	Ser	Ser	Leu	Asn	Pro	Val	Lys	Glu	His	Gly	Val	Leu	
				850					855					860		
ttt	gaa	tgt	tca	cct	gga	aac	tgg	act	gat	cag	aaa	aaa	gca	cca	cca	2701
Phe	Glu	Cys	Ser	Pro	Gly	Asn	Trp	Thr	Asp	Gln	Lys	Lys	Ala	Pro	Pro	
			865					870					875			
gtt	atg	gct	tac	tgg	gta	gta	ggg	aga	ctt	ttt	ctt	cat	cca	aaa	cct	2749
Val	Met	Ala	Tyr	Trp	Val	Val	Gly	Arg	Leu	Phe	Leu	His	Pro	Lys	Pro	
		880					885					890				
caa	gaa	ctt	tat	gtc	tgt	ttt	cat	gac	tca	gtc	aca	gaa	att	gcc	att	2797
Gln	Glu	Leu	Tyr	Val	Cys	Phe	His	Asp	Ser	Val	Thr	Glu	Ile	Ala	Ile	



895	900	905	
gaa ata gct ttt aaa ttg ttc ttt ggg tta acc ttg tag ctgtgctttc			2846
Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr Leu *			
910	915	920	
ttgatgcgta gaaacacgtg catggaggat caaacactgt cagaattgct gaaatcaata			2906
cacaaagaga taaagtttag cttcttttta ctattcaata ttgaacataa tattgttaaa			2966
tattgagatg aaatgctggt ggatttgata cattaaatct taatgtaata ttgtaagact			3026
tttgagaata tacttgatta aaatgtgaaa gaagggttg ttaacttatt gctatttttg			3086
tatataatgt taatttattg actagtttga aataatgtga agtgtttttt atatcagatt			3146
aatataggaa atgtttattc ttgaaaaata aaaaaaaaaa			3186

<210> 207  
 <211> 1595  
 <212> DNA  
 <213> Homo sapiens  
  
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 <222> (306)..(1496)  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(1595)  
 <223> n = a,t,c or g

<400> 207			
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gtggaaacat gtcttgcgac acccaccagc gactgctaca acccagcggc ggcgntgntg			120
gtcacggagc tggggccggg ggcagcccg gagctggctg gggccctgc aaggaccgtc			180
tcgggcctgc ccagccaaga gtgtgtgcaa cacatcgggtg ctgagcagca gcctgcagtc			240
actggagtat ctcatcaacg acatccggcc gccctgcatc aaggagcaga tgctgggcaa			300
gggct	atg aga cgg tgg ccg tgc ccc ggc tac tcg acc acc agc atg		347
	Met Arg Arg Trp Pro Cys Pro Gly Tyr Ser Thr Thr Ser Met		
	1 5 10		
ccc aca tcc gcc tac ccg tct aca gat aag gcc tgc ctg cgg aca tac			395
Pro Thr Ser Ala Tyr Pro Ser Thr Asp Lys Ala Cys Leu Arg Thr Tyr			
15	20	25	30
gga cat gcg gac agg gcg cag agc cgg gag gca ggc cgc aga aca ggg			443
Gly His Ala Asp Arg Ala Gln Ser Arg Glu Ala Gly Arg Arg Thr Gly			
	35	40	45



cac cac ttt cac cca aac ttg tat att tat tac aat ttt ctg cat ctt His His Phe His Pro Asn Leu Tyr Ile Tyr Tyr Asn Phe Leu His Leu 275 280 285	1163
gag gaa ggg gcg tca ttt tcc tgt tcg cac aaa ggc acc aca ggg gct Glu Glu Gly Ala Ser Phe Ser Cys Ser His Lys Gly Thr Thr Gly Ala 290 295 300	1211
aac agt ggg cct gca atc tta gat ccc atc ctt gcc ttc ttc gag gga Asn Ser Gly Pro Ala Ile Leu Asp Pro Ile Leu Ala Phe Phe Glu Gly 305 310 315	1259
tct ctt ggg acc ctc ctg gtt tta act ggg agg ccc aga cca act cct Ser Leu Gly Thr Leu Leu Val Leu Thr Gly Arg Pro Arg Pro Thr Pro 320 325 330	1307
ttc ctg caa acc acc ctc caa ggc ctg tcc cac acg atc aag gca ggg Phe Leu Gln Thr Thr Leu Gln Gly Leu Ser His Thr Ile Lys Ala Gly 335 340 345 350	1355
aaa gat agg cag gag tcc cct cac gaa gtc ctc aag tcc tgg ccc ctc Lys Asp Arg Gln Glu Ser Pro His Glu Val Leu Lys Ser Trp Pro Leu 355 360 365	1403
tgg cgc tct gga agc ggt act gta tct ctc tcc aag gcc tgg tca agc Trp Arg Ser Gly Ser Gly Thr Val Ser Leu Ser Lys Ala Trp Ser Ser 370 375 380	1451
act aag tgc att tac aaa tct ctg aga atg ttt ttt tta tac taa aat Thr Lys Cys Ile Tyr Lys Ser Leu Arg Met Phe Phe Leu Tyr * 385 390 395	1499
tgaccattat attctactgt gagaagtgc gtcctgcacta tattgtttta aaaacgaaga	1559
gaaagaagaa aaaggaaaac acagaaaaaa aaaaaa	1595

<210> 208  
<211> 1463  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (288)..(1235)

<400> 208 aaaataaccc tactaaagg gaataagctt gcggccgccc ggggagccgc gggagaggcg	60
gcggcggggg gaggaggag aggagggcc agccggcggc acgggaggcc cggttttgaa	120
gccgcttctc tgcccagatt aggtttcgcc cagcgcaatt tctttctcta tgtactttgc	180
gaataagttt cggagcatcg gttaacagcc tatgggtgaa atttggtttt cattcatgaa	240

tgagaaatta ttcttgacag aagtatttta aaagaaaaat ctttacg	atg gcc tca	296
	Met Ala Ser	
	1	
gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt gcc ctg tta		344
Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe Ala Leu Leu		
5 10 15		
caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga aaa ggt aaa		392
Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly Lys Gly Lys		
20 25 30 35		
ggt cga aat act gga aag tct caa act tta gga agc aag tca act aca		440
Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys Ser Thr Thr		
40 45 50		
aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa cag caa cag		488
Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu Gln Gln Gln		
55 60 65		
agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa att ccc cag		536
Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys Ile Pro Gln		
70 75 80		
aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt cca ttg tca		584
Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu Pro Leu Ser		
85 90 95		
aac cca gta cag aag gat tca cga gaa gaa aat tgg caa gag tgg aga		632
Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln Glu Trp Arg		
100 105 110 115		
caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca gat ctt gag		680
Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala Asp Leu Glu		
120 125 130		
aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac aaa aag gag		728
Lys Ala Leu Leu Ser Lys Leu Glu Tyr Glu Glu His Lys Lys Glu		
135 140 145		
tat gaa gat gct gaa aat act tca act cag tcc aaa gtt atg aat aaa		776
Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val Met Asn Lys		
150 155 160		
aaa gat aaa aga aag aat cat cag gga aaa gac aga cct ctc aca gta		824
Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro Leu Thr Val		
165 170 175		
tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa aag act gag		872
Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys Lys Thr Glu		
180 185 190 195		
gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag tta gag ctt		920
Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys Leu Glu Leu		
200 205 210		
gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta atc act caa		968

Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val Ile Thr Gln	
215 220 225	
tgg gag gca aag tat aag gaa gta aag gca aga aat gca caa tta ttg	1016
Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala Gln Leu Leu	
230 235 240	
aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa ata ctt ctg	1064
Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu Ile Leu Leu	
245 250 255	
caa gtt gat gaa tca caa agt atc aag aat gag ctc act att cag gtg	1112
Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr Ile Gln Val	
260 265 270 275	
act tca ctt cat gct gca tta gaa caa gaa aga tct aaa gtg aaa gta	1160
Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys Val Lys Val	
280 285 290	
tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa ggg aaa aga	1208
Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys Gly Lys Arg	
295 300 305	
aac tct gaa tcc gac cag tgt agg tga ttaca ttagcctttg aagtcaacac	1260
Asn Ser Glu Ser Asp Gln Cys Arg *	
310 315	
aaagtttaaa acttccagga ttttgcaaag ttgtatatat ttaatgctgt gcaactgcta	1320
aactatgcag tttttgttga aggaactaaa agcaactagc tccctaattgg tctataat	1380
tatttctttt ggcttaaagt gaaaaagaag aatagagatt ccagcagatt cagtgggtgt	1440
cactatccaa cttctatcac ttg	1463

<210> 209  
 <211> 751  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (160)..(399)

<400> 209	
cttccctttc ctgggaaaga aattcaatct tgttttctct tttattattg gattctctat	60
tctacagtta tgccccaata gtagccaaag gaaaaagggg gaagatgata gtttgactaa	120
acaaatacca gttcatacat tcttgttcca ataggagtt atg gga gga aaa att	174
Met Gly Gly Lys Ile	
1 5	
att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt	222



cctaacaagc acgcagttcc tgatgattgg cctcaggtcc cagagagctc cagcaggtgt 480  
aggagtccat gggcctgaca cctttgctgg tctctgctgg atcccgacga agtcaggtcc 540  
tttctggaaa ggggttcgaa gtccacatac tctccgact acccccagga agtacgtcct 600  
tgggtgtgtg tttgggggag tgagaggaat gaagaaccac tccccctata gcctggccat 660  
actccccaaag atgaggggcag taaggtgctg aggaccctgg aagtaacttg cttttctcaa 720  
cttctcagga gaaggccatc agcatttggg agtcaaagaa tttctttttt gaacttgagc 780  
ctctgccagg ggcctgggaa gctgtcaagg ag atg gcc agc cta caa aac act 833  
Met Ala Ser Leu Gln Asn Thr  
1 5  
gac gtc ttc atc tgc aca agc ccc atc aag atg ttc aag tac tgt ccc 881  
Asp Val Phe Ile Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro  
10 15 20  
tat gag aag tat gcc tgg gtg gag aag tac ttt ggc cct gac ttt ctg 929  
Tyr Glu Lys Tyr Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu  
25 30 35  
gag cag att gtg ctg acc aga gac aag acc gtg gtc tct gct gac ctt 977  
Glu Gln Ile Val Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu  
40 45 50 55  
ctc ata gac gac cgg ccg gac atc aca ggg gcc gag cca acc ccc agc 1025  
Leu Ile Asp Asp Arg Pro Asp Ile Thr Gly Ala Glu Pro Thr Pro Ser  
60 65 70  
tgg gag cat gtc ctc ttc acc gcc tgc cac aac cag cac ctg cag ctg 1073  
Trp Glu His Val Leu Phe Thr Ala Cys His Asn Gln His Leu Gln Leu  
75 80 85  
cag ccc ccc cgc cgc agg ctg cac tgc tgg gcg gac gac tgg aag gcc 1121  
Gln Pro Pro Arg Arg Arg Leu His Ser Trp Ala Asp Asp Trp Lys Ala  
90 95 100  
att ctg gac agc aag cgg ccc tgc tga gctgg actgtgcttc gggctcctct 1173  
Ile Leu Asp Ser Lys Arg Pro Cys \*  
105 110  
gtggggctct gacctcaggg ctcccagctc ggggcctgtg gggccagtat gctggctctgg 1233  
gagtcctctc tagactcctg ggccccatga cctcctgctg catgtccctt cccttcccca 1293  
gccccctgcca ggccttaacc tgatcacggg gcagggctgg gccctctggg cgcttgagaca 1353  
taacaacgtg gtcccaggcc gttcagcctg acctcaggca gcaggcacca agctgccaga 1413  
agcccagggg ctcaggacaa ggaggagttt aggccactgt tcagggggct ggtggccgtc 1473  
ttcactccct aaggcaagtt ttttaaggca aaaggggggt ccctgttccc aaagtgttga 1533

gccatcagca aggaggacca ggaacccggc gattgaggtg cttccaggtg gggacaagcc 1593  
 ccttttggtt tcagccacag cacccttat tccaggtgcc ctgccaacc tgctcacccc 1653  
 acatgacctt ttgtgtattc agcaaacct cattaggtga cagcggtccc caggctttgt 1713  
 gctggggggac gatactggcc ctggcctcga ccagcttaaa ggtttttcac acctttgttc 1773  
 ccagggtccc gctcagggcc cagcaaaaag tccgtaggct tgaacatgtg ttgagggcat 1833  
 gaaaaataaa tgctgttcat gtgtgtagct caaaaaaaaa aaa 1876

<210> 211  
 <211> 3051  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (527) .. (2308)

<400> 211  
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 caagcactgg catgtggccc tcccagaccg ggtcacaaga cgccagtgca agtgctggtt 120  
 aaccaggggt gctaaaaata accaggccca aatggaccag aagcaactcc catggacttt 180  
 ggcttgcagt catggtcaga agagatacag gcacagatcc cactattacg aaggagccaa 240  
 aatatctgcc aagataaaaa tggaagtaac tcctctggat ttatgtgtcc aggggtggat 300  
 atggaaagac ttgtgaagta ttaatcaaaa atcaccgag gctttttcag actattattc 360  
 aaatgacaca gaatgaagac ctccgagaaa acatgtacgg caagttctgg agcatttgtc 420  
 tcagcacagt gaaagccagt acctaaagat tctaacaagc cttgctgaag ttgctacaac 480  
 aaatggtcac aaactgctta gcctctctag caattatgat gctcaa atg aag agc 535  
 Met Lys Ser  
 1  
 ctt tta agg att gtg aga atg ttt tgt cac gtc ttt cga att ggt cca 583  
 Leu Leu Arg Ile Val Arg Met Phe Cys His Val Phe Arg Ile Gly Pro  
 5 10 15  
 tcc tcc ccc agt aat gga att gat atg ggc tac aat ggg aat aaa act 631  
 Ser Ser Pro Ser Asn Gly Ile Asp Met Gly Tyr Asn Gly Asn Lys Thr  
 20 25 30 35  
 cca aaa agc cag gtg ttc aag cct ctg gaa ttg ctt tgg cac tcg tta 679  
 Pro Lys Ser Gln Val Phe Lys Pro Leu Glu Leu Leu Trp His Ser Leu  
 40 45 50



gat gaa tgg cta gtt tta ata gcc cca gaa ttg atg aaa aac aaa aga Asp Glu Trp Leu Val Leu Ile Ala Pro Glu Leu Met Lys Asn Lys Arg	727
55 60 65	
gac tca aca gag atc act tct att tta ctg aaa caa aaa ggc caa gat Asp Ser Thr Glu Ile Thr Ser Ile Leu Leu Lys Gln Lys Gly Gln Asp	775
70 75 80	
caa gat gct gct tcc att cct cca ttt gaa cct cca gga cct ggg agc Gln Asp Ala Ala Ser Ile Pro Pro Phe Glu Pro Pro Gly Pro Gly Ser	823
85 90 95	
tat gaa aat ctg tcc act ggc aca agg gaa tct aaa cca gat gct ctt Tyr Glu Asn Leu Ser Thr Gly Thr Arg Glu Ser Lys Pro Asp Ala Leu	871
100 105 110 115	
gca ggg aga cag gaa gcc agt gca gat tgt cag gat gtt att tct atg Ala Gly Arg Gln Glu Ala Ser Ala Asp Cys Gln Asp Val Ile Ser Met	919
120 125 130	
aca gct aac cgg cta agt gct gtc att caa gct ttt tac atg tgc tgt Thr Ala Asn Arg Leu Ser Ala Val Ile Gln Ala Phe Tyr Met Cys Cys	967
135 140 145	
tct tgt cag atg cct ccg gga atg act tca cct cgt ttc att gaa ttt Ser Cys Gln Met Pro Pro Gly Met Thr Ser Pro Arg Phe Ile Glu Phe	1015
150 155 160	
gtc tgc aaa cat gat gaa gtt tta aaa tgc ttt gtt aat aga aat ccc Val Cys Lys His Asp Glu Val Leu Lys Cys Phe Val Asn Arg Asn Pro	1063
165 170 175	
aaa att ata ttt gac cac ttt cac ttt ctc ctt gaa tgt cct gag ttg Lys Ile Ile Phe Asp His Phe His Phe Leu Leu Glu Cys Pro Glu Leu	1111
180 185 190 195	
atg tca aga ttc atg cat atc ata aaa gca cag cct ttt aaa gat cgc Met Ser Arg Phe Met His Ile Ile Lys Ala Gln Pro Phe Lys Asp Arg	1159
200 205 210	
tgt gaa tgg ttc tat gaa cat ttg cat tca gga cag cca gat tca gat Cys Glu Trp Phe Tyr Glu His Leu His Ser Gly Gln Pro Asp Ser Asp	1207
215 220 225	
atg gtg cac agg cca gtg aat gaa aat gat atc ctg ctg gtt cac aga Met Val His Arg Pro Val Asn Glu Asn Asp Ile Leu Leu Val His Arg	1255
230 235 240	
gat tct att ttt agg agt agc tgt gaa gtt gtg tca aaa gca aat tgt Asp Ser Ile Phe Arg Ser Ser Cys Glu Val Val Ser Lys Ala Asn Cys	1303
245 250 255	
gca aag cta aag caa ggg att gct gta cgg ttc cat gga gaa gaa ggc Ala Lys Leu Lys Gln Gly Ile Ala Val Arg Phe His Gly Glu Glu Gly	1351
260 265 270 275	
atg ggt caa ggt gtt gtg cgt gag tgg ttt gat att ctg tcc aat gag	1399

Met	Gly	Gln	Gly	Val	Arg	Glu	Trp	Phe	Asp	Ile	Leu	Ser	Asn	Glu		
280				285				290								
ata	gtc	aat	cct	gat	tat	gca	ttg	ttt	acc	cag	tca	gct	gat	gga	aca	1447
Ile	Val	Asn	Pro	Asp	Tyr	Ala	Leu	Phe	Thr	Gln	Ser	Ala	Asp	Gly	Thr	
295				300				305								
act	ttt	cag	cct	aat	agc	aac	tct	tat	gta	aat	cct	gat	cac	ttg	aac	1495
Thr	Phe	Gln	Pro	Asn	Ser	Asn	Ser	Tyr	Val	Asn	Pro	Asp	His	Leu	Asn	
310				315				320								
tat	ttt	cgg	ttt	gct	ggg	cag	atc	ttg	gga	tta	gcg	ttg	aac	cac	agg	1543
Tyr	Phe	Arg	Phe	Ala	Gly	Gln	Ile	Leu	Gly	Leu	Ala	Leu	Asn	His	Arg	
325				330				335								
cag	ctg	gtc	aat	att	tac	ttc	aca	cga	tcc	ttc	tac	aag	cac	att	ctt	1591
Gln	Leu	Val	Asn	Ile	Tyr	Phe	Thr	Arg	Ser	Phe	Tyr	Lys	His	Ile	Leu	
340				345				350				355				
ggt	att	cct	gta	aat	tac	caa	gat	gtg	gca	tcc	att	gat	cca	gaa	tat	1639
Gly	Ile	Pro	Val	Asn	Tyr	Gln	Asp	Val	Ala	Ser	Ile	Asp	Pro	Glu	Tyr	
360				365				370								
gcg	aaa	aat	ttg	caa	tgg	att	tta	gat	aat	gat	ata	agt	gat	ctg	ggt	1687
Ala	Lys	Asn	Leu	Gln	Trp	Ile	Leu	Asp	Asn	Asp	Ile	Ser	Asp	Leu	Gly	
375				380				385								
cta	gaa	cta	act	ttt	tct	gtt	gag	act	gat	gtg	ttt	gga	gca	atg	gaa	1735
Leu	Glu	Leu	Thr	Phe	Ser	Val	Glu	Thr	Asp	Val	Phe	Gly	Ala	Met	Glu	
390				395				400								
gag	gtg	cct	ttg	aaa	cct	ggg	ggt	ggg	agt	att	ctt	gtg	aca	caa	aat	1783
Glu	Val	Pro	Leu	Lys	Pro	Gly	Gly	Gly	Ser	Ile	Leu	Val	Thr	Gln	Asn	
405				410				415								
aat	aaa	gcg	gag	tac	gtc	cag	ctt	gtt	act	gaa	ctt	cga	atg	aca	aga	1831
Asn	Lys	Ala	Glu	Tyr	Val	Gln	Leu	Val	Thr	Glu	Leu	Arg	Met	Thr	Arg	
420				425				430				435				
gcc	att	cag	cct	cag	atc	aat	gct	ttt	tta	cag	ggc	ttt	cat	atg	ttc	1879
Ala	Ile	Gln	Pro	Gln	Ile	Asn	Ala	Phe	Leu	Gln	Gly	Phe	His	Met	Phe	
440				445				450								
att	cca	ccc	tcc	ctc	ata	cag	ctt	ttt	gat	gaa	tat	gaa	ttg	gag	cta	1927
Ile	Pro	Pro	Ser	Leu	Ile	Gln	Leu	Phe	Asp	Glu	Tyr	Glu	Leu	Glu	Leu	
455				460				465								
ctg	ctt	tct	ggc	atg	cca	gaa	att	gat	gtg	agt	gat	tgg	ata	aaa	aat	1975
Leu	Leu	Ser	Gly	Met	Pro	Glu	Ile	Asp	Val	Ser	Asp	Trp	Ile	Lys	Asn	
470				475				480								
aca	gaa	tac	aca	agt	ggc	tat	gaa	aga	gaa	gat	cca	gtt	att	cag	tgg	2023
Thr	Glu	Tyr	Thr	Ser	Gly	Tyr	Glu	Arg	Glu	Asp	Pro	Val	Ile	Gln	Trp	
485				490				495								
ttc	tgg	gaa	gtt	gta	gaa	gac	att	act	caa	gag	gag	aga	gtt	ctt	ctc	2071
Phe	Trp	Glu	Val	Val	Glu	Asp	Ile	Thr	Gln	Glu	Glu	Arg	Val	Leu	Leu	

500	505	510	515	
tta cag ttt gtt acg ggc agt tcc agg gtc cca cat ggt ggg ttt gct				2119
Leu Gln Phe Val Thr Gly Ser Ser Arg Val Pro His Gly Gly Phe Ala				
	520	525	530	
aat atc atg ggt gga agt gga ttg caa aac ttt aca atc gct gct gtg				2167
Asn Ile Met Gly Gly Ser Gly Leu Gln Asn Phe Thr Ile Ala Ala Val				
	535	540	545	
cca tat act cca aat ctt tta cca act tca agc aca tgc atc aac atg				2215
Pro Tyr Thr Pro Asn Leu Leu Pro Thr Ser Ser Thr Cys Ile Asn Met				
	550	555	560	
ctc aag tta cct gaa tac cca agt aaa gaa ata ctc aag gac aga ctt				2263
Leu Lys Leu Pro Glu Tyr Pro Ser Lys Glu Ile Leu Lys Asp Arg Leu				
	565	570	575	
ctt gtg gca cta cat tgt ggc agc tat ggt tac aca atg gca taa tga				2311
Leu Val Ala Leu His Cys Gly Ser Tyr Gly Thr Met Ala *				
	580	585	590	
agtctggaaa actcctctga ctactgatgc acaattcaga atggcagaag taatttgga				2371
aaatgtcaac aaaaaagcag cctaaatgca acccataggc agggctgatg cttccaattt				2431
ataaaggatc atcagggtttt ctgtttctct cttttccctt ttatgttttc tctgtttgta				2491
tacaattaga aaatataaaa tcacagtaga ttttattttt taaaatgcta actgaaagta				2551
atagagactg tccttttttca taattaattt tatccaagat tgtattaagg caaaatctga				2611
ttctacattc cacctctgct atgtaactgt cttgttaaaa ggggtgttttc tcctaatttc				2671
tgatatatta tatgaggtca tccagctggg gtgttctttt gcatgtaaac tgccatttat				2731
attttagaaa actattgtat agaatggatt tagattgtct ataaagccac aaatacgtat				2791
tttgccacag tgtattctat attgcaatga tttttttagc attttaatat tttaatatat				2851
attgtaaaat ttagactgat gatactaaca gttgatgaaa tgacatatataa tttatatatg				2911
aaagcttacg ctatatgtga tgaattattt gcatctttca gtggccagtt ttccatatgt				2971
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taaaatgtaa aaaaaaaaaa				3051

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 <212> DNA  
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 <220>

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 <222> (634)..(1122)

<220>  
 <221> misc\_feature  
 <222> (1)...(1435)  
 <223> n = a,t,c or g

<400> 212

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ggtgtacacg agtggagaac tgacacaggc gcctgcaaat cagccgggag ttcctggcct	120
tggctcctcc tccagcccct tggctctctg ctgctcccc cggggcagga gaaagaagga	180
aagagggcca ggggtcccct gccccaccac tttccatgat gacaagagat gggaaggtag	240
ccaggcagca acagtgtacg gcgacattgg agcggacctc acggcgacct caatttccac	300
tgcgcctcct cccagagctt aagaagctgc aggcctgtgg tgcccagcac caagtgcaga	360
tggacacggg tcttcatccc cttccttggc accttccatt taagccaaac attagaaatg	420
taaagaaggg cttgtttctg gagtttccag tttgttccat tcatctactc agagcatctt	480
ctttggacaa cactgtctgc agctgtgggc ccactccaag gggaggcgat ggactgtagg	540
tctgtggagc tcagcacagg gctgtgccac ggacgcgggt gtcagtgaag tcacgcgcac	600
tttcagatgg aattctcctc cccgatgtga aca atg aac gac ggt gtc act ttc	654
Met Asn Asp Gly Val Thr Phe	
1 5	
ata gga ttg tcc tgg agc cca cgg aga cgc ggg ctt ggg att caa cgt	702
Ile Gly Leu Ser Trp Ser Pro Arg Arg Arg Gly Leu Gly Ile Gln Arg	
10 15 20	
gat gct gag cgg atc ttc tct gct tca gac cag gcc tca tgt ggc ttc	750
Asp Ala Glu Arg Ile Phe Ser Ala Ser Asp Gln Ala Ser Cys Gly Phe	
25 30 35	
act att cat cca cac ata gat gct gca gag aca ctg agg gga ctc aca	798
Thr Ile His Pro His Ile Asp Ala Ala Glu Thr Leu Arg Gly Leu Thr	
40 45 50 55	
aat gca cct gtg cag aag gtg tca acg tgg aca aac aca ggc agg gaa	846
Asn Ala Pro Val Gln Lys Val Ser Thr Trp Thr Asn Thr Gly Arg Glu	
60 65 70	
act ccc atg agc ccg tgt gcc aca tgc agt gag gga act ttg gtg gct	894
Thr Pro Met Ser Pro Cys Ala Thr Cys Ser Glu Gly Thr Leu Val Ala	
75 80 85	
gag tct ggg cgg ggg tgg gct ggg ggc tca atc gat ttc cac cga gtg	942
Glu Ser Gly Arg Gly Trp Ala Gly Gly Ser Ile Asp Phe His Arg Val	
90 95 100	

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tgt ctc caa atc ttt gct gga agt gca ggc aag ggg caa ggc ttg gac      990
Cys Leu Gln Ile Phe Ala Gly Ser Ala Gly Lys Gly Gln Gly Leu Asp
    105                110                115

acc agc gtc gct gtt cct cca ggc tgg gct gat ccc ttt tta ttt cca      1038
Thr Ser Val Ala Val Pro Pro Gly Trp Ala Asp Pro Phe Leu Phe Pro
    120                125                130                135

agt cac agg agc ctg ttc cct gaa atc ctg ggg aag tgt ggt gag gtg      1086
Ser His Arg Ser Leu Phe Pro Glu Ile Leu Gly Lys Cys Gly Glu Val
           140                145                150

gcc ccg tgc cgt cga atc ccc atc ctg gtt tac tga agtg cagaagtgac      1136
Ala Pro Cys Arg Arg Ile Pro Ile Leu Val Tyr  *
           155                160

ataagtgcctt gtgaatcagc agggagctct tggccttgac tccctgtgca gatgagccca      1196

gggcgccagc tccttgctgg agaactcctt tgtccatttg cacgtatgga tctttcctca      1256

ctgcttgatg ttttgaactc tcttctttgc gggtattaat gagatactca aagggtggtca      1316

tcttcttggc ctctatttca gccacgagct tccatggagg ggccaaactc tccatgcttc      1376

tttccctaaa caccaacacc gtgagagccg atgtcttggtg actatttctg gagactggg      1435

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<211> 1600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (469)..(1380)

<400> 213
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gaaaaaaaaa gaaaaaatat atattatata ttaaatggcg aaaatggtaa attttatgtt      120

atgtgtatatt caccacaatt taagaaatat gtaatttgag gcttggagaa ttttaattaag      180

tgatttatct gatgttaact tacagctgat acatggtaga gctgcatttt aatctcagtc      240

atctggctct ttttaaaaca attacagaga aaactttatt ttgggccatt taggaggttt      300

agatcatttt gatcatcttc agctgtcttc tcttcacata caggaaaggc cttggaaagc      360

agtcgttgcg ccagacagcc cagggaagag cggcagcctg aggacctagg gccacctgct      420

gttccctggg attcatgtcc ttctggggag gagggaggac ccaggaca atg gct gct      477
                                Met Ala Ala
                                1

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gtt cat gat ctg gag atg gag agc atg aat ctg aat atg ggg aga gag	525
Val His Asp Leu Glu Met Glu Ser Met Asn Leu Asn Met Gly Arg Glu	
5 10 15	
atg aaa gaa gag ctg gag gaa gag gag aaa atg aga gag gat ggg gga	573
Met Lys Glu Glu Leu Glu Glu Glu Glu Lys Met Arg Glu Asp Gly Gly	
20 25 30 35	
ggt aaa gat cgg gcc aag agt aaa aag gtc cac agg att gtc tca aaa	621
Gly Lys Asp Arg Ala Lys Ser Lys Lys Val His Arg Ile Val Ser Lys	
40 45 50	
tgg atg ctg ccc gaa aag tcc cga gga aca tac ttg gag aga gct aac	669
Trp Met Leu Pro Glu Lys Ser Arg Gly Thr Tyr Leu Glu Arg Ala Asn	
55 60 65	
tgc ttc ccg cct ccc gtg ttc atc atc tcc atc agc ctg gcc gag ctg	717
Cys Phe Pro Pro Pro Val Phe Ile Ile Ser Ile Ser Leu Ala Glu Leu	
70 75 80	
gca gtg ttt att tac tat gct gtg tgg aag cct cag aaa cag tgg atc	765
Ala Val Phe Ile Tyr Tyr Ala Val Trp Lys Pro Gln Lys Gln Trp Ile	
85 90 95	
acg ttg gac aca ggc atc ttg gag agt ccc ttt atc tac agt cct gag	813
Thr Leu Asp Thr Gly Ile Leu Glu Ser Pro Phe Ile Tyr Ser Pro Glu	
100 105 110 115	
aag agg gag gaa gcc tgg agg ttt atc tca tac atg ctg gta cat gct	861
Lys Arg Glu Glu Ala Trp Arg Phe Ile Ser Tyr Met Leu Val His Ala	
120 125 130	
gga gtt cag cac atc ttg ggg aat ctt tgt atg cag ctt gtt ttg ggt	909
Gly Val Gln His Ile Leu Gly Asn Leu Cys Met Gln Leu Val Leu Gly	
135 140 145	
att ccc ttg gaa atg gtc cac aaa ggc ctc cgt gtg ggg ctg gtg tac	957
Ile Pro Leu Glu Met Val His Lys Gly Leu Arg Val Gly Leu Val Tyr	
150 155 160	
ctg gca gga gtg att gca ggg tcc ctt gcc agc tcc atc ttt gac cca	1005
Leu Ala Gly Val Ile Ala Gly Ser Leu Ala Ser Ser Ile Phe Asp Pro	
165 170 175	
ctc aga tat ctt gtg gga gct tca gga gga gtc tat gct ctg atg gga	1053
Leu Arg Tyr Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Met Gly	
180 185 190 195	
ggc tat ttt atg aat gtt ctg gtg aat ttt caa gaa atg att cct gcc	1101
Gly Tyr Phe Met Asn Val Leu Val Asn Phe Gln Glu Met Ile Pro Ala	
200 205 210	
ttt gga att ttc aga ctg ctg atc atc atc ctg ata att gtg ttg gac	1149
Phe Gly Ile Phe Arg Leu Leu Ile Ile Ile Leu Ile Ile Val Leu Asp	
215 220 225	
atg gga ttt gct ctc tat aga agg ttc ttt gtt cct gaa gat ggg tct	1197

Met Gly Phe Ala Leu Tyr Arg Arg Phe Phe Val Pro Glu Asp Gly Ser  
230 235 240

ccg gtg tct ttt gca gct cac att gca ggt gga ttt gct gga atg tcc 1245  
Pro Val Ser Phe Ala Ala His Ile Ala Gly Gly Phe Ala Gly Met Ser  
245 250 255

att ggc tac acg gtg ttt agc tgc ttt gat aaa gca ctg atg aaa gat 1293  
Ile Gly Tyr Thr Val Phe Ser Cys Phe Asp Lys Ala Leu Met Lys Asp  
260 265 270 275

cca agg ttt tgg ata gca att gct gca tat tta gct tgt gtc tta ttt 1341  
Pro Arg Phe Trp Ile Ala Ile Ala Ala Tyr Leu Ala Cys Val Leu Phe  
280 285 290

gct gtg ttt ttc aac att ttc cta tct cca gca aac tga cctgccccta 1390  
Ala Val Phe Phe Asn Ile Phe Leu Ser Pro Ala Asn \*

295 300

ttgtaagtca attaataaaa agagccatct ggaggaaata ataaaaaaaaa ggaagactct 1450

atgaagaaac agagaagtct cagcaaaggc taacaatttt atatagagga caaaacagca 1510

ttaaactcat cagttgcaaa gattgcctat aaaaggacct taggatttaa ggaaggggct 1570

tcttaatgta gaaagggaaa aaaaaaaaaa 1600

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<212> DNA  
<213> Homo sapiens

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<222> (232)..(1086)

<400> 214

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ttgaaaaagc tgcattgcagt tggaagggat cttcagatgg tgctgggtgac tttctgttcc 120

ttttggagtt gacatgcatg tggattggag gaaaaataat caacatatat tctcctttcg 180

tactgttttaa atcacaggaa gaagcggctt taagacaaag atcaaacc aa a atg aca 237  
Met Thr  
1

act gct cac ttt tac tgt caa tac tgc aca gca tca ctt ctt ggg aag 285  
Thr Ala His Phe Tyr Cys Gln Tyr Cys Thr Ala Ser Leu Leu Gly Lys  
5 10 15

aaa tat gta cta aag gat gac agt cca tac tgt gtt aca tgt tat gat 333  
Lys Tyr Val Leu Lys Asp Asp Ser Pro Tyr Cys Val Thr Cys Tyr Asp  
20 25 30

cgt gta ttt tct aac tat tgc gag gaa tgc aaa aaa cca att gaa tct	381
Arg Val Phe Ser Asn Tyr Cys Glu Glu Cys Lys Lys Pro Ile Glu Ser	
35 40 45 50	
gat tct aag gat ctt tgt tac aaa gac cgg cac tgg cat gaa gga tgc	429
Asp Ser Lys Asp Leu Cys Tyr Lys Asp Arg His Trp His Glu Gly Cys	
55 60 65	
ttc aag tgc acc aaa tgc aat cac tct ttg gtg gaa aag cct ttt gct	477
Phe Lys Cys Thr Lys Cys Asn His Ser Leu Val Glu Lys Pro Phe Ala	
70 75 80	
gcc aag gat gag cgc ctg ctg tgc acg gag tgc tat tct aac gag tgc	525
Ala Lys Asp Glu Arg Leu Leu Cys Thr Glu Cys Tyr Ser Asn Glu Cys	
85 90 95	
tcc tcc aag tgc ttc cac tgc aag agg acc atc atg cct ggt tcc cgc	573
Ser Ser Lys Cys Phe His Cys Lys Arg Thr Ile Met Pro Gly Ser Arg	
100 105 110	
aaa atg gaa ttt aag gga aac tac tgg cat gaa acc tgt ttt gtg tgt	621
Lys Met Glu Phe Lys Gly Asn Tyr Trp His Glu Thr Cys Phe Val Cys	
115 120 125 130	
gag aat tgc cga caa cct ata ggg aca aag cct ttg atc tcc aaa gag	669
Glu Asn Cys Arg Gln Pro Ile Gly Thr Lys Pro Leu Ile Ser Lys Glu	
135 140 145	
agt ggc aat tat tgt gtg cca tgt ttt gag aag gag ttt gct cac tac	717
Ser Gly Asn Tyr Cys Val Pro Cys Phe Glu Lys Glu Phe Ala His Tyr	
150 155 160	
tgc aac ttt tgt aag aag gtg ata act tca ggt ggg ata aca ttt tgt	765
Cys Asn Phe Cys Lys Lys Val Ile Thr Ser Gly Gly Ile Thr Phe Cys	
165 170 175	
gac cag cta tgg cat aaa gag tgt ttt ctg tgt agt ggc tgt agg aaa	813
Asp Gln Leu Trp His Lys Glu Cys Phe Leu Cys Ser Gly Cys Arg Lys	
180 185 190	
gat ctc tgt gaa gaa cag ttc atg tcc aga gac gac tat cca ttc tgc	861
Asp Leu Cys Glu Glu Gln Phe Met Ser Arg Asp Asp Tyr Pro Phe Cys	
195 200 205 210	
atg gac tgc tac aac cat ctt tat gcc aac aag tgt gta gcc tgt tcc	909
Met Asp Cys Tyr Asn His Leu Tyr Ala Asn Lys Cys Val Ala Cys Ser	
215 220 225	
aaa ccc att agt ggt ctc aca ggt gcc aag ttt atc tgc ttt caa gac	957
Lys Pro Ile Ser Gly Leu Thr Gly Ala Lys Phe Ile Cys Phe Gln Asp	
230 235 240	
agc cag tgg cat agc gaa tgc ttt aac tgc ggg aaa tgc tct gtc tcc	1005
Ser Gln Trp His Ser Glu Cys Phe Asn Cys Gly Lys Cys Ser Val Ser	
245 250 255	



ttg gtg ggt aaa ggc ttc ctg acc cag aac aag gaa atc ttc tgc caa 1053  
 Leu Val Gly Lys Gly Phe Leu Thr Gln Asn Lys Glu Ile Phe Cys Gln  
 260 265 270  
 aaa tgt ggc tcc gga atg gac act gac atc tag gagacagt ccttgcccac 1104  
 Lys Cys Gly Ser Gly Met Asp Thr Asp Ile \*  
 275 280 285  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(1920)

<400> 215

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 1 5 10 15

ctc ctg ctg ctc ctg atg ctg gga tgc gtc ctg atg atg gtg gcg atg 96  
 Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met  
 20 25 30

ttg cac cct ccc cac cac acc ctg cac cag act gtc aca gcc caa gcc 144  
 Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala  
 35 40 45

agc aag cac agc cct gaa gcc agg tac cgc ctg gac ttt ggg gaa tcc 192  
 Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser  
 50 55 60

cag gat tgg gta ctg gaa gct gag gat gag ggt gaa gag tac agc cct 240  
 Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro  
 65 70 75 80

ctg gag ggc ctg cca ccc ttt atc tca ctg cgg gag gat cag ctg ctg 288  
 Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu  
 85 90 95

gtg gcc gtg gcc tta ccc cag gcc aga agg aac cag agc cag ggc agg 336  
 Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg  
 100 105 110

aga ggt ggg agc tac cgc ctc atc aag cag cca agg agg cag gat aag 384  
 Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys  
 115 120 125

gaa gcc cca aag agg gac tgg ggg gct gat gag gac ggg gag gtg tct 432  
 Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser

130	135	140	
gaa gaa gag gag ttg acc ccg ttc agc ctg gac cca cgt ggc ctc cag Glu Glu Glu Glu Leu Thr Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln 145 150 155 160			480
gag gca ctc agt gcc cgc atc ccc ctc cag agg gct ctg ccc gag gtg Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val 165 170 175			528
cgg cac cca ctg tgt ctg cag cag cac cct cag gac agc ctg ccc aca Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr 180 185 190			576
gcc agc gtc atc ctc tgt ttc cat gat gag gcc tgg tcc act ctc ctg Ala Ser Val Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu 195 200 205			624
cgg act gta cac agc atc ctc gac aca gtg ccc agg gcc ttc ctg aag Arg Thr Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys 210 215 220			672
gag atc atc ctc gtg gac gac ctc agc cag caa gga caa ctc aag tct Glu Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser 225 230 235 240			720
gct ctc agc gaa tat gtg gcc agg ctg gag ggg gtg aag tta ctc agg Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu Arg 245 250 255			768
agc aac aag agg ctg ggt gcc atc agg gcc cgg atg ctg ggg gcc acc Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly Ala Thr 260 265 270			816
aga gcc acc ggg gat gtg ctc gtc ttc atg gat gcc cac tgc gag tgc Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His Cys Glu Cys 275 280 285			864
cac cca ggc tgg ctg gag ccc ctc ctc agc aga ata gct ggt gac agg His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile Ala Gly Asp Arg 290 295 300			912
agc cga gtg gta tct ccg gtg ata gat gtg att gac tgg aag act ttc Ser Arg Val Val Ser Pro Val Ile Asp Val Ile Asp Trp Lys Thr Phe 305 310 315 320			960
cag tat tac ccc tca aag gac ctg cag cgt ggg gtg ttg gac tgg aag Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg Gly Val Leu Asp Trp Lys 325 330 335			1008
ctg gat ttc cac tgg gaa cct ttg cca gag cat gtg agg aag gcc ctc Leu Asp Phe His Trp Glu Pro Leu Pro Glu His Val Arg Lys Ala Leu 340 345 350			1056
cag tcc ccc ata agc ccc atc agg agc cct gtg gtg ccc gga gag gtg Gln Ser Pro Ile Ser Pro Ile Arg Ser Pro Val Val Pro Gly Glu Val 355 360 365			1104

gtg gcc atg gac aga cat tac ttc caa aac act gga gcg tat gac tct	1152
Val Ala Met Asp Arg His Tyr Phe Gln Asn Thr Gly Ala Tyr Asp Ser	
370 375 380	
ctt atg tcg ctg cga ggt ggt gaa aac ctc gaa ctg tct ttc aag gcc	1200
Leu Met Ser Leu Arg Gly Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala	
385 390 395 400	
tgg ctc tgt ggt ggc tct gtt gaa atc ctt ccc tgc tct cgg gta gga	1248
Trp Leu Cys Gly Gly Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly	
405 410 415	
cac atc tac caa aat cag gat tcc cat tcc ccc ctc gac cag gag gcc	1296
His Ile Tyr Gln Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala	
420 425 430	
acc ctg agg aac agg gtt cgc att gct gag acc tgg ctg ggg tca ttc	1344
Thr Leu Arg Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe	
435 440 445	
aaa gaa acc ttc tac aag cat agc cca gag gcc ttc tcc ttg agc aag	1392
Lys Glu Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys	
450 455 460	
gct gag aag cca gac tgc atg gaa cgc ttg cag ctg caa agg aga ctg	1440
Ala Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	
465 470 475 480	
ggt tgt cgg aca ttc cac tgg ttt ctg gct aat gtc tac cct gag ctg	1488
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu Leu	
485 490 495	
tac cca tct gaa ccc agg ccc agt ttc tct gga aag ctc cac aac act	1536
Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His Asn Thr	
500 505 510	
gga ctt ggg ctc tgt gca gac tgc cag gca gaa ggg gac atc ctg ggc	1584
Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp Ile Leu Gly	
515 520 525	
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Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg Gln Gln Gln Tyr	
530 535 540	
ctg cag cac acc agc agg aag gag att cac ttt ggc agc cca cag cac	1680
Leu Gln His Thr Ser Arg Lys Glu Ile His Phe Gly Ser Pro Gln His	
545 550 555 560	
ctg tgc ttt gct gtc agg cag gag cag gtg att ctt cag aac tgc acg	1728
Leu Cys Phe Ala Val Arg Gln Glu Gln Val Ile Leu Gln Asn Cys Thr	
565 570 575	
gag gaa ggc ctg gcc atc cac cag cag cac tgg gac ttc cag gag aat	1776
Glu Glu Gly Leu Ala Ile His Gln Gln His Trp Asp Phe Gln Glu Asn	
580 585 590	

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Gly Met Ile Val His Ile Leu Ser Gly Lys Cys Met Glu Ala Val Val
      595                      600                      605

caa gaa aac aat aaa gat ttg tac ctg cgt ccg tgt gat gga aaa gcc      1872
Gln Glu Asn Asn Lys Asp Leu Tyr Leu Arg Pro Cys Asp Gly Lys Ala
      610                      615                      620

cgc cag cag tgg cgt ttt gac cag atc aat gct gtg gat gaa cga tga      1920
Arg Gln Gln Trp Arg Phe Asp Gln Ile Asn Ala Val Asp Glu Arg *
      625                      630                      635                      640

atgtcaatgt cagaaggaaa agagaatttt ggccatcaaa atccagctcc aagtgaactt      1980

aaagagctta tataatttcat gaagctgata cttttgtgtg tgtgctcctg gtgttaggag      2040

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ccccactga agggcaaagt ccagcggatt ctacactgga ggtggacgga gccccctgcc      180

cccttc      atg gtg ggg ctg ccg ggg cct gac gtg gag ccc agc ctc cct      228
      Met Val Gly Leu Pro Gly Pro Asp Val Glu Pro Ser Leu Pro
      1                      5                      10

cca cct aag ccc ctg gag ggc atc cct gag aga gag ttc ttt gtc aag      276
Pro Pro Lys Pro Leu Glu Gly Ile Pro Glu Arg Glu Phe Phe Val Lys
      15                      20                      25                      30

tgg gca ggg ctg tcc tac tgg cat tgc tcc tgg gtg aag gag cta cag      324
Trp Ala Gly Leu Ser Tyr Trp His Cys Ser Trp Val Lys Glu Leu Gln
      35                      40                      45

ctg gag ctg tac cac acg gtg atg tat cgc aac tac caa aga aag aac      372
Leu Glu Leu Tyr His Thr Val Met Tyr Arg Asn Tyr Gln Arg Lys Asn
      50                      55                      60

gac atg gat gag ccg ccc ccc ttt gac tac ggc tct ggg gat gaa gac      420
Asp Met Asp Glu Pro Pro Pro Phe Asp Tyr Gly Ser Gly Asp Glu Asp

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65	70	75	
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gag gag cgc ttc tac cgc tat ggc atc aag cca gag tgg atg atg att Glu Glu Arg Phe Tyr Arg Tyr Gly Ile Lys Pro Glu Trp Met Met Ile 95 100 105 110			516
cac cga atc ctg aac cat agc ttt gac aag aag ggg gat gtg cac tac His Arg Ile Leu Asn His Ser Phe Asp Lys Lys Gly Asp Val His Tyr 115 120 125			564
ctg atc aag tgg aaa gac ctg ccc tat gac cag tgc acc tgg gag atc Leu Ile Lys Trp Lys Asp Leu Pro Tyr Asp Gln Cys Thr Trp Glu Ile 130 135 140			612
gat gac atc gac atc ccc tac tac gac aac ctc aag cag gcc tac tgg Asp Asp Ile Asp Ile Pro Tyr Tyr Asp Asn Leu Lys Gln Ala Tyr Trp 145 150 155			660
ggc cac agg gag ctg atg ctg gga gaa gac acc agg ctg ccc aag agg Gly His Arg Glu Leu Met Leu Gly Glu Asp Thr Arg Leu Pro Lys Arg 160 165 170			708
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ccg gac acg ccc att gtg gac ccc acg gtc aag ttc gac aag cag cca Pro Asp Thr Pro Ile Val Asp Pro Thr Val Lys Phe Asp Lys Gln Pro 195 200 205			804
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agc gcg ccc ctc tcc acc atc atc aac tgg gaa cgc gag ttt gag atg Ser Ala Pro Leu Ser Thr Ile Ile Asn Trp Glu Arg Glu Phe Glu Met 275 280 285			1044
tgg gcg ccc gac ttc tac gtg gtc acc tac acg ggg gac aag gag agc Trp Ala Pro Asp Phe Tyr Val Val Thr Tyr Thr Gly Asp Lys Glu Ser 290 295 300			1092

cgc tcg gtg att cgg gag aac gag ttt tcc ttt gag gac aac gcc att	1140
Arg Ser Val Ile Arg Glu Asn Glu Phe Ser Phe Glu Asp Asn Ala Ile	
305 310 315	
cgg agt ggg aag aag gta ttc cgt atg aag aaa gaa gtg cag atc aaa	1188
Arg Ser Gly Lys Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys	
320 325 330	
ttc cac gtg ctg ctc acc tcc tat gag ctc atc acc atc gac cag gcc	1236
Phe His Val Leu Leu Thr Ser Tyr Glu Leu Ile Thr Ile Asp Gln Ala	
335 340 345 350	
atc ctg ggc tcc atc gag tgg gcc tgc ctg gtg gta gat gag gcc cac	1284
Ile Leu Gly Ser Ile Glu Trp Ala Cys Leu Val Val Asp Glu Ala His	
355 360 365	
cgc ctc aag aac aac cag tcc aag ttt ttt agg gtc tta aac agc tac	1332
Arg Leu Lys Asn Asn Gln Ser Lys Phe Phe Arg Val Leu Asn Ser Tyr	
370 375 380	
aag att gat tac aag ctg ctg ctg aca ggg acc ccc ctt cag aac aac	1380
Lys Ile Asp Tyr Lys Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn	
385 390 395	
ctg gag gag ctg ttc cat ctc ctc aac ttc ctg act cca gag agg ttc	1428
Leu Glu Glu Leu Phe His Leu Leu Asn Phe Leu Thr Pro Glu Arg Phe	
400 405 410	
aac aac ctg gag ggc ttc ctg gag gag ttt gct gac atc tcc aag gaa	1476
Asn Asn Leu Glu Gly Phe Leu Glu Glu Phe Ala Asp Ile Ser Lys Glu	
415 420 425 430	
gac cag atc aag aag ctg cat gac ctg ctg ggg ccg cac atg ctc agg	1524
Asp Gln Ile Lys Lys Leu His Asp Leu Leu Gly Pro His Met Leu Arg	
435 440 445	
cgg ctc aag gct gac gtg ttc aag aac atg ccg gcc aag acc gag ctc	1572
Arg Leu Lys Ala Asp Val Phe Lys Asn Met Pro Ala Lys Thr Glu Leu	
450 455 460	
att gtc cgg gtg gag ctg agc cag atg cag aag aag tac tac aag ttc	1620
Ile Val Arg Val Glu Leu Ser Gln Met Gln Lys Lys Tyr Tyr Lys Phe	
465 470 475	
atc ctc aca cgg aac ttt gag gca ctg aac tcc aag ggg ggc ggc aac	1668
Ile Leu Thr Arg Asn Phe Glu Ala Leu Asn Ser Lys Gly Gly Gly Asn	
480 485 490	
caa gta tcg ctg ctc aac atc atg atg gac ctg aaa aag tgc tgc aac	1716
Gln Val Ser Leu Leu Asn Ile Met Met Asp Leu Lys Lys Cys Cys Asn	
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His Pro Tyr Leu Phe Pro Val Ala Ala Val Glu Ala Pro Val Leu Pro	
515 520 525	

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Asn Gly Ser Tyr Asp Gly Ser Ser Leu Val Lys Ser Ser Gly Lys Leu	
530 535 540	
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Met Leu Leu Gln Lys Met Leu Lys Lys Leu Arg Asp Glu Gly His Arg	
545 550 555	
gtg ctc atc ttc tcc cag atg acc aag atg ctg gac ctc ctg gag gac	1908
Val Leu Ile Phe Ser Gln Met Thr Lys Met Leu Asp Leu Leu Glu Asp	
560 565 570	
ttc ctg gag tac gaa ggc tac aag tat gag cgg att gat ggt ggc atc	1956
Phe Leu Glu Tyr Glu Gly Tyr Lys Tyr Glu Arg Ile Asp Gly Gly Ile	
575 580 585 590	
acc ggg ggc ctc cgg cag gag gca atc gac aga ttc aat gcc ccc ggg	2004
Thr Gly Gly Leu Arg Gln Glu Ala Ile Asp Arg Phe Asn Ala Pro Gly	
595 600 605	
gcc cag cag ttc tgc ttc ctc ctc tca acc cgg gca ggt ggt ctg ggc	2052
Ala Gln Gln Phe Cys Phe Leu Leu Ser Thr Arg Ala Gly Leu Gly	
610 615 620	
atc aac ctg gcc acg gcg gac act gtc atc atc tac gac tcg gac tgg	2100
Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile Tyr Asp Ser Asp Trp	
625 630 635	
aac ccg cac aat gac atc cag gcc ttc agc cgc gcc cac cgc atc ggc	2148
Asn Pro His Asn Asp Ile Gln Ala Phe Ser Arg Ala His Arg Ile Gly	
640 645 650	
cag aac aag aag gtg atg atc tac cgc ttc gtg act cgg gcc tcg gtg	2196
Gln Asn Lys Lys Val Met Ile Tyr Arg Phe Val Thr Arg Ala Ser Val	
655 660 665 670	
gag gag cgc atc acg cag gtg gcc aag cgc aag atg atg ctc acc cac	2244
Glu Glu Arg Ile Thr Gln Val Ala Lys Arg Lys Met Met Leu Thr His	
675 680 685	
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Leu Val Val Arg Pro Gly Leu Gly Ser Lys Ser Gly Ser Met Thr Lys	
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Gln Glu Leu Asp Asp Ile Leu Lys Phe Gly Thr Glu Glu Leu Phe Lys	
705 710 715	
gac gac gtg gag ggc atg atg tct cag ggc cag agg ccg gtc aca ccc	2388
Asp Asp Val Glu Gly Met Met Ser Gln Gly Gln Arg Pro Val Thr Pro	
720 725 730	
atc cct gat gtc cag tcc tcc aaa ggg ggg aac ttg gcc gcc agt gca	2436
Ile Pro Asp Val Gln Ser Ser Lys Gly Gly Asn Leu Ala Ala Ser Ala	
735 740 745 750	
aag aag aag cac ggt agc acc ccg cca ggt gac aac aag gac gtg gag	2484

Lys	Lys	Lys	His	Gly	Ser	Thr	Pro	Pro	Gly	Asp	Asn	Lys	Asp	Val	Glu		
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Asp	Ser	Ser	Val	Ile	His	Tyr	Asp	Asp	Ala	Ala	Ile	Ser	Lys	Leu	Leu		
			770					775					780				
gac	cgg	aac	cag	gac	gct	aca	gat	gac	acg	gag	cta	cag	aac	atg	aac	2580	
Asp	Arg	Asn	Gln	Asp	Ala	Thr	Asp	Asp	Thr	Glu	Leu	Gln	Asn	Met	Asn		
			785					790					795				
gag	tac	ctg	agc	tcc	ttc	aag	gtg	gcg	cag	tac	gtg	gtg	cgc	gag	gag	2628	
Glu	Tyr	Leu	Ser	Ser	Phe	Lys	Val	Ala	Gln	Tyr	Val	Val	Arg	Glu	Glu		
	800					805					810						
gac	ggc	gtg	gag	gag	gtg	gag	cgg	gaa	atc	atc	aag	cag	gag	gag	aac	2676	
Asp	Gly	Val	Glu	Glu	Val	Glu	Arg	Glu	Ile	Ile	Lys	Gln	Glu	Glu	Asn		
	815				820					825					830		
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Val	Asp	Pro	Asp	Tyr	Trp	Glu	Lys	Leu	Leu	Arg	His	His	Tyr	Glu	Gln		
				835					840					845			
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Gln	Gln	Glu	Asp	Leu	Ala	Arg	Asn	Leu	Gly	Lys	Gly	Lys	Arg	Ile	Arg		
			850					855					860				
aag	cag	gtc	aac	tac	aac	gat	gcc	tcc	cag	gag	gac	cag	gag	tgg	cag	2820	
Lys	Gln	Val	Asn	Tyr	Asn	Asp	Ala	Ser	Gln	Glu	Asp	Gln	Glu	Trp	Gln		
			865				870					875					
gat	gag	ctc	tct	gat	aac	cag	tca	gaa	tat	tcc	att	ggc	tct	gag	gat	2868	
Asp	Glu	Leu	Ser	Asp	Asn	Gln	Ser	Glu	Tyr	Ser	Ile	Gly	Ser	Glu	Asp		
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gag	gat	gag	gac	ttt	gaa	gag	agg	ccg	gaa	ggg	cag	agt	gga	cga	cga	2916	
Glu	Asp	Glu	Asp	Phe	Glu	Glu	Arg	Pro	Glu	Gly	Gln	Ser	Gly	Arg	Arg		
	895				900					905					910		
caa	tcc	cgg	agg	cag	ctg	aag	agt	gac	agg	gac	aag	ccc	ctg	ccc	ccg	2964	
Gln	Ser	Arg	Arg	Gln	Leu	Lys	Ser	Asp	Arg	Asp	Lys	Pro	Leu	Pro	Pro		
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ctt	ctc	gcc	cga	gtt	ggt	ggc	aac	atc	gag	gtg	ctg	ggc	ttc	aat	gcc	3012	
Leu	Leu	Ala	Arg	Val	Gly	Gly	Asn	Ile	Glu	Val	Leu	Gly	Phe	Asn	Ala		
			930					935					940				
cga	cag	cgg	aag	gcc	ttt	ctg	aac	gcc	atc	atg	cgc	tgg	ggc	atg	ccc	3060	
Arg	Gln	Arg	Lys	Ala	Phe	Leu	Asn	Ala	Ile	Met	Arg	Trp	Gly	Met	Pro		
			945				950					955					
ccg	cag	gac	gcc	ttc	aac	tcc	cac	tgg	ctg	gtg	cgg	gac	ctt	cga	ggg	3108	
Pro	Gln	Asp	Ala	Phe	Asn	Ser	His	Trp	Leu	Val	Arg	Asp	Leu	Arg	Gly		
	960					965					970						
aag	agc	gag	aag	gag	ttt	aga	gcc	tat	gtg	tcc	ctc	ttc	atg	cgg	cac	3156	
Lys	Ser	Glu	Lys	Glu	Phe	Arg	Ala	Tyr	Val	Ser	Leu	Phe	Met	Arg	His		



975	980	985	990	
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Leu Cys Glu Pro Gly Ala Asp Gly Ala Glu Thr Phe Ala Asp Gly Val	995	1000	1005	
ccc cgg gag ggc ctc tcc agg cag cac gtg ctg acc cgc atc ggg gtc				3252
Pro Arg Glu Gly Leu Ser Arg Gln His Val Leu Thr Arg Ile Gly Val	1010	1015	1020	
atg tca cta gtt agg aag aag gtt cag gag ttt gag cat gtc aac ggg				3300
Met Ser Leu Val Arg Lys Lys Val Gln Glu Phe Glu His Val Asn Gly	1025	1030	1035	
aag tac agc acc cca gac ttg atc cct gag ggg ccc gag ggg aag aag				3348
Lys Tyr Ser Thr Pro Asp Leu Ile Pro Glu Gly Pro Glu Gly Lys Lys	1040	1045	1050	
ccg ggc gag gtg atc tcc tcg gac ccc aac aca cca gtg ccc gcc agc				3396
Pro Gly Glu Val Ile Ser Ser Asp Pro Asn Thr Pro Val Pro Ala Ser	1055	1060	1065	1070
cct gcc cac ctc ctg cca gcc ccg ctg ggc ctg cca gac aaa atg gaa				3444
Pro Ala His Leu Leu Pro Ala Pro Leu Gly Leu Pro Asp Lys Met Glu	1075	1080	1085	
gcc cag ctg ggc tac atg gat gag aaa gac ccc ggg gca cag aag cca				3492
Ala Gln Leu Gly Tyr Met Asp Glu Lys Asp Pro Gly Ala Gln Lys Pro	1090	1095	1100	
agg cag ccc ctg gaa gtc cag gcc ctt cca gcc gcc ttg gat aga gtg				3540
Arg Gln Pro Leu Glu Val Gln Ala Leu Pro Ala Ala Leu Asp Arg Val	1105	1110	1115	
gag agt gag gac aag cac gag agc cca gcc agc aag gag aga gcc cga				3588
Glu Ser Glu Asp Lys His Glu Ser Pro Ala Ser Lys Glu Arg Ala Arg	1120	1125	1130	
gag gag cgg cca gag gag acg gag aag gcc ccg ccc tcc ccg gag cag				3636
Glu Glu Arg Pro Glu Glu Thr Glu Lys Ala Pro Pro Ser Pro Glu Gln	1135	1140	1145	1150
ctg ccg aga gag gag gtg ctt cct gag aag gag aag atc ctg gac aag				3684
Leu Pro Arg Glu Glu Val Leu Pro Glu Lys Glu Lys Ile Leu Asp Lys	1155	1160	1165	
ctg gag ctg agc ttg atc cac agc aga ggg gac agt tcc gaa ctc agg				3732
Leu Glu Leu Ser Leu Ile His Ser Arg Gly Asp Ser Ser Glu Leu Arg	1170	1175	1180	
cca gat gac acc aag gct gag gag aag gag ccc att gaa aca cag caa				3780
Pro Asp Asp Thr Lys Ala Glu Glu Lys Glu Pro Ile Glu Thr Gln Gln	1185	1190	1195	
aat ggt gac aaa gag gaa gat gac gag ggg aag aag gag gac aag aag				3828
Asn Gly Asp Lys Glu Glu Asp Asp Glu Gly Lys Lys Glu Asp Lys Lys	1200	1205	1210	



tac agc aac aac ttt ggg ccc aac ttc cgg ggc cct gga ccg gga ggg	4548
Tyr Ser Asn Asn Phe Gly Pro Asn Phe Arg Gly Pro Gly Pro Gly Gly	
1440 1445 1450	
att gtc aac tac aac cag atg ccc ctg ggg ccc tat gtg acc gat atc	4596
Ile Val Asn Tyr Asn Gln Met Pro Leu Gly Pro Tyr Val Thr Asp Ile	
1455 1460 1465 1470	
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Met Ala Ser Pro Asp Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp	
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gtg ccc tcg ggg gtc gcg ctg ttc ctc acc atc cct ttc gcc ttc ttc	155
Val Pro Ser Gly Val Ala Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe	
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ctg ccc gag ctg ata ttt ggg ttc ttg gtc tgg acc atg gta gcc gcc	203
Leu Pro Glu Leu Ile Phe Gly Phe Leu Val Trp Thr Met Val Ala Ala	
35 40 45	
acc cac ata gta tac ccc ttg ctg caa gga tgg gtg atg tat gtc tcg	251
Thr His Ile Val Tyr Pro Leu Leu Gln Gly Trp Val Met Tyr Val Ser	
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ctc acc tcg ttt ctc atc tcc ttg atg ttc ctg ttg tct tac ttg ttt	299
Leu Thr Ser Phe Leu Ile Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe	
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gga ttt tac aaa aga ttt gaa tcc tgg aga gtt ctg gac agc ctg tac	347
Gly Phe Tyr Lys Arg Phe Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr	
80 85 90 95	
cac ggg acc act ggc atc ctg tac atg agc gct gcc gtc cta caa gta	395
His Gly Thr Thr Gly Ile Leu Tyr Met Ser Ala Ala Val Leu Gln Val	
100 105 110	

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cat gcc acg att gtt tct gag aaa ctg ctg gac cca aga att tac tac      443
His Ala Thr Ile Val Ser Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr
      115                      120                      125

att aat tcg gca gcc tcg ttc ttc gcc ttc atc gcc acg ctg ctc tac      491
Ile Asn Ser Ala Ala Ser Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr
      130                      135                      140

att ctc cat gcc ttc agc atc tat tac cac tga tgcacagg cgccaggcca      542
Ile Leu His Ala Phe Ser Ile Tyr Tyr His *
      145                      150

agggggaaat gctctttgaa agctccaatt attggtcccc aaaagcagct tccaacgttt      602

gccatctgga tgacaaacgg aagatccact aaaacgtcca cgggattaac agaacgtcct      662

tgcagactga gcgatgacac cacactttgt ttggacattt aaattcactc tgctgaatag      722

gaggaagctt ttctttttcc tgggaaaaca actgtctctt ggaattatct gaccatgaac      782

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aggggaatac tcagtctgat cttttttttg tttgttttat tttgtttttt ttgagacgga      962

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ccaggcgcgc ccgctgctcg gtggcaggag ggccggcgga gcgcc      atg gcc tgc      174
                                   Met Ala Cys
                                   1

atc ctg aag aga aag tct gtg att gct gtg agc ttc ata gca gcg ttc      222
Ile Leu Lys Arg Lys Ser Val Ile Ala Val Ser Phe Ile Ala Ala Phe
      5                      10                      15

ctt ttc ctg ctg gtt gtg cgt ctt gta aat gaa gtg aat ttc cca ttg      270
Leu Phe Leu Leu Val Val Arg Leu Val Asn Glu Val Asn Phe Pro Leu

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Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile Pro Phe Ser	40	45	50	
tac aca tac agg cgg ccc ctt cga act cac tat gga tac ata aat gtg				366
Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr Ile Asn Val	55	60	65	
aag aca caa gag cct ttg caa ctg gac tgt gac ctt tgt gcc ata gtg				414
Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys Ala Ile Val	70	75	80	
tca aac tca ggt cag atg gtt ggc cag aag gtg gga aat gag ata gat				462
Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn Glu Ile Asp	85	90	95	
cga tcc tcc tgc att tgg aga atg aac aat gcc ccc acc aaa ggt tat				510
Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr Lys Gly Tyr	100	105	110	115
gaa gaa gat gtc ggc cgc atg acc atg att cga gtt gtg tcc cat acc				558
Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val Ser His Thr	120	125	130	
agc gtt cct ctt ttg cta aaa aac cct gat tat ttt ttc aag gaa gcg				606
Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe Lys Glu Ala	135	140	145	
aat act act att tgt gtt att tgg gga cct ttc cgc aat atg agg aaa				654
Asn Thr Thr Ile Cys Val Ile Trp Gly Pro Phe Arg Asn Met Arg Lys	150	155	160	
gat ggc aat ggc atc gtt tac aac atg ttg aaa aag aca gtt ggt atc				702
Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr Val Gly Ile	165	170	175	
tat ccg aat gcc caa ata tac gtg acc aca gag aag cgc atg agt tac				750
Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg Met Ser Tyr	180	185	190	195
tgt gat gga gtt ttt aag aag gaa act ggg aag gac agg ggg cat gca				798
Cys Asp Gly Val Phe Lys Lys Glu Thr Gly Lys Asp Arg Gly His Ala	200	205	210	
agg cga ctg ctg att tct aca gac act ttt taa gcgattac cagtgtctggc				849
Arg Arg Leu Leu Ile Ser Thr Asp Thr Phe *	215	220		
aagtggaact acctttccgg tcctcttaca agcatccagt cacttgctga aatgtcataa				909
gcgatataaa cctgctgaca ggccaggatc attgcatctc ctgcctcctc cttccacgta				969
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ctt gct tac agt gac tca gct ggt agc ttt tta aaa gaa gta gac cga Leu Ala Tyr Ser Asp Ser Ala Gly Ser Phe Leu Lys Glu Val Asp Arg 155 160 165	653
gac ata gaa caa ata gta aag tgt aca gac aat aag aga gag aac ctc Asp Ile Glu Gln Ile Val Lys Cys Thr Asp Asn Lys Arg Glu Asn Leu 170 175 180	701
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gat aac aaa aac act caa cgt aaa gac ccc tat tat gga gca gac tgg Asp Asn Lys Asn Thr Gln Arg Lys Asp Pro Tyr Tyr Gly Ala Asp Trp 200 205 210	797
gga ata ggg tgg tgg aca gct gta gtg ata atg ttg ata gta ggt ata Gly Ile Gly Trp Trp Thr Ala Val Val Ile Met Leu Ile Val Gly Ile 215 220 225 230	845
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caa gat tct cag tca cct gct gct caa cag gaa aca tag caattagctc Gln Asp Ser Gln Ser Pro Ala Ala Gln Gln Glu Thr *	1086
295 300 305	
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ccaataatag cttcaaaggc agaatttaga gagattgagg atgcttttgt ttttaacaaa	1206
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 gccgagggat cctccgagg acaccccagc agtggacggc agcacagaca cggacagg 178  
 atg ccc ttg aag ctc tac ttg cct ggt ggt aat tcc agg atg acc cag 226  
 Met Pro Leu Lys Leu Tyr Leu Pro Gly Gly Asn Ser Arg Met Thr Gln  
 1 5 10 15  
 gag agg ctg gaa aga gcg ttc aaa cgg cag ggc agc cag ccc gca cct 274  
 Glu Arg Leu Glu Arg Ala Phe Lys Arg Gln Gly Ser Gln Pro Ala Pro  
 20 25 30  
 gtc agg aaa aat cag ttg ctg ccg tct gac aag gtg gat ggt gag ctg 322  
 Val Arg Lys Asn Gln Leu Leu Pro Ser Asp Lys Val Asp Gly Glu Leu  
 35 40 45  
 ggt gcc ctg cgg ctc gag gat gtg gag gat gag ttg ata agg gaa gag 370  
 Gly Ala Leu Arg Leu Glu Asp Val Glu Asp Glu Leu Ile Arg Glu Glu  
 50 55 60  
 gtc atc ctg tcg cca gtc cca tca gtg ctc aag ttg cag aca gca tca 418  
 Val Ile Leu Ser Pro Val Pro Ser Val Leu Lys Leu Gln Thr Ala Ser  
 65 70 75 80  
 aaa cca att gac ctc tca gta gca aag gaa ata aag acc ctt ctg ttt 466  
 Lys Pro Ile Asp Leu Ser Val Ala Lys Glu Ile Lys Thr Leu Leu Phe  
 85 90 95

ggt tcc agc ttt tgc tgt ttc aat gaa gaa tgg aaa ctt cag agt ttt Gly Ser Ser Phe Cys Cys Phe Asn Glu Glu Trp Lys Leu Gln Ser Phe 100 105 110	514
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Phe	Leu	Lys	Thr	Pro	Arg	Phe	Pro	Ile	Trp	Val	Val	Cys	Ser	Glu	Ser	
				340				345					350			
cac	ttc	agc	atc	ctc	ttt	agc	ctg	cag	ccg	ggg	ctc	ctg	cgt	gac	tgg	1282
His	Phe	Ser	Ile	Leu	Phe	Ser	Leu	Gln	Pro	Gly	Leu	Leu	Arg	Asp	Trp	
		355					360					365				
agg	act	gag	agg	ctc	ttt	gac	ttg	tac	tac	tac	gat	ggc	ctg	gcc	aac	1330
Arg	Thr	Glu	Arg	Leu	Phe	Asp	Leu	Tyr	Tyr	Tyr	Asp	Gly	Leu	Ala	Asn	
	370					375					380					
cag	cag	gag	cag	atc	cgg	ctg	acc	att	gac	acc	acc	caa	acc	atc	tct	1378
Gln	Gln	Glu	Gln	Ile	Arg	Leu	Thr	Ile	Asp	Thr	Thr	Gln	Thr	Ile	Ser	
385					390				395					400		
gag	gac	aca	gac	aac	gac	ctt	gtc	cca	ccc	ctc	gag	ctc	tgc	atc	aga	1426
Glu	Asp	Thr	Asp	Asn	Asp	Leu	Val	Pro	Pro	Leu	Glu	Leu	Cys	Ile	Arg	
				405				410					415			
acc	aag	tgg	aag	ggg	gca	tca	gtg	aac	tgg	aac	ggc	tca	gac	ccc	atc	1474
Thr	Lys	Trp	Lys	Gly	Ala	Ser	Val	Asn	Trp	Asn	Gly	Ser	Asp	Pro	Ile	
			420					425					430			
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Leu	*															
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              Met Ser Leu Ser Arg Pro Gly Glu Thr Glu Pro Ile His
              1          5          10

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Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His
  15          20          25

acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc 505
Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Leu Gln Ser Pro
  30          35          40          45

cag gtg agt gag aag agg agt tgt ggg agg agg aga gaa ggg aag cga 553
Gln Val Ser Glu Lys Arg Ser Cys Gly Arg Arg Arg Glu Gly Lys Arg
          50          55          60

tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta 602
Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg  *
          65          70          75

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        Met Pro Ser Leu Glu Val Ile Thr Leu Arg Tyr Leu Ala Pro
        1          5          10

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Ala Val Met Leu Ser Leu Gly Pro Gly Ser Arg Gly Arg Ala Ser Arg	
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ccc tcc agt ggg acc cag cac tgt gac ata acc tgg aaa cct cca aca	203
Pro Ser Ser Gly Thr Gln His Cys Asp Ile Thr Trp Lys Pro Pro Thr	
35 40 45	
cag act gag ggc ggc ttc cag aag ggg agg ggc cgg gac agc gag agc	251
Gln Thr Glu Gly Gly Phe Gln Lys Gly Arg Gly Arg Asp Ser Glu Ser	
50 55 60	
tgg gcc tac cct gtg gcc ccc atg ttc agc cct cct tcc tca gag cct	299
Trp Ala Tyr Pro Val Ala Pro Met Phe Ser Pro Pro Ser Ser Glu Pro	
65 70 75	
cac ctg ggc ctc ctg atg gct cct gtc ccc tgc ctg ccc tgc tgt acg	347
His Leu Gly Leu Leu Met Ala Pro Val Pro Cys Leu Pro Cys Cys Thr	
80 85 90	
cct gcc cac cct tgg cct gtg tgc tcc gat aag cca ttg ctg tgt tca	395
Pro Ala His Pro Trp Pro Val Cys Ser Asp Lys Pro Leu Leu Cys Ser	
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Leu Gly Gln Ser Val Val Glu Pro Ser *	
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aga att cat aca gga gag aaa cct tat gaa tgt gat ata tgt ggg aaa Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asp Ile Cys Gly Lys 350 355 360	1165
gat ttt agc cat cat gca tca ctc act cag cat caa aga gta cat tct Asp Phe Ser His His Ala Ser Leu Thr Gln His Gln Arg Val His Ser 365 370 375 380	1213
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aaggtagata aattcacgaa gatgaggaga aaccagtgc aaaaagcctga aaattccaaa	3182
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atggagctga aaaacacagc atgagaactt cgtgaagcat acagaagaaa aaccttcagc	3482
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cacattcaat gggttgcata cccatgaatt ctaaaacttc atcctctttt gtccctttcg	3962
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<210> 224
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (578)..(916)

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gcagaggagg cttaaggctg gcctgggaga gattcttggc ctagctccca gcacggagcc 180
ttgcttgtgt cccagggcgg cactaaccag aaccagaaaa ggaaatcttt ggccctcggg 240
gagaattatg ccaattatct gtctggttcc tgtctttgaa aatgcccgaga tgttggttta 300
caaatcagga agctgtcttg gggcaatctc tgttccctct ttgatgcaga gagcctttct 360
ctgtaaacac tggagagcag ggcttcactg tctggctccc ctccgcctc ttgcaggaag 420
gactagatgc tgctgatcag ctgatcatgg ctgagccggg tagagcttgg ggctctccta 480
agaggtcacc cactgggagg gagcttcaca gctgttcttt tgaccagga aggagctctt 540
tcaggactgt ggcaccagca gccgtggccc tctgcc atg cca ttg ttc cca ctt 595

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Met Pro Leu Phe Pro Leu  
1 5

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ccc tgc cct tgg gag tct tgg aga cag ctg act agc tgc cct gag ggg      643
Pro Cys Pro Trp Glu Ser Trp Arg Gln Leu Thr Ser Cys Pro Glu Gly
          10          15          20

tcc acc gct ctc acc ttc tca ctg gtg gct gct gcc att ctc ctg ggc      691
Ser Thr Ala Leu Thr Phe Ser Leu Val Ala Ala Ala Ile Leu Leu Gly
          25          30          35

tct gca cag aaa gct ttg gtc ctt ctg aaa gcc act ctg ccc ctt cct      739
Ser Ala Gln Lys Ala Leu Val Leu Leu Lys Ala Thr Leu Pro Leu Pro
          40          45          50

gca gca cca gat ccc cct gag ccg gta ctg ctg cct cca cct ggg cca      787
Ala Ala Pro Asp Pro Pro Glu Pro Val Leu Leu Pro Pro Pro Gly Pro
          55          60          65          70

aga cta gtc ttg gtg ttc acc ctt ctt cgt gct tca gaa agt agg gat      835
Arg Leu Val Leu Val Phe Thr Leu Leu Arg Ala Ser Glu Ser Arg Asp
          75          80          85

atc tgg gga cat gac tgt gtt tcc ctg ggg tcc ttt cag aag aga ctt      883
Ile Trp Gly His Asp Cys Val Ser Leu Gly Ser Phe Gln Lys Arg Leu
          90          95          100

agg aag ctc ctg ctc agg aat ctg gcc ctc tga aagagccc cttcaaagca      934
Arg Lys Leu Leu Leu Arg Asn Leu Ala Leu *
          105          110

gcctggggcag caggtaacgt gggtttccctt gcggccccct cctcccagct gcatagactc      994

gtgggtttgaa gtgaacagat cttgtccgga ac      1026

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<210> 225  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (70)..(609)

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accgccaag      atg gtg gtg ggc gcg ttc cct atg gcg aag ctg cta tac      108
                Met Val Val Gly Ala Phe Pro Met Ala Lys Leu Leu Tyr
                1          5          10

ttg ggc atc cgg cag gtc agc aag ccg ctt gcc aac cgt att aag gag      156
Leu Gly Ile Arg Gln Val Ser Lys Pro Leu Ala Asn Arg Ile Lys Glu
          15          20          25

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gcc gcc cgc cga agc gag ttc ttc aag acc tat atc tgc ctc ccg ccg	204
Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu Pro Pro	
30 35 40 45	
gct caa ctg tat cac tgg gtg gag atg cgg acc aag atg cgc atc atg	252
Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met	
50 55 60	
ggc ttc cgg ggc acg gtc atc aag ccg ctg aac gag gag gcg gca gct	300
Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala	
65 70 75	
gag ctg ggc gca gag ctg ctg ggc gaa gcc acc atc ttc atc gtg ggc	348
Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly	
80 85 90	
ggc ggc tgc cta gtg ctg gag tac tgg cgc cac cag gcg cag cag cgc	396
Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg	
95 100 105	
cac aag gag gag gag cag cgt gct gcc tgg aac gcg ctg cgg gac gag	444
His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu	
110 115 120 125	
gtg ggc cac ctg gcg ctg gcg ctg gaa gcg ctg cag gcg cag gtg cag	492
Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln	
130 135 140	
gcg gcg ccg cca cag ggc gcc ctg gag gaa ctg cgc aca gag ctg caa	540
Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu Leu Gln	
145 150 155	
gag gtg cgc gcc cag ctc tgc aat ccc ggc cgg tcc gct tcc cac gca	588
Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser His Ala	
160 165 170	
gtg cct gcg tcc aag aaa tag ga gcttgctgga tggaacctga atttggacat	641
Val Pro Ala Ser Lys Lys *	
175 180	
ggcctatgta cctaacgtgg ccttcttccc gcaccaccct tgccctgcgct ggcccagtg	701
aaaccaccag gatcttgatg caacttggca tttggttacc cctgctgata agagcagcca	761
ttacctgcca ctgggaccag caggtgaagc gttgcaacat agccccctcc atcatccttc	821
acctcctatc cccactcca aaccaggacg acctgcaagg tcccagccag caggacaccg	881
tgggcactct ggcaaataaa aaaatggaac ctggtcttga gctgaatcaa tgtgttattg	941
ttacccccac ccccggttta cctgatcagt gttaaccttt actgggacac tcatctgtta	1001
caactggaaca ccttcttctt tttgtcaatc ggcacagacc actgtaagga aatgcagtgt	1061
gttgcaagtgg ccttttctcc ccctcacctt ctaaggtcag ctctagctga gcatcagtgc	1121

tctcttaagg aggaaaaaaa cgggtgcggtg gggagcggtg gctcacgcct gtaatcctag 1181  
caccttggga ggccgaggcg ggcggatcac ttgaggtcag gagttccaga ccagcctggc 1241  
caacatggtg aaactccgtc tttcta 1267

<210> 226  
<211> 1813  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (494)..(1126)

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agatcagcct caacaagatg atgagacccc ttctctacaa aagaaattat aaaaaattag 180  
tcaggtgtgg tagtacacac ctatagcccc agctactcag gaggctgaag cgggaggatc 240  
acttgaggcc aggagtttga ggccatagtg agcaaggatc atgccactgc cctccagcct 300  
gggcaacaac gagaccctgt ctctaaaaaa taaataaaaa ctagttcctc gcccgcctggg 360  
tgctgaagtt gggcggatgg cagcaaaccg gctccgctag aggaccgagc cgcccagccc 420  
cgctcccccg gacccatcgg cgcgctgccc acacctccag gcgaccggcc aactgggtcc 480  
tgaagtagct gaa atg cga aaa agg cag cag tcc caa aat gaa gga aca 529  
Met Arg Lys Arg Gln Gln Ser Gln Asn Glu Gly Thr  
1 5 10  
cct gcc gtg tct caa gct cct gga aac cag agg ccc aac aac acc tgt 577  
Pro Ala Val Ser Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys  
15 20 25  
tgc ttt tgt tgg tgc tgt tgt tgc agc tgc tcc tgc ctc act gtg agg 625  
Cys Phe Cys Trp Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg  
30 35 40  
aat gaa gaa aga ggg gaa aat gcg gga aga ccc aca cac act aca aaa 673  
Asn Glu Glu Arg Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys  
45 50 55 60  
atg gag agt atc cag gtc cta gag gaa tgc caa aac ccc act gca gag 721  
Met Glu Ser Ile Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu  
65 70 75  
gaa gtc ttg tcc tgg tct caa aat ttt gac aag atg atg aag gcc cca 769  
Glu Val Leu Ser Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro

80	85	90	
gca gga aga aac ctt ttc aga gag ttc ctc cga aca gaa tac agt gaa			817
Ala Gly Arg Asn Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu			
95	100	105	
gag aac cta ctt ttc tgg ctt gct tgt gaa gac tta aag aag gag cag			865
Glu Asn Leu Leu Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln			
110	115	120	
aac aaa aaa gta att gaa gaa aag gct agg atg ata tat gaa gat tac			913
Asn Lys Lys Val Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr			
125	130	135	140
att tct ata cta tca cca aaa gag gtc agt ctt gat tct cga gtt aga			961
Ile Ser Ile Leu Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg			
145	150	155	
gag gtg atc aat aga aat ctg ttg gat ccc aat cct cac atg tat gaa			1009
Glu Val Ile Asn Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu			
160	165	170	
gat gcc caa ctt cag ata tat act tta atg cac aga gat tct ttt cca			1057
Asp Ala Gln Leu Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro			
175	180	185	
agg ttt ttg aac tct caa att tat aag tca ttt gtt gaa agt act gct			1105
Arg Phe Leu Asn Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala			
190	195	200	
ggc tct tct tct gaa tct taa tg ttcatttaaa aacaatcatt ttggagggct			1158
Gly Ser Ser Ser Glu Ser *			
205	210		
gagatgggaa ataaaagtag ttaaataaca tcagaaactg agttcctgga gaactacagt			1218
ttagcattcc tcaggctact gtgaaaacac aaccgttatg gtctttgtct ccatttttat			1278
caagggttttc catgggttaag tttggagaaa ataccacaca aaacaatgaa ttgccaaatt			1338
gtttgtttta ttcaagactc attctacttg caagcaaagt gtattttgtag tcctatgaac			1398
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ctttgtttgt tggaaaaacc taatggggaa tcctctggtg gtccttgcca aaactgtgga			1758
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (170)..(2119)

<400> 227

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agacagagct gtgaaccaac cccgctcacg gctaacaagc ccacccacc      atg gcg      175
                                     Met Ala
                                     1

agc ccc act ctg agc ccc gac tcc tca tcc cag gag gcc ctg tcg gcc      223
Ser Pro Thr Leu Ser Pro Asp Ser Ser Ser Gln Glu Ala Leu Ser Ala
          5                      10                      15

ccc acc tgc tcc cca acc tct gac tcc gag aac ctc agc ccc gat gag      271
Pro Thr Cys Ser Pro Thr Ser Asp Ser Glu Asn Leu Ser Pro Asp Glu
          20                      25                      30

ctg gag ctg ctg gcc aag ctc gaa gag cag aac cgg ctc ctg gag gcc      319
Leu Glu Leu Leu Ala Lys Leu Glu Glu Gln Asn Arg Leu Leu Glu Ala
          35                      40                      45                      50

gac tcc aag tcc atg cgc tcc atg aat ggc tcg cgg cgg aac agt ggc      367
Asp Ser Lys Ser Met Arg Ser Met Asn Gly Ser Arg Arg Asn Ser Gly
          55                      60                      65

tcc tcg cta gtg tcc agc tcc tcg gcc tcc tcc aac ctg agc cac ctg      415
Ser Ser Leu Val Ser Ser Ser Ser Ala Ser Ser Asn Leu Ser His Leu
          70                      75                      80

gag gag gac acg tgg atc ctg tgg ggc cgg atc gcc aac gag tgg gag      463
Glu Glu Asp Thr Trp Ile Leu Trp Gly Arg Ile Ala Asn Glu Trp Glu
          85                      90                      95

gag tgg cgg cgc agg aag gag aag ctg ctc aag gag ctg atc cgc aag      511
Glu Trp Arg Arg Arg Lys Glu Lys Leu Leu Lys Glu Leu Ile Arg Lys
          100                      105                      110

ggc atc ccc cac cac ttc cgg gcc atc gtg tgg cag ctt ctg tgc agc      559
Gly Ile Pro His His Phe Arg Ala Ile Val Trp Gln Leu Leu Cys Ser
          115                      120                      125                      130

gcc acg gac atg ccc gtc aag aac cag tac tcc gag ctg ctc aag atg      607
Ala Thr Asp Met Pro Val Lys Asn Gln Tyr Ser Glu Leu Leu Lys Met
          135                      140                      145

tcc tcg ccg tgc gag aag ctg atc cgc agg gac atc gcc cgc acc tac      655

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Ser	Ser	Pro	Cys	Glu	Lys	Leu	Ile	Arg	Arg	Asp	Ile	Ala	Arg	Thr	Tyr		
			150					155					160				
ccg	gaa	cac	gag	ttc	ttc	aag	ggc	cag	gac	agc	ctg	ggc	cag	gag	gtc	703	
Pro	Glu	His	Glu	Phe	Phe	Lys	Gly	Gln	Asp	Ser	Leu	Gly	Gln	Glu	Val		
		165					170					175					
ctc	ttc	aac	gtc	atg	aag	gca	tac	tcg	ctg	gta	gac	cgg	gag	gtg	ggc	751	
Leu	Phe	Asn	Val	Met	Lys	Ala	Tyr	Ser	Leu	Val	Asp	Arg	Glu	Val	Gly		
		180				185					190						
tac	tgc	cag	gga	agc	gcc	ttc	atc	gtg	ggc	ctg	ctc	ctc	atg	cag	atg	799	
Tyr	Cys	Gln	Gly	Ser	Ala	Phe	Ile	Val	Gly	Leu	Leu	Leu	Met	Gln	Met		
195					200				205						210		
cct	gag	gag	gag	gcc	ttc	tgt	gtg	ttc	gtg	cgg	ctg	atg	cag	gag	tac	847	
Pro	Glu	Glu	Glu	Ala	Phe	Cys	Val	Phe	Val	Arg	Leu	Met	Gln	Glu	Tyr		
				215					220				225				
cgg	ctg	cgg	gag	ctc	ttc	aaa	ccc	agc	atg	gcc	gag	ctc	ggg	ctc	tgc	895	
Arg	Leu	Arg	Glu	Leu	Phe	Lys	Pro	Ser	Met	Ala	Glu	Leu	Gly	Leu	Cys		
			230					235					240				
atc	tat	cag	ttc	gag	tac	atg	ctg	cag	gag	cag	ctc	cca	gac	ctc	aac	943	
Ile	Tyr	Gln	Phe	Glu	Tyr	Met	Leu	Gln	Glu	Gln	Leu	Pro	Asp	Leu	Asn		
		245					250					255					
acc	cac	ttc	cgt	tcc	caa	agc	ttc	cac	aca	tcc	atg	tat	gcc	tcg	tcc	991	
Thr	His	Phe	Arg	Ser	Gln	Ser	Phe	His	Thr	Ser	Met	Tyr	Ala	Ser	Ser		
		260				265					270						
tgg	ttc	ctc	aca	ctg	ttc	ctg	acc	acc	ttc	cca	ctc	ccc	gtc	gcc	acc	1039	
Trp	Phe	Leu	Thr	Leu	Phe	Leu	Thr	Thr	Phe	Pro	Leu	Pro	Val	Ala	Thr		
275					280					285					290		
cgg	gtc	ttt	gac	atc	ttc	atg	tat	gag	ggg	ctg	gag	atc	gtg	ttc	cga	1087	
Arg	Val	Phe	Asp	Ile	Phe	Met	Tyr	Glu	Gly	Leu	Glu	Ile	Val	Phe	Arg		
			295						300				305				
gtg	ggc	ctc	gcc	ctg	ctg	cag	gtg	aac	cag	gcg	gag	ctg	atg	cag	ctg	1135	
Val	Gly	Leu	Ala	Leu	Leu	Gln	Val	Asn	Gln	Ala	Glu	Leu	Met	Gln	Leu		
			310				315						320				
gac	atg	gag	ggg	atg	tcc	cag	tac	ttc	cag	aga	gtg	atc	ccc	cac	cag	1183	
Asp	Met	Glu	Gly	Met	Ser	Gln	Tyr	Phe	Gln	Arg	Val	Ile	Pro	His	Gln		
		325					330					335					
ttc	gac	agc	tgc	ccg	gac	aag	ctg	gtc	ctc	aaa	gcc	tac	cag	gtc	aag	1231	
Phe	Asp	Ser	Cys	Pro	Asp	Lys	Leu	Val	Leu	Lys	Ala	Tyr	Gln	Val	Lys		
		340				345					350						
tac	aac	ccc	aag	aag	atg	aag	agg	ctg	gag	aag	gag	tac	gca	gcc	atg	1279	
Tyr	Asn	Pro	Lys	Lys	Met	Lys	Arg	Leu	Glu	Lys	Glu	Tyr	Ala	Ala	Met		
355					360					365					370		
aag	agc	aag	gag	atg	gag	gag	cag	atc	gag	atc	aaa	aga	ctt	cgg	acg	1327	
Lys	Ser	Lys	Glu	Met	Glu	Glu	Gln	Ile	Glu	Ile	Lys	Arg	Leu	Arg	Thr		



375	380	385	
gag aac cgg ctc ctg aaa cag cgg att gaa acc cta gag aag gag agc Glu Asn Arg Leu Leu Lys Gln Arg Ile Glu Thr Leu Glu Lys Glu Ser 390 395 400			1375
gct gct ctg gct gat agg tta atc cag ggg caa gtg aca cgg gcg cag Ala Ala Leu Ala Asp Arg Leu Ile Gln Gly Gln Val Thr Arg Ala Gln 405 410 415			1423
gag gcg gag gag aac tac gtc atc aag cgg gag ctg gcg gtg gtg cgg Glu Ala Glu Glu Asn Tyr Val Ile Lys Arg Glu Leu Ala Val Val Arg 420 425 430			1471
cag cag tgc agc tcg gcg gcc gag gac ctg cag aag gca cag agc acc Gln Gln Cys Ser Ser Ala Ala Glu Asp Leu Gln Lys Ala Gln Ser Thr 435 440 445 450			1519
atc cgg cag cta cag gag cag cag gag aac ccc cgc ctc aca gaa gac Ile Arg Gln Leu Gln Glu Gln Gln Glu Asn Pro Arg Leu Thr Glu Asp 455 460 465			1567
ttc gtg tcc cac ctg gag acc gag ctg gag cag tcg agg ctg cgg gag Phe Val Ser His Leu Glu Thr Glu Leu Glu Gln Ser Arg Leu Arg Glu 470 475 480			1615
acg gag aca ctg ggg gcc ctt cgg gag atg cag gac aag gtt ctc gac Thr Glu Thr Leu Gly Ala Leu Arg Glu Met Gln Asp Lys Val Leu Asp 485 490 495			1663
atg gaa aag agg aac agc tcg ctg ccc gac gag aac aat gtg gcg cag Met Glu Lys Arg Asn Ser Ser Leu Pro Asp Glu Asn Asn Val Ala Gln 500 505 510			1711
ctg cag gag gag ctg aag gcg ctc aag gtg cgg gaa ggc cag gcg gtg Leu Gln Glu Glu Leu Lys Ala Leu Lys Val Arg Glu Gly Gln Ala Val 515 520 525 530			1759
gcc tcg acg cga gag ctt aaa ctg cag ctg cag gag ctc tcg gac acc Ala Ser Thr Arg Glu Leu Lys Leu Gln Leu Gln Glu Leu Ser Asp Thr 535 540 545			1807
tgg cag gac cag atc gag gag ctg aag acc gag gtg cgg ctg ctg aag Trp Gln Asp Gln Ile Glu Glu Leu Lys Thr Glu Val Arg Leu Leu Lys 550 555 560			1855
ggc ccg ccg ccc ttc gag gac ccg ctg gct ttc gat ggg ctg agc ctg Gly Pro Pro Pro Phe Glu Asp Pro Leu Ala Phe Asp Gly Leu Ser Leu 565 570 575			1903
gcg cgg cac ttg gac gag gac tcg ctg ccg tcg tcg gac gag gag cta Ala Arg His Leu Asp Glu Asp Ser Leu Pro Ser Ser Asp Glu Glu Leu 580 585 590			1951
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<400> 228

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agcagcgagg acacctgcag aaatacattc ccaaagcaag gctgggcggc cgtgtgaagt    180

aagcaatggc ctcagttttg cttctgtttt ggatgaacac caccacatag ggcttgaatg    240

tgaaagaaga ccctctatct gtctgttccg gggcagcctg gtagtaaaac actgttgaat    300

gggccacagt ttcagcagac catcaggtga      atg gga cca gtc tct ctt ctt    351
                               Met Gly Pro Val Ser Leu Leu
                               1                               5

cca aaa tat cag aag tta aac act tgg aac gga gat ttg gcc aag atg      399
Pro Lys Tyr Gln Lys Leu Asn Thr Trp Asn Gly Asp Leu Ala Lys Met
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acc cat tta cag gct gga ctc agt cca gag act ata gag aaa gct cgc      447
Thr His Leu Gln Ala Gly Leu Ser Pro Glu Thr Ile Glu Lys Ala Arg
          25                      30                      35

ctg gaa ctg aat gaa aac ccc gat gtt tta cat cag gat att cag caa      495
Leu Glu Leu Asn Glu Asn Pro Asp Val Leu His Gln Asp Ile Gln Gln
          40                      45                      50                      55

gtc agg gac atg atc atc acc agg cct gac att gga ttt tta cgt aca      543
Val Arg Asp Met Ile Ile Thr Arg Pro Asp Ile Gly Phe Leu Arg Thr
          60                      65                      70

gat gat gcc ttc atc ctg aga ttt ctc cga gcc agg aag ttt cac caa      591
Asp Asp Ala Phe Ile Leu Arg Phe Leu Arg Ala Arg Lys Phe His Gln
          75                      80                      85

gcg gat gcc ttt aga ctc ctg gct cag tat ttc cag tac cgc cag cta      639
Ala Asp Ala Phe Arg Leu Leu Ala Gln Tyr Phe Gln Tyr Arg Gln Leu
          90                      95                      100

aac ctg gac atg ttc aaa aac ttc aag gca gat gat ccc ggc att aag      687
Asn Leu Asp Met Phe Lys Asn Phe Lys Ala Asp Asp Pro Gly Ile Lys
          105                      110                      115

agg gct ctg atc gat ggg ttc ccc ggg gtg ctg gaa aac cga gac cat      735
Arg Ala Leu Ile Asp Gly Phe Pro Gly Val Leu Glu Asn Arg Asp His
          120                      125                      130                      135

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tac ggc agg aag att ctt ttg ctg ttt gca gcc aat tgg gat cag agt	783
Tyr Gly Arg Lys Ile Leu Leu Leu Phe Ala Ala Asn Trp Asp Gln Ser	
140 145 150	
agg aac tcc ttc aca gac atc ctt cgt gcc atc ctg ctg tca ttg gaa	831
Arg Asn Ser Phe Thr Asp Ile Leu Arg Ala Ile Leu Leu Ser Leu Glu	
155 160 165	
gtc cta atc gaa gat ccg gag ctt cag ata aat ggc ttc att tta att	879
Val Leu Ile Glu Asp Pro Glu Leu Gln Ile Asn Gly Phe Ile Leu Ile	
170 175 180	
ata gac tgg agt aat ttt tcc ttc aaa caa gcc tcc aaa ctg aca cct	927
Ile Asp Trp Ser Asn Phe Ser Phe Lys Gln Ala Ser Lys Leu Thr Pro	
185 190 195	
tca atc ctt aaa ctg gcc att gaa ggg ttg cag gac agc ttt cct gcc	975
Ser Ile Leu Lys Leu Ala Ile Glu Gly Leu Gln Asp Ser Phe Pro Ala	
200 205 210 215	
cgc ttt gga gga gtc cac ttt gtc aac cag ccc tgg tac att cat gcc	1023
Arg Phe Gly Gly Val His Phe Val Asn Gln Pro Trp Tyr Ile His Ala	
220 225 230	
ctc tac aca ctc atc aag cca ttt ctt aaa gac aag acc agg aaa cgg	1071
Leu Tyr Thr Leu Ile Lys Pro Phe Leu Lys Asp Lys Thr Arg Lys Arg	
235 240 245	
att ttc ctg cat gga aac aat tta aac agc ctt cac cag cta ata cac	1119
Ile Phe Leu His Gly Asn Asn Leu Asn Ser Leu His Gln Leu Ile His	
250 255 260	
cct gaa ttt ttg ccc tct gaa ttt gga gga act ctt cct ccc tta tga	1167
Pro Glu Phe Leu Pro Ser Glu Phe Gly Gly Thr Leu Pro Pro Leu *	
265 270 275	
catgggaact tgggcccgga cggtactcgg tcccgaactac agcgatgaaa atgactatac	1227
tcacacatcc tataatgcaa tgcacgtgaa gcatacgtcc tcgaatctgg agagagaatg	1287
ctcaccgaag ctgatgaaaa gatctcagtc tgtggtagaa gctgggaccc tgaaacatga	1347
ggagaaggga gagaatgaga acaccagcc actcctggct ctggactgaa ccctgagtca	1407
ccccaatgct cctgcacact ggccttcagt ggtatcagcc acccaggaag cacatgcaca	1467
actgacccat gcagacacgt gtgttctgct tgacacaagg tcctccactc ctgaaccctc	1527
gcagtgactg tcaccagcca tcggtctgag cagccaaagt tggacaaaga cttgagagat	1587
gctttttttt tccccagtg aggggactgg aggatgatgc aaggcattta tgtaaaaaag	1647
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aaaaaaaaaa aa	1719

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agtcagattc tgactctgca taccctctcca	171
atg gct ttc gcc acc ccc aaa	
Met Ala Phe Ala Thr Pro Lys	
1 5	
tca ctt gga gta aaa gcc gaa gtc ctt cca gca gct tac cag gtg ctg	219
Ser Leu Gly Val Lys Ala Glu Val Leu Pro Ala Ala Tyr Gln Val Leu	
10 15 20	
cat gat cca gac tcc ttc tta gcc ctc tgg ctc tcc tgc tgc tct cct	267
His Asp Pro Asp Ser Phe Leu Ala Leu Trp Leu Ser Cys Cys Ser Pro	
25 30 35	
tct tca ttt ctc tct agc cac acc agc ttt ctt gct gag agc act ggg	315
Ser Ser Phe Leu Ser Ser His Thr Ser Phe Leu Ala Glu Ser Thr Gly	
40 45 50 55	
tgc tct gtc tac act att ctc caa aat atc cat atg gtt tgt cct cct	363
Cys Ser Val Tyr Thr Ile Leu Gln Asn Ile His Met Val Cys Pro Pro	
60 65 70	
tca ttt act ttc ttg aat tcc acg gtc tca gtg aga tta cct tgg cat	411
Ser Phe Thr Phe Leu Asn Ser Thr Val Ser Val Arg Leu Pro Trp His	
75 80 85	
cct agt taa agctgct gcctgtcctc tcaccctgcg tcttgcagtc ccctttctag	467
Pro Ser *	
90	
cgccccctcc ctttttctat agcactcttc aacttctaac atacttttaa aacataattt	527
ccttgatatgt tttgctgag	546

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<220>

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<400> 230

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cagccgccag cgcgccccgt cggcagctct ccactctcac gtctctccgt gaaccccggtg      180
agcgggtgtgc agccacc  atg ttc agc tgg ctg aag cgg ggc ggg gca cgg      230
                      Met Phe Ser Trp Leu Lys Arg Gly Gly Ala Arg
                      1           5           10

ggc cag cag ccc gag gcc atc cgc acg gtg acc tcg gcc ctc aag gag      278
Gly Gln Gln Pro Glu Ala Ile Arg Thr Val Thr Ser Ala Leu Lys Glu
                      15           20           25

ctg tac cgc acg aag ctg ctg ccg ctg gag gag cac tac cgc ttt ggg      326
Leu Tyr Arg Thr Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe Gly
                      30           35           40

gcc ttc cac tcg ccg gcc ctg gag gac gca gac ttc gac ggc aag ccc      374
Ala Phe His Ser Pro Ala Leu Glu Asp Ala Asp Phe Asp Gly Lys Pro
                      45           50           55

atg gtg ctg gtg gcc ggc cag tac agc acg ggc aag acc agc ttc atc      422
Met Val Leu Val Ala Gly Gln Tyr Ser Thr Gly Lys Thr Ser Phe Ile
                      60           65           70           75

cag tac ctg ctg gag cag gag gtg ccc ggc tcc cgc gtg ggg cct gag      470
Gln Tyr Leu Leu Glu Gln Glu Val Pro Gly Ser Arg Val Gly Pro Glu
                      80           85           90

ccc acc acc gac ttc ttt gtg gcc gtc atg cac ggc gac act gag ggc      518
Pro Thr Thr Asp Phe Phe Val Ala Val Met His Gly Asp Thr Glu Gly
                      95           100          105

acc gtg ccc ggc aac gcc ctc gtc gtg gac ccg gac aag ccc ttc cgc      566
Thr Val Pro Gly Asn Ala Leu Val Val Asp Pro Asp Lys Pro Phe Arg
                      110          115          120

aaa ctc aac cct ttc gga aac acc ttc ctc aac agg ttc atg tgt gcc      614
Lys Leu Asn Pro Phe Gly Asn Thr Phe Leu Asn Arg Phe Met Cys Ala
                      125          130          135

cag ctc cct aat cag gtc ctg gag agc atc agc atc atc gac acc ccg      662
Gln Leu Pro Asn Gln Val Leu Glu Ser Ile Ser Ile Ile Asp Thr Pro
                      140          145          150          155

ggt atc ctg tcg ggt gcc aag cag aga gtg agc cgc ggc tac gac ttc      710
Gly Ile Leu Ser Gly Ala Lys Gln Arg Val Ser Arg Gly Tyr Asp Phe
                      160          165          170

ccg gcc gtg ctg cgc tgg ttc gcg gag cgc gtg gac ctc atc atc ctg      758
Pro Ala Val Leu Arg Trp Phe Ala Glu Arg Val Asp Leu Ile Ile Leu
                      175          180          185

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ctc ttt gat gcg cac aag ctg gag atc tcg gac gag ttc tca gag gcc	806
Leu Phe Asp Ala His Lys Leu Glu Ile Ser Asp Glu Phe Ser Glu Ala	
190 195 200	
atc ggc gcg ttg cgg ggc cat gag gac aag atc cgc gtg gtg ctc aac	854
Ile Gly Ala Leu Arg Gly His Glu Asp Lys Ile Arg Val Val Leu Asn	
205 210 215	
aag gcc gac atg gtg gag acg cag cag ctg atg cgc gtc tac ggc gcg	902
Lys Ala Asp Met Val Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala	
220 225 230 235	
ctc atg tgg gcg ctg ggc aag gtg gtg ggc acg ccc gag gtg ctg cgc	950
Leu Met Trp Ala Leu Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg	
240 245 250	
gtc tac atc ggc tcc ttc tgg tcc cag ccc ctc ctc gtg ccc gac aac	998
Val Tyr Ile Gly Ser Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn	
255 260 265	
cgg cgc ctc ttc gag ctg gag gag cag gac ctc ttc cgc gac atc cag	1046
Arg Arg Leu Phe Glu Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln	
270 275 280	
ggc ctg ccc cgg cac gca gcc ttg cgc aag ctc aac gac ctg gtg aag	1094
Gly Leu Pro Arg His Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys	
285 290 295	
agg gcc cgg ctg gtg cga gtt cac gct tac atc atc agc tac ctg aag	1142
Arg Ala Arg Leu Val Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys	
300 305 310 315	
aag gag atg ccc tct gtg ttt ggg aag gag aac aag aag aag cag ctg	1190
Lys Glu Met Pro Ser Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu	
320 325 330	
atc ctc aaa ctg ccc gtc atc ttt gcg aag att cag ctg gaa cat cac	1238
Ile Leu Lys Leu Pro Val Ile Phe Ala Lys Ile Gln Leu Glu His His	
335 340 345	
atc tcc cct ggg gac ttt cct gat tgc cag aaa atg cag gag ctg ctg	1286
Ile Ser Pro Gly Asp Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu	
350 355 360	
atg gcg cac gac ttc acc aag ttt cac tcg ctg aag ccg aag ctg cta	1334
Met Ala His Asp Phe Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu	
365 370 375	
gag gca ctg gac gag atg ctg acg cac gac atc gcc aag ctc atg ccc	1382
Glu Ala Leu Asp Glu Met Leu Thr His Asp Ile Ala Lys Leu Met Pro	
380 385 390 395	
ctg ctg cgg cag gag gag ctg gag agc acc gag gtg ggc gtg cag ggg	1430
Leu Leu Arg Gln Glu Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly	
400 405 410	

ggc gct ttt gag ggc acc cac atg ggc ccg ttt gtg gag cgg gga cct	1478
Gly Ala Phe Glu Gly Thr His Met Gly Pro Phe Val Glu Arg Gly Pro	
415 420 425	
gac gag gcc atg gag gac ggc gag gag ggc tcg gac gac gag gcc gag	1526
Asp Glu Ala Met Glu Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu	
430 435 440	
tgg gtg gtg acc aaa gac aag tcc aaa tac gac gag atc ttc tac aac	1574
Trp Val Val Thr Lys Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn	
445 450 455	
ctg gcg cct gcc gac ggc aag ctg agc ggc tcc aag gcc aag acc tgg	1622
Leu Ala Pro Ala Asp Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp	
460 465 470 475	
atg gtg ggg acc aag ctc ccc aac tca gtg ctg ggg cgc atc tgg aag	1670
Met Val Gly Thr Lys Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys	
480 485 490	
ctc agc gat gtg gac cgc gac ggc atg ctg gat gat gaa gag ttc gcg	1718
Leu Ser Asp Val Asp Arg Asp Gly Met Leu Asp Asp Glu Phe Ala	
495 500 505	
ctg gcc agc cac ctc atc gag gcc aag ctg gaa ggc cac ggg ctg ccc	1766
Leu Ala Ser His Leu Ile Glu Ala Lys Leu Glu Gly His Gly Leu Pro	
510 515 520	
gcc aac ctg ccc cgt cgc ctg gtg cca ccc tcc aag cga cgc cac aag	1814
Ala Asn Leu Pro Arg Arg Leu Val Pro Pro Ser Lys Arg Arg His Lys	
525 530 535	
ggc tcc gcc gag tga gccggggcccc cctcccatgg ccctgctgtg gctccccagc	1869
Gly Ser Ala Glu *	
540	
tccagtcggc tgcacgcaca ccctgctcc ggctcacaca cgccctgcct gccctccctg	1929
cccagctgta aggaccgggg gtctccctcc tctactaccgc cagacacccc ggtggaagca	1989
tttagagggg accacgggag ggacaaggct tctctgtccg cccttcacac ctccagcctc	2049
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tcattcaaatt atttattgag cacctactat gtgcccagcc ctgtttctagg cactgggcat	2169
taccatagag aacaaaatag acaaatacat ctgccctcat ggaaggtgac gttcccagga	2229
gagggcacct acacagtcac gcaaacacac actaattcct ggcagggccc ccagcccctc	2289
ccctggctga gcagccctgt ggctgaaatg actagcagat aaacagaccc ccttctgctc	2349
cgttccctcc tgcccagcca ggcaacaccc tcaaccggct ccatcacatc ctccaggtctc	2409
gggaccatgg ggggctcaga ggggagacac acctactgct tcttcagatg ggcccctccg	2469
cagccccttc ccttgctcgg ggaaagcccc caattctgcc cacacccatt tatttccttc	2529





cgg gtc cgc ggg gcg ctt gat aca cag aaa tgc agt cca gag aaa agt	276
Arg Val Arg Gly Ala Leu Asp Thr Gln Lys Cys Ser Pro Glu Lys Ser	
15 20 25	
gcc tca ttt ttc agt aaa gtg aca tat tcc tgg ttt agc aga gta att	324
Ala Ser Phe Phe Ser Lys Val Thr Tyr Ser Trp Phe Ser Arg Val Ile	
30 35 40 45	
act tta ggc tat aag aga cct ttg gaa aga gag gat ctt ttt gaa cta	372
Thr Leu Gly Tyr Lys Arg Pro Leu Glu Arg Glu Asp Leu Phe Glu Leu	
50 55 60	
aag gaa agt gat tcc ttc tgc act gcg tgt ccc atc ttt gaa aaa caa	420
Lys Glu Ser Asp Ser Phe Cys Thr Ala Cys Pro Ile Phe Glu Lys Gln	
65 70 75	
tgg aga aag gaa gtt tta agg aat caa gag agg caa aaa gta aag gta	468
Trp Arg Lys Glu Val Leu Arg Asn Gln Glu Arg Gln Lys Val Lys Val	
80 85 90	
tct tgt tat aaa gag gca cat atc aag aaa cca tct cta ctc tat gca	516
Ser Cys Tyr Lys Glu Ala His Ile Lys Lys Pro Ser Leu Leu Tyr Ala	
95 100 105	
ttg tgg aac acc ttt aaa tcc atc ctg att caa gtt gcc tta ttc aaa	564
Leu Trp Asn Thr Phe Lys Ser Ile Leu Ile Gln Val Ala Leu Phe Lys	
110 115 120 125	
gtg ttt gct gat att ttg tcc ttc act agc cca ctc ata atg aag caa	612
Val Phe Ala Asp Ile Leu Ser Phe Thr Ser Pro Leu Ile Met Lys Gln	
130 135 140	
att atc att ttc tgt gaa cac agc tca gat ttt ggc tgg aat ggc tat	660
Ile Ile Ile Phe Cys Glu His Ser Ser Asp Phe Gly Trp Asn Gly Tyr	
145 150 155	
ggc tat gca gtg gca ctt ctt gtt gta gtc ttt ttg caa act ctg att	708
Gly Tyr Ala Val Ala Leu Leu Val Val Phe Leu Gln Thr Leu Ile	
160 165 170	
ctt cag caa tat caa cgt ttt aac atg ctc acc tca gca aaa gtt aag	756
Leu Gln Gln Tyr Gln Arg Phe Asn Met Leu Thr Ser Ala Lys Val Lys	
175 180 185	
aca gct gta aat gga ctg atc tac aaa aag gcc tta ctt tta tca aat	804
Thr Ala Val Asn Gly Leu Ile Tyr Lys Lys Ala Leu Leu Leu Ser Asn	
190 195 200 205	
gtt tct cga caa aag ttt tcc act ggg gaa att att aac ttg atg tca	852
Val Ser Arg Gln Lys Phe Ser Thr Gly Glu Ile Ile Asn Leu Met Ser	
210 215 220	
gca act cat gga ctt gac agc aaa cct caa tct cct ctg gtc tgc ccc	900
Ala Thr His Gly Leu Asp Ser Lys Pro Gln Ser Pro Leu Val Cys Pro	
225 230 235	

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Phe Ser Asn Pro Asn Gly Arg Ile Ser Pro Leu Ala Arg Ala Gly Ser
      240                      245                      250

agc agt gtt agc agg ggt ggc agt cct tgt gtt tgt tat acc aat aaa      996
Ser Ser Val Ser Arg Gly Gly Ser Pro Cys Val Cys Tyr Thr Asn Lys
      255                      260                      265

tgc ttt agc tgc aac taa aataaa aaagttaaag gtaaaaaaat gactgcctca    1050
Cys Phe Ser Cys Asn *
      270                      275

tgttacatgt gtcaaacagg agctgagttt tctgacttga gttaacaatc accatctcgc    1110

taattatata gagagagtta caaatggaag tcatcgaatt ttatcattta cttattcact    1170

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agcagtgagg ggaaatgaca agtccagctc tcatgagggg tagtggagga gacaggcatt    1290

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Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys
      5                      10                      15

cac caa ccc cat aaa gtg aca cag tac aag aag ggc aag gat tct ctg      154
His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu
      20                      25                      30

tac gcc cag gga aag cgg cgt tat gac agg aag cag agt ggc tat ggt      202
Tyr Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly
      35                      40                      45

ggg caa act aag ccg att ttc cgg aaa aag gct aaa act aca aag aag      250
Gly Gln Thr Lys Pro Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys
      50                      55                      60                      65

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gtc aag tgt gct gca atc att ggt cac tcc ttc cat ata gat ttg ctg 307  
Val Lys Cys Ala Ala Ile Ile Gly His Ser Phe His Ile Asp Leu Leu  
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cag cac ctg ctg cct ggc tgg gat aaa aat aag cta ctt cag gtc ttg 355  
Gln His Leu Leu Pro Gly Trp Asp Lys Asn Lys Leu Leu Gln Val Leu  
70 75 80 85

aga gct ctt gtg gat ata cat gtg ctg tgc tgg tct gac aag agc caa 403  
Arg Ala Leu Val Asp Ile His Val Leu Cys Trp Ser Asp Lys Ser Gln  
90 95 100

gag ctt cct gct gag ccc ata tta atg cct tcc tct atc gac atc att 451  
Glu Leu Pro Ala Glu Pro Ile Leu Met Pro Ser Ser Ile Asp Ile Ile  
105 110 115

gat gga acc aaa gag aag aag aca aag tta gat ggt ggg tca gcc tct 499  
Asp Gly Thr Lys Glu Lys Lys Thr Lys Leu Asp Gly Gly Ser Ala Ser  
120 125 130

ctt ctg agg cta caa gaa gaa tta tcc cta cca cag gca gca ctg aaa 547  
Leu Leu Arg Leu Gln Glu Glu Leu Ser Leu Pro Gln Ala Ala Leu Lys  
135 140 145

cag aca ata gac agc ttc cac ccc act aca cgc ctg cag caa cac agc 595  
Gln Thr Ile Asp Ser Phe His Pro Thr Thr Arg Leu Gln Gln His Ser  
150 155 160 165

ccg gct gca cag gct ctg gta tgc gac cat cat gct tgc agt agc ccg 643  
Pro Ala Ala Gln Ala Leu Val Cys Asp His His Ala Cys Ser Ser Pro  
170 175 180

gtc ttt gca cgg cta cct cta gag cac ctt cag aaa tgc cct taa gca 691  
Val Phe Ala Arg Leu Pro Leu Glu His Leu Gln Lys Cys Pro \*  
185 190 195

tgctgggggtc acgtgtcatg caaaccttgg acagatgact gaacctctct atgccttggt 751

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atg gca tca tgc acc tcc ctc cca gct cct ggc tct cgg cct aag aag	286
Met Ala Ser Ser Thr Ser Leu Pro Ala Pro Gly Ser Arg Pro Lys Lys	
1 5 10 15	
cct cta ggc aag atg gct gac tgg ttc agg cag acc ctg ctg aag aag	334
Pro Leu Gly Lys Met Ala Asp Trp Phe Arg Gln Thr Leu Leu Lys Lys	
20 25 30	
ccc aag aag agg ccc aac tcc cca gaa agc acc tcc agc gat gct tca	382
Pro Lys Lys Arg Pro Asn Ser Pro Glu Ser Thr Ser Ser Asp Ala Ser	
35 40 45	
cag cct acc tca cag gac agc cca cta ccc cca agc ctc agc tca gtc	430
Gln Pro Thr Ser Gln Asp Ser Pro Leu Pro Pro Ser Leu Ser Ser Val	
50 55 60	
acg tct ccc agc ctg cca ccc aca cat gcg agt gac agt ggc agt agt	478
Thr Ser Pro Ser Leu Pro Thr His Ala Ser Asp Ser Gly Ser Ser	
65 70 75 80	
cgc tgg agc aaa gac tat gac gtc tgc gtg tgc cac agt gag gaa gac	526
Arg Trp Ser Lys Asp Tyr Asp Val Cys Val Cys His Ser Glu Glu Asp	
85 90 95	
ctg gtg gcc gcc cag gac ctg gtc tcc tac ttg gaa ggc agc act gcc	574
Leu Val Ala Ala Gln Asp Leu Val Ser Tyr Leu Glu Gly Ser Thr Ala	
100 105 110	
agc ctg cgc tgc ttc ctg caa ctc cgg gat gca acc cca ggc ggc gct	622
Ser Leu Arg Cys Phe Leu Gln Leu Arg Asp Ala Thr Pro Gly Gly Ala	
115 120 125	
ata gtg tcc gag ctg tgc cag gca ctg agc agt agt cac tgc cgg gtg	670
Ile Val Ser Glu Leu Cys Gln Ala Leu Ser Ser Ser His Cys Arg Val	
130 135 140	
ctg ctc atc acg ccg ggc ttc ctt cag gac ccc tgg tgc aag tac cag	718
Leu Leu Ile Thr Pro Gly Phe Leu Gln Asp Pro Trp Cys Lys Tyr Gln	
145 150 155 160	
atg ctg cag gcc ctg acc gag gct cca ggg gcc gag ggc tgc acc atc	766
Met Leu Gln Ala Leu Thr Glu Ala Pro Gly Ala Glu Gly Cys Thr Ile	
165 170 175	
ccc ctg ctg tgc ggc ctc agc aga gct gct tac cca cct gag ctc cga	814
Pro Leu Leu Ser Gly Leu Ser Arg Ala Ala Tyr Pro Pro Glu Leu Arg	
180 185 190	
ttc atg tac tac gtc gat ggc agg ggc cct gat ggt ggc ttt cgt caa	862
Phe Met Tyr Tyr Val Asp Gly Arg Gly Pro Asp Gly Gly Phe Arg Gln	
195 200 205	

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gtc aaa gaa gct gtc atg cgt tgt aag cta cta cag gag gga gaa ggg      910
Val Lys Glu Ala Val Met Arg Cys Lys Leu Leu Gln Glu Gly Glu Gly
    210                      215                      220

gaa cgg gat tca gct aca gta ttt gat cta ctt tga cttt taggagacag      960
Glu Arg Asp Ser Ala Thr Val Phe Asp Leu Leu *
    225                      230                      235

ccctgtagcc tagtagttca aagcgcagct tctggaagag gctgtcgggg tttgtatcct    1020

ggctcctgcc cttattaacc cataaaaagt aacttgggtca agttaaaaaa aaaaaaa    1077

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<210> 235
<211> 916
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (169)..(738)

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<400> 235
agctggctag cgtttaaact taagcttggg accgagctcg gatccactag tccagtgtgg      60
tggaattcca cagcccgagta actttgctag tacctcttga gtgcaagggtg gagaattaag    120
atctggattt gagacggagc acggaacatt tcactcaggg gaagagct atg aac atg      177
                               Met Asn Met
                               1

ctg act gcc agc ctg ttg agg gca gtc ata gcc tcc atc tgt gtt gta      225
Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val
    5                      10                      15

tcc agc atg gct cag aag gta act caa gcg cag act gaa att tct gtg      273
Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val
    20                      25                      30                      35

gtg gag aag gag gat gtg acc ttg gac tgt gtg tat gaa acc cgt gat      321
Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp
                40                      45                      50

act act tat tac tta ttc tgg tac aag caa cca cca agt gga gaa ttg      369
Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu
                55                      60                      65

gtt ttc ctt att cgt cgg aac tct ttt gat gag caa aat gaa ata agt      417
Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser
    70                      75                      80

ggg cgg tat tct tgg aac ttc cag aaa tcc acc agt tcc ttc aac ttc      465
Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe
    85                      90                      95

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acc atc aca gcc tca caa gtc gtg gac tca gca gta tac ttc tgt gct	513
Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala	
100 105 110 115	
ctg agt gag gcg gcc caa gaa acc agt ggc tct agg ttg acc ttt ggg	561
Leu Ser Glu Ala Ala Gln Glu Thr Ser Gly Ser Arg Leu Thr Phe Gly	
120 125 130	
gaa gga aca cag ctc aca gtg aat cct gat atc cag aac cct gac cct	609
Glu Gly Thr Gln Leu Thr Val Asn Pro Asp Ile Gln Asn Pro Asp Pro	
135 140 145	
gcc gtg tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc	657
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys	
150 155 160	
cta ttc acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat	705
Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp	
165 170 175	
tct gat gtg tat atc aca gac aaa ctg tgc tag actgtgag gctagggatt	756
Ser Asp Val Tyr Ile Thr Asp Lys Leu Cys *	
180 185 190	
tcagaaccac cgggttgggc ctggagcaac aaatctgact ttgcatgggc aacgccttca	816
acaacaggct tatttcagaa gaacccttct tccccagccc caaaagggtcc cttgatggca	876
agctgccccga gaaagctttg aaacagatac caacctaaac	916
<210> 236	
<211> 876	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (38)..(547)	
<400> 236	
agtgtggtgg aattcgggag ccctgccccca ggggccc atg cag aat gcc acc aag	55
Met Gln Asn Ala Thr Lys	
1 5	
tat ggc aac atg aca gag gac cat gtg atg cac ctg ctc cag aat gct	103
Tyr Gly Asn Met Thr Glu Asp His Val Met His Leu Leu Gln Asn Ala	
10 15 20	
gac ccc ctg aag gtg tac ccg cca ctg aag ggg agc ttc ccg gag aac	151
Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly Ser Phe Pro Glu Asn	
25 30 35	
ctg aga cac ctt aag aac acc atg gag acc ata gac tgg aag gtc ttt	199
Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile Asp Trp Lys Val Phe	



40	45	50	
gag agc tgg atg cac cat tgg ctc ctg ttt gaa atg agc agg cac tcc			247
Glu Ser Trp Met His His Trp Leu Leu Phe Glu Met Ser Arg His Ser			
55	60	65	70
ttg gag caa aag ccc act gac gct cca ccg aaa gta ctg acc aag tgc			295
Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys Val Leu Thr Lys Cys			
	75	80	85
cag gaa gag gtc agc cac atc cct gct gtc cac ccg ggt tca ttc agg			343
Gln Glu Glu Val Ser His Ile Pro Ala Val His Pro Gly Ser Phe Arg			
	90	95	100
ccc aag tgc gac gag aac ggc aac tat ctg cca ctc cag tgc tat ggg			391
Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro Leu Gln Cys Tyr Gly			
	105	110	115
agc atc ggc tac tgc tgg tgt gtc ttc ccc aac ggc acg gag gtc ccc			439
Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn Gly Thr Glu Val Pro			
	120	125	130
aac acc aga agc cgc ggg cac cat aac tgc agt gag tca ctg gaa ctg			487
Asn Thr Arg Ser Arg Gly His His Asn Cys Ser Glu Ser Leu Glu Leu			
	135	140	145
gag gac ccg tct tct ggg ctg ggt gtg acc aag cag gat ctg ggc cca			535
Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Leu Gly Pro			
	155	160	165
gtc ccc atg tga gag cagcagaggc ggtcttcaac atcctgccag cccacacag			590
Val Pro Met *			
	170		
ctacagcttt cttgctccct tcagcccca gccctcccc catctccac cctgtacctc			650
atcccatgag accctggtgc ctggctcttt cgtcaccctt ggacaagaca aaccaagtcg			710
gaacagcaga taacaatgca gcaaggccct gctgcccaat ctccatctgt caacaggggc			770
ggtcgacgcg gccgcgaatt cggatcctcg agagatctct ttttttgggt ttggtggggt			830
gtcttcatca tcggatatata taggtatata catcggccta tcaagg			876

<210> 237  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (168)..(419)  
  
 <400> 237

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gtccgtgcgc accgcccggc gtccaggtga gtctcccatc tgcagagacg cggacgcgcc      60
ggcccgcagt tggcctgcgg agcgcggtgg acggtttggc gcccaccagg cgatcaatac      120
tttgattttt taatttctag atttggcaat tcttcgctga agtcac  atg agc ttt      176
                                         Met Ser Phe
                                         1

ttc caa ctc ctg atg aaa agg aag gaa ctc att ccc ttg gtg gtg ttc      224
Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val Val Phe
      5              10              15

atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat tct ctt      272
Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr Ser Leu
      20              25              30              35

tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa cct tgg      320
Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu Pro Trp
              40              45              50

gaa act gtg gac cct act gta cct caa aag ctt ata aca atc aac caa      368
Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile Asn Gln
              55              60              65

caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg acc aaa      416
Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val Thr Lys
              70              75              80

tga cgag cctcgcctc tttcttctga agagtactct ataaatctag tggaaacatt      473
*

tctgcacaaa ctagattctg gacaccagtg tgcggaaatg cttctgctac atttttaggg      533

tttgtctaca ttttttgggc tctggataag gaattaaagg agtgcagcaa taactgcact      593

gtctaaaagt ttgtgcttat tttcttgtaa atttgaatat tgcattattga aatttttggt      653

tatgatctat gaatgttttt cttaaaattt acaaagcttt gtaaattaga ttttctttaa      713

taaaatgccca tttgtgcaag atttctcaaa aaaaaaaaaa      753

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<210> 238  
 <211> 1395  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (50)..(1060)

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<400> 238
gagtgggtgga attccgctgg cctcgcctcg tgcgcgcctc cctccccgc  atg cag      55
                                         Met Gln

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ccc gcc gag cgc tgc cgg gtc ccc agg atc gac ccg tac gga ttc gag	103
Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly Phe Glu	
5 10 15	
cgg cct gag gac ttc gac gac gcc gcc tac gag aag ttt ttc tcc agc	151
Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe Ser Ser	
20 25 30	
tac ctg gtc acg ctc acc cgc agg gcg atc aaa tgg tcc cgg ctg ctg	199
Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg Leu Leu	
35 40 45 50	
cag ggc ggg ggc gtc ccc agg agc cgg aca gtg aag cgc tat gtc cgg	247
Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr Val Arg	
55 60 65	
aaa ggg gtc ccg ctg gag cac cgt gcc cgc gtc tgg atg gtg ctg agt	295
Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val Leu Ser	
70 75 80	
ggg gcc cag gcg cag atg gac cag aat ccc ggc tac tac cac cag ctt	343
Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His Gln Leu	
85 90 95	
ctc cag gga gag aga aac ccc agg ctg gag gac gcc atc agg aca gac	391
Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg Thr Asp	
100 105 110	
ctg aac cgg acc ttc ccc gac aac gtg aag ttc cgg aag acc acg gac	439
Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr Thr Asp	
115 120 125 130	
ccc tgc tta cag agg acc ctg tac aat gtg ctg ctg gca tat ggg cac	487
Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr Gly His	
135 140 145	
cat aac cag gga gtg ggc tac tgc cag gga atg aat ttt ata gca gga	535
His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile Ala Gly	
150 155 160	
tat ctg att ctt ata aca aat aat gaa gaa gaa tct ttt tgg ctg tta	583
Tyr Leu Ile Leu Ile Thr Asn Asn Glu Glu Glu Ser Phe Trp Leu Leu	
165 170 175	
gat gct ctt gtt gga aga ata cta cca gat tac tac agc ccg gcc atg	631
Asp Ala Leu Val Gly Arg Ile Leu Pro Asp Tyr Tyr Ser Pro Ala Met	
180 185 190	
ctg ggc ctg aag acc gac cag gag gtc ctc ggg gag ctg gtg cgg gcg	679
Leu Gly Leu Lys Thr Asp Gln Glu Val Leu Gly Glu Leu Val Arg Ala	
195 200 205 210	
aag ctg ccg gct gtg ggg gcc ctg atg gag cgt ctc ggt gtg ctg tgg	727
Lys Leu Pro Ala Val Gly Ala Leu Met Glu Arg Leu Gly Val Leu Trp	
215 220 225	





gtttctatattt acatattcca ttaattctat tagtttgaat tagatttttaa gtccaatttt 120  
gaaaagcttg cagaattttct tctgaaatta cttaaaatta ctgtatgcat aaacttacia 180  
aaacat atg cta tac caa ggc aga gaa aag aaa aaa agt gaa gtg gct 228  
Met Leu Tyr Gln Gly Arg Glu Lys Lys Lys Ser Glu Val Ala  
1 5 10  
aca aag gtc cct ggg gca tca cct gct cac cta gga acc agg agt act 276  
Thr Lys Val Pro Gly Ala Ser Pro Ala His Leu Gly Thr Arg Ser Thr  
15 20 25 30  
gga tac tgt tcc gtt act ggt aac cta tct gga tgt aaa ggt tca taa 324  
Gly Tyr Cys Ser Val Thr Gly Asn Leu Ser Gly Cys Lys Gly Ser \*  
35 40 45  
gttacaatgc tttttttgtt taaaaaaaaa aaaaagtctg tacttttacia gccaaaagtg 384  
aaaatgccac acatcctctt tacgctttca tgtacactaa gtcactccat ttggttgata 444  
ccaataatga tagctcctgt gtataatatt ttcataaaatc atactcagta agcaaatctc 504  
tcaagcagcc agcatatgca gc 526

<210> 241  
<211> 3744  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (27)..(3161)

<400> 241  
aagagctgcc tcccaggagggt gtctac atg gtg cag ccc cag ggg tgc agc gat 53  
Met Val Gln Pro Gln Gly Cys Ser Asp  
1 5  
gag gaa gac cac gcg gag gag ccc tcc aag gac ggc ggt gcc ctg gag 101  
Glu Glu Asp His Ala Glu Glu Pro Ser Lys Asp Gly Gly Ala Leu Glu  
10 15 20 25  
gag aag gat tcg gac ggg gca gcc tcc aag gag gac agc ggc ccc agc 149  
Glu Lys Asp Ser Asp Gly Ala Ala Ser Lys Glu Asp Ser Gly Pro Ser  
30 35 40  
acc agg cag gct tca gga gag gcc tcc tcg ctg cgg gac tac gcg gcc 197  
Thr Arg Gln Ala Ser Gly Glu Ala Ser Ser Leu Arg Asp Tyr Ala Ala  
45 50 55  
tcc acc atg acc gag ttc ctc ggc atg ttt ggc tat gat gac cag aac 245  
Ser Thr Met Thr Glu Phe Leu Gly Met Phe Gly Tyr Asp Asp Gln Asn  
60 65 70

acg cgg gac gag ctg gcc agg aag atc agc ttt gag aag ctg cac gcg Thr Arg Asp Glu Leu Ala Arg Lys Ile Ser Phe Glu Lys Leu His Ala 75 80 85	293
ggc tcc acc ccg gag gca gcc acc tcc tcc atg ctg ccc acc tcc gag Gly Ser Thr Pro Glu Ala Ala Thr Ser Ser Met Leu Pro Thr Ser Glu 90 95 100 105	341
gat acc ctc agc aag cgg gcc cgg ttc tct aag tat gag gag tac atc Asp Thr Leu Ser Lys Arg Ala Arg Phe Ser Lys Tyr Glu Glu Tyr Ile 110 115 120	389
cgc aag ctc aag gct gcc gag cag ctc tcc tgg ccg gcc ccc agc acc Arg Lys Leu Lys Ala Gly Glu Gln Leu Ser Trp Pro Ala Pro Ser Thr 125 130 135	437
aag acc gag gag cgg gtg gcc aag gag gtg gtg gcc acc ctg ccc gcc Lys Thr Glu Glu Arg Val Gly Lys Glu Val Val Gly Thr Leu Pro Gly 140 145 150	485
ctg cgg ctg ccc agc agc acg gcc cac ctg gag acc aag gcc acc atc Leu Arg Leu Pro Ser Ser Thr Ala His Leu Glu Thr Lys Ala Thr Ile 155 160 165	533
ctg ccc ctg ccg tcg cac agc agt gtc cag atg cag aac ctg gta gcc Leu Pro Leu Pro Ser His Ser Ser Val Gln Met Gln Asn Leu Val Ala 170 175 180 185	581
cgg gcc tcc aag tac gac ttc ttc atc caa aaa ctg aag acc gcc gag Arg Ala Ser Lys Tyr Asp Phe Phe Ile Gln Lys Leu Lys Thr Gly Glu 190 195 200	629
aat ctg cgg ccc cag aac ggg agc acc tac aag aag cca tcc aag tac Asn Leu Arg Pro Gln Asn Gly Ser Thr Tyr Lys Lys Pro Ser Lys Tyr 205 210 215	677
gac ctg gag aat gtc aag tac ctg cac ctc ttc aaa ccc ggg gag gcc Asp Leu Glu Asn Val Lys Tyr Leu His Leu Phe Lys Pro Gly Glu Gly 220 225 230	725
agc ccc gac atg gcc ggg gcc atc gcc ttc aag aca gcc aag gtg ggg Ser Pro Asp Met Gly Gly Ala Ile Ala Phe Lys Thr Gly Lys Val Gly 235 240 245	773
cgc cct tcc aag tac gac gtc cgg gcc atc cag aag cca gcc ccc gcc Arg Pro Ser Lys Tyr Asp Val Arg Gly Ile Gln Lys Pro Gly Pro Ala 250 255 260 265	821
aag gtt ccg ccc acc ccc agc ctg gct ccc gca ccc ctc gcc agc gtg Lys Val Pro Pro Thr Pro Ser Leu Ala Pro Ala Pro Leu Ala Ser Val 270 275 280	869
ccc agt gcc ccc aac gcc ccc ggg cca ggg cca gag cct cct gcc tcc Pro Ser Ala Pro Asn Ala Pro Gly Pro Gly Pro Glu Pro Pro Ala Ser 285 290 295	917
ctg tcc ttc aac act ccc gag tac ctg aag tca acc ttc tcc aaa aca	965

Leu	Ser	Phe	Asn	Thr	Pro	Glu	Tyr	Leu	Lys	Ser	Thr	Phe	Ser	Lys	Thr		
		300					305					310					
gac	tcc	atc	acc	acg	ggg	acc	gtc	tcc	act	gtc	aag	aac	gga	ctg	ccc		1013
Asp	Ser	Ile	Thr	Thr	Gly	Thr	Val	Ser	Thr	Val	Lys	Asn	Gly	Leu	Pro		
		315				320					325						
aca	gat	aaa	cca	gcc	gtc	act	gaa	gat	gta	aac	att	tac	cag	aaa	tat		1061
Thr	Asp	Lys	Pro	Ala	Val	Thr	Glu	Asp	Val	Asn	Ile	Tyr	Gln	Lys	Tyr		
		330			335					340					345		
att	gcc	agg	ttc	tcg	ggc	agc	cag	cac	tgt	ggc	cac	atc	cac	tgt	gcc		1109
Ile	Ala	Arg	Phe	Ser	Gly	Ser	Gln	His	Cys	Gly	His	Ile	His	Cys	Ala		
				350					355					360			
tac	cag	tac	cgc	gag	cac	tac	cac	tgc	ctt	gac	cct	gag	tgt	aac	tac		1157
Tyr	Gln	Tyr	Arg	Glu	His	Tyr	His	Cys	Leu	Asp	Pro	Glu	Cys	Asn	Tyr		
			365					370					375				
cag	agg	ttc	acg	agt	aag	cag	gac	gtg	atc	cgc	cac	tac	aac	atg	cac		1205
Gln	Arg	Phe	Thr	Ser	Lys	Gln	Asp	Val	Ile	Arg	His	Tyr	Asn	Met	His		
		380					385					390					
aag	aag	cgc	gac	aac	tcc	ctg	cag	cac	ggc	ttc	atg	cgt	ttc	agc	ccg		1253
Lys	Lys	Arg	Asp	Asn	Ser	Leu	Gln	His	Gly	Phe	Met	Arg	Phe	Ser	Pro		
		395				400					405						
ctg	gac	gac	tgc	agc	gtc	tac	tac	cac	ggc	tgc	cac	ctc	aat	ggg	aag		1301
Leu	Asp	Asp	Cys	Ser	Val	Tyr	Tyr	His	Gly	Cys	His	Leu	Asn	Gly	Lys		
					415					420				425			
agc	acc	cac	tat	cac	tgc	atg	cag	gtg	ggc	tgt	aac	aag	gtg	tac	acg		1349
Ser	Thr	His	Tyr	His	Cys	Met	Gln	Val	Gly	Cys	Asn	Lys	Val	Tyr	Thr		
				430					435					440			
agc	acg	tct	gac	gtg	atg	acc	cac	gag	aac	ttc	cac	aag	aag	aat	acc		1397
Ser	Thr	Ser	Asp	Val	Met	Thr	His	Glu	Asn	Phe	His	Lys	Lys	Asn	Thr		
			445					450					455				
cag	ctc	att	aac	gac	ggc	ttc	cag	cgc	ttc	cga	gcc	acc	gaa	gac	tgt		1445
Gln	Leu	Ile	Asn	Asp	Gly	Phe	Gln	Arg	Phe	Arg	Ala	Thr	Glu	Asp	Cys		
		460					465					470					
ggc	aca	gcc	gac	tgc	cag	ttc	tac	gga	cag	aag	acc	acg	cac	ttc	cac		1493
Gly	Thr	Ala	Asp	Cys	Gln	Phe	Tyr	Gly	Gln	Lys	Thr	Thr	His	Phe	His		
		475				480					485						
tgc	agg	cgc	ccc	ggc	tgc	aca	ttc	act	ttc	aag	aac	aag	tgt	gac	atc		1541
Cys	Arg	Arg	Pro	Gly	Cys	Thr	Phe	Thr	Phe	Lys	Asn	Lys	Cys	Asp	Ile		
		490			495					500				505			
gag	aag	cac	aag	agc	tac	cac	atc	aag	gac	gat	gcc	tac	gcc	aag	gac		1589
Glu	Lys	His	Lys	Ser	Tyr	His	Ile	Lys	Asp	Asp	Ala	Tyr	Ala	Lys	Asp		
				510					515					520			
ggc	ttc	aag	aag	ttc	tac	aag	tac	gag	gag	tgc	aag	tac	gag	ggc	tgc		1637
Gly	Phe	Lys	Lys	Phe	Tyr	Lys	Tyr	Glu	Glu	Cys	Lys	Tyr	Glu	Gly	Cys		





gcc ctc aag ccc tct gcc acc ttt gac cca gga agc ggg cag cag gtc Ala Leu Lys Pro Ser Ala Thr Phe Asp Pro Gly Ser Gly Gln Gln Val 765 770 775	2357
acc cca gcc agg ttc ccc ccg gcc caa gtg aag ccg gaa ccc ggt gag Thr Pro Ala Arg Phe Pro Pro Ala Gln Val Lys Pro Glu Pro Gly Glu 780 785 790	2405
agc acc ggc gcc cca ggc ccc cac gaa gcc tcc cag gac cgc agt cta Ser Thr Gly Ala Pro Gly Pro His Glu Ala Ser Gln Asp Arg Ser Leu 795 800 805	2453
gac ctg act gtg aag gag ccc agc aac gaa tca aat ggc cac gca gtc Asp Leu Thr Val Lys Glu Pro Ser Asn Glu Ser Asn Gly His Ala Val 810 815 820 825	2501
ccg gca aat tca tct ctt tta tcc tcg ctt atg aat aag atg tct cag Pro Ala Asn Ser Ser Leu Leu Ser Ser Leu Met Asn Lys Met Ser Gln 830 835 840	2549
ggc aac cct ggc ctg ggc agc ctg ctg aac atc aag gcg gaa gcg gag Gly Asn Pro Gly Leu Gly Ser Leu Leu Asn Ile Lys Ala Glu Ala Glu 845 850 855	2597
ggg agc ccc gct gcg gag ccc tcg ccc ttc cta ggc aag gcc gtg aag Gly Ser Pro Ala Ala Glu Pro Ser Pro Phe Leu Gly Lys Ala Val Lys 860 865 870	2645
gcg ctg gtt cag gag aag ttg gca gag ccc tgg aag gtg tac ctg cgc Ala Leu Val Gln Glu Lys Leu Ala Glu Pro Trp Lys Val Tyr Leu Arg 875 880 885	2693
agg ttt ggt aca aag gac ttc tgt gac ggc cag tgt gac ttc ctc cac Arg Phe Gly Thr Lys Asp Phe Cys Asp Gly Gln Cys Asp Phe Leu His 890 895 900 905	2741
aag gcc cac ttc cac tgc gtg gtg gag gaa tgc ggc gcg ctc ttc agc Lys Ala His Phe His Cys Val Val Glu Glu Cys Gly Ala Leu Phe Ser 910 915 920	2789
acc ttg gac ggg gcc atc aag cac gca aac ttc cac ttc cgg aca gag Thr Leu Asp Gly Ala Ile Lys His Ala Asn Phe His Phe Arg Thr Glu 925 930 935	2837
gga gga gca gca aaa gga aac aca gag gct gcc ttt ccg gcc tcg gcc Gly Gly Ala Ala Lys Gly Asn Thr Glu Ala Ala Phe Pro Ala Ser Ala 940 945 950	2885
gcc gag acc aaa cct ccc atg gcc ccc tcg tcc cct ccg gtc cct cct Ala Glu Thr Lys Pro Pro Met Ala Pro Ser Ser Pro Pro Val Pro Pro 955 960 965	2933
gtc acc acg gcc acg gtg tcc tct ctg gag ggg ccc gct ccc agc ccg Val Thr Thr Ala Thr Val Ser Ser Leu Glu Gly Pro Ala Pro Ser Pro 970 975 980 985	2981

gcc tcc gtg ccc tcc acc ccc acc ctg ctc gcc tgg aag cag ctg gct	3029
Ala Ser Val Pro Ser Thr Pro Thr Leu Leu Ala Trp Lys Gln Leu Ala	
990 995 1000	
tcc acc ata ccc cag atg cct cag atc cca gcg tca gtg cct cac ctg	3077
Ser Thr Ile Pro Gln Met Pro Gln Ile Pro Ala Ser Val Pro His Leu	
1005 1010 1015	
ccc gcc tcg ccc ttg gca acg act tct cta gag aac gcc aag ccc cag	3125
Pro Ala Ser Pro Leu Ala Thr Thr Ser Leu Glu Asn Ala Lys Pro Gln	
1020 1025 1030	
gtc aaa ccc gga ttc ctc cag ttc cag gag aag tga gtcc ctgatgagc	3175
Val Lys Pro Gly Phe Leu Gln Phe Gln Glu Lys *	
1035 1040 1045	
cgaggagtcgc gcgttcccct cgcgtctcgg gagtaggtgc tagcaagggc gctaggaggc	3235
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tgatgtcctt ctagccaaag atgctgctgc tctacctca ctgcctgtcc cagagcaggc	3355
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tgacaaggag ggctgcgtct cctccgagc ctccgtattg gcctcctctg tggctcacac	3535
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cgtcactggc ctgcacagtg gtctgagctc ttgggtggaa gggaccctcc tcaatggatg	3655
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 <213> Homo sapiens

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aaagctttta gagttctgat gcctatttaa gtaaattaac tcttttcccc ccaaattct	180
taggcttgaa g atg cag tgg acg cca gag cat gcc cag tgg cca gaa cag	230
Met Gln Trp Thr Pro Glu His Ala Gln Trp Pro Glu Gln	

1	5	10	
cac ttt gac atc acc tca acc act cgg tct cct gcc cac aaa gtt gaa His Phe Asp Ile Thr Ser Thr Thr Arg Ser Pro Ala His Lys Val Glu 15 20 25			278
gcc tac aga ggt cat ctg cag cgc acc tat cag tac gcc tgg gcg aat Ala Tyr Arg Gly His Leu Gln Arg Thr Tyr Gln Tyr Ala Trp Ala Asn 30 35 40 45			326
gat gac ata tct gct ctg act gca tcc aac cta cta aaa aaa tat gca Asp Asp Ile Ser Ala Leu Thr Ala Ser Asn Leu Leu Lys Lys Tyr Ala 50 55 60			374
gag aag tat tcc ggc att ttg gaa ggt cct gtg gac cga ccc gta ctc Glu Lys Tyr Ser Gly Ile Leu Glu Gly Pro Val Asp Arg Pro Val Leu 65 70 75			422
agc aac tat tcg gac aca cca tca gga cta gtg aac ggt cgg aaa aat Ser Asn Tyr Ser Asp Thr Pro Ser Gly Leu Val Asn Gly Arg Lys Asn 80 85 90			470
gaa agt gaa ccc tgg cag cct tcc ttg aat tca gaa gct gtt tat ccc Glu Ser Glu Pro Trp Gln Pro Ser Leu Asn Ser Glu Ala Val Tyr Pro 95 100 105			518
atg aac tgt gtt ccg gat gtt atc act gcc agc aaa gct gga gtc agt Met Asn Cys Val Pro Asp Val Ile Thr Ala Ser Lys Ala Gly Val Ser 110 115 120 125			566
tca gcc ctc cct cca gca gat gtc tct gcg agt ata gga agc tct cct Ser Ala Leu Pro Pro Ala Asp Val Ser Ala Ser Ile Gly Ser Ser Pro 130 135 140			614
ggg gta gcc agc aac ctg aca gaa cct agt tat tca agt agt acc tgt Gly Val Ala Ser Asn Leu Thr Glu Pro Ser Tyr Ser Ser Ser Thr Cys 145 150 155			662
gga agc cac act gta ccc agt ctt cat gca ggg ctc cca tct cag gaa Gly Ser His Thr Val Pro Ser Leu His Ala Gly Leu Pro Ser Gln Glu 160 165 170			710
tat gcc cca gga tac aac gga tca tat ttg cat tct act tat agt agc Tyr Ala Pro Gly Tyr Asn Gly Ser Tyr Leu His Ser Thr Tyr Ser Ser 175 180 185			758
cag cca gca cct gca ctt cct tca cct cat ccg tct cct ttg cat agc Gln Pro Ala Pro Ala Leu Pro Ser Pro His Pro Ser Pro Leu His Ser 190 195 200 205			806
tct ggg cta cta cag ccc cca cca cca cct cct ccg cca cca gcc ttg Ser Gly Leu Leu Gln Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu 210 215 220			854
gtc cca ggc tac aat ggg act tct aac ctc tcc agt tac agc tat ccg Val Pro Gly Tyr Asn Gly Thr Ser Asn Leu Ser Ser Tyr Ser Tyr Pro 225 230 235			902

tct gct agc tat cct cct cag act gct gtg ggg tct ggg tac agc cct Ser Ala Ser Tyr Pro Pro Gln Thr Ala Val Gly Ser Gly Tyr Ser Pro 240 245 250	950
ggg ggg gca ccg cct ccg cct tca gcg tac ctg cct tca gga att cct Gly Gly Ala Pro Pro Pro Pro Ser Ala Tyr Leu Pro Ser Gly Ile Pro 255 260 265	998
gct ccc acc ccc cta ccc ccc acc act gtt cct ggc tac acc tac cag Ala Pro Thr Pro Leu Pro Pro Thr Thr Val Pro Gly Tyr Thr Tyr Gln 270 275 280 285	1046
ggc cat ggt ttg aca cct att gca ccg tcg gct ctg aca aac agt tca Gly His Gly Leu Thr Pro Ile Ala Pro Ser Ala Leu Thr Asn Ser Ser 290 295 300	1094
gca agt tct ctc aaa agg aaa gct ttc tac atg gca ggg caa gga gat Ala Ser Ser Leu Lys Arg Lys Ala Phe Tyr Met Ala Gly Gln Gly Asp 305 310 315	1142
atg gac tcc agt tat gga aat tac agc tat ggc caa cag aga tct aca Met Asp Ser Ser Tyr Gly Asn Tyr Ser Tyr Gly Gln Gln Arg Ser Thr 320 325 330	1190
cag agt cct atg tac aga atg ccc gac aac agc att tca aac aca aat Gln Ser Pro Met Tyr Arg Met Pro Asp Asn Ser Ile Ser Asn Thr Asn 335 340 345	1238
cgg ggg aat ggc ttt gac aga agt gct gaa aca tca tcc tta gca ttt Arg Gly Asn Gly Phe Asp Arg Ser Ala Glu Thr Ser Ser Leu Ala Phe 350 355 360 365	1286
aag cca acg aag cag cta atg tcc tct gaa cag caa agg aaa ttc agc Lys Pro Thr Lys Gln Leu Met Ser Ser Glu Gln Gln Arg Lys Phe Ser 370 375 380	1334
agc cag tcc agt agg gct ctg acc cct cct tcc tac agt act gct aaa Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr Ser Thr Ala Lys 385 390 395	1382
aat tca ttg gga tca aga tcc agt gaa tcc ttt ggg aag tac aca tcg Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly Lys Tyr Thr Ser 400 405 410	1430
cca gta atg agt gag cat ggg gac gag cac agg cag ctc ctc tct cac Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln Leu Leu Ser His 415 420 425	1478
cca atg caa ggc cct gga ctc cgt gca gct acc tca tcc aac cac tct Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser Ser Asn His Ser 430 435 440 445	1526
gtg gac gag caa ctg aag aat act gac acg cac ctc atc gac ctg gta Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu Ile Asp Leu Val 450 455 460	1574

acc aat gag att atc acc caa gga cct cca gtg gac tgg aat gac att	1622
Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp Trp Asn Asp Ile	
465 470 475	
gct ggt ctc gac ctg gtg aag gct gtc att aaa gag gag gtt tta tgg	1670
Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu Glu Val Leu Trp	
480 485 490	
cca gtg ttg agg tca gac gcg ttc agt gga ctg acg gcc tta cct cgg	1718
Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr Ala Leu Pro Arg	
495 500 505	
agc atc ctt tta ttt gga cct cgg ggg aca ggc aaa aca tta ttg ggc	1766
Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys Thr Leu Leu Gly	
510 515 520 525	
aga tgc atc gct agt cag ctg ggg gcc aca ttt ttc aaa att gcc ggt	1814
Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe Lys Ile Ala Gly	
530 535 540	
tct gga cta gtc gcc aag tgg tta gga gaa gca gag aaa att atc cat	1862
Ser Gly Leu Val Ala Lys Trp Leu Gly Glu Ala Glu Lys Ile Ile His	
545 550 555	
gcc tct ttt ctt gtg gcc agg tgt cgc cag ccc tcg gtg att ttt gtt	1910
Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser Val Ile Phe Val	
560 565 570	
agt gac att gac atg ctt ctc tcc tct caa gtg aat gag gaa cat agt	1958
Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn Glu Glu His Ser	
575 580 585	
cca gtc agt cgg atg aga acc gaa ttt ctg atg caa ctg gac act gta	2006
Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln Leu Asp Thr Val	
590 595 600 605	
cta act tcg gct gag gac caa atc gta gta att tgt gcc acc agt aaa	2054
Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys Ala Thr Ser Lys	
610 615 620	
cca gaa gaa ata gat gaa tcc ctt cgg agg tac ttc atg aaa cga ctt	2102
Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe Met Lys Arg Leu	
625 630 635	
tta atc cca ctt cct gac agc aca gcg agg cac cag ata ata gta caa	2150
Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln Ile Ile Val Gln	
640 645 650	
ctg ctc tca cag cac aat tac tgt ctc aat gac aag gag ttt gca ctg	2198
Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys Glu Phe Ala Leu	
655 660 665	
ctc gtc cag cgc aca gaa ggc ttt tct gga cta gat gtg gct cat ttg	2246
Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp Val Ala His Leu	
670 675 680 685	
tgt cag gaa gca gtg gtg ggc ccc ctc cat gcc atg cca gcc aca gac	2294

Cys Gln Glu Ala Val Val Gly Pro Leu His Ala Met Pro Ala Thr Asp	
690	695 700
ctt tca gcc att atg ccc agc cag ttg agg ccc gtt aca tat caa gac	2342
Leu Ser Ala Ile Met Pro Ser Gln Leu Arg Pro Val Thr Tyr Gln Asp	
705	710 715
ttt gaa aat gct ttc tgc aag att cag cct agc ata tct caa aag gag	2390
Phe Glu Asn Ala Phe Cys Lys Ile Gln Pro Ser Ile Ser Gln Lys Glu	
720	725 730
ctt gat atg tat gtt gaa tgg aac aaa atg ttt ggt tgc agt cag tga	2438
Leu Asp Met Tyr Val Glu Trp Asn Lys Met Phe Gly Cys Ser Gln *	
735	740 745
taacttcttt ag	2450

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (168)..(437)

<400> 243

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aagttttaag tattcaggca attcatgata ccttgttgaa ataaagc atg cag act	176
	Met Gln Thr
	1
cat aaa aac ttg tat ata atc aaa ata aag ttc tac aaa tgg gaa aga	224
His Lys Asn Leu Tyr Ile Ile Lys Ile Lys Phe Tyr Lys Trp Glu Arg	
5	10 15
gga tta tta tca ggg tat att aag gtg tta gac tta caa aag aag tgc	272
Gly Leu Leu Ser Gly Tyr Ile Lys Val Leu Asp Leu Gln Lys Lys Cys	
20	25 30 35
ata att aat tac tca ttt aaa att aat tct ata ccc att agc ttg gca	320
Ile Ile Asn Tyr Ser Phe Lys Ile Asn Ser Ile Pro Ile Ser Leu Ala	
40	45 50
aca gat aaa ata aaa gca tgc aac agt gct ttc tta gtc gac gcg gcc	368
Thr Asp Lys Ile Lys Ala Cys Asn Ser Ala Phe Leu Val Asp Ala Ala	
55	60 65
gcg aat tcg gat cct cga gag atc tct ttt ttt ggg ttt ggt ggg gta	416
Ala Asn Ser Asp Pro Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val	
70	75 80

tct tca tca tcg aat aga tag ttatatacat catgctcttc aattaaaa	465
Ser Ser Ser Ser Asn Arg *	
85 90	

<210> 244  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (83)..(829)

<400> 244

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gcggcccggc ctcggggcag cc atg gac tcg cag gaa ttg aag act ttg att	112
Met Asp Ser Gln Glu Leu Lys Thr Leu Ile	
1 5 10	
aat tac tat tgt caa gag aga tat ttc cat cat gta tta ctg gtt gcc	160
Asn Tyr Tyr Cys Gln Glu Arg Tyr Phe His His Val Leu Leu Val Ala	
15 20 25	
agt gaa gga att aag agg tat gga agt gat cca gtc ttc agg ttt tat	208
Ser Glu Gly Ile Lys Arg Tyr Gly Ser Asp Pro Val Phe Arg Phe Tyr	
30 35 40	
cat gcc tat ggc aca tta atg gaa ggt aaa act caa gaa gct ctt cga	256
His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu Arg	
45 50 55	
gaa ttt gag gct att aaa aat aaa caa gat gta tca ctt tgt tct cta	304
Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser Leu	
60 65 70	
ctt gca ctg ata tat gcc cat aaa atg agt cct aat cca gat aga gaa	352
Leu Ala Leu Ile Tyr Ala His Lys Met Ser Pro Asn Pro Asp Arg Glu	
75 80 85 90	
gct att ctg gaa tca gat gcc aga gtg aag gaa caa cgt aaa gga gct	400
Ala Ile Leu Glu Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala	
95 100 105	
gga gag aaa gcc tta tac cat gca ggc tta ttt tta tgg cac att ggt	448
Gly Glu Lys Ala Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly	
110 115 120	
cgc cat gat aaa gca agg gaa tat att gac aga atg atc aaa ata tca	496
Arg His Asp Lys Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser	
125 130 135	



gat ggt agt aaa cag gga cac gtt ttg aaa gca tgg ctt gat att aca 544  
 Asp Gly Ser Lys Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr  
 140 145 150

aga gga aaa gag cct tac act aaa aaa gca ctg aag tat ttt gaa gag 592  
 Arg Gly Lys Glu Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu  
 155 160 165 170

gga ctc caa gat ggg aat gat act ttt gct ctg ctg ggt aag gca caa 640  
 Gly Leu Gln Asp Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Ala Gln  
 175 180 185

tgc ctt gag atg cgc cag aat tat tca ggt gcc ctg gag act gtg aac 688  
 Cys Leu Glu Met Arg Gln Asn Tyr Ser Gly Ala Leu Glu Thr Val Asn  
 190 195 200

cag ata atc gtg aat ttt ccg agc ttc ctt cct gct ttt gtt aag aaa 736  
 Gln Ile Ile Val Asn Phe Pro Ser Phe Leu Pro Ala Phe Val Lys Lys  
 205 210 215

atg aaa tta caa cta gcc ttg cag gat tgg gac cag aca gtt gag aca 784  
 Met Lys Leu Gln Leu Ala Leu Gln Asp Trp Asp Gln Thr Val Glu Thr  
 220 225 230

gca aaa ggt tgc tgc tcc aag ata gcc aaa atg tgg aag cac tga gaa 832  
 Ala Lys Gly Cys Cys Ser Lys Ile Ala Lys Met Trp Lys His \*  
 235 240 245

tgcaggcact ctactatgtg tgtagagagg gggatataga gaaggcttcc accaagctgg 892

aaaacttggg aaatgcattg gatgccatgg aaccacagaa tgctcaactt ttctataaca 952

ttacactcgc cttcagcaga acttgtggac gtagtcaact tattcttcaa aaaattcaaa 1012

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taccaatt 1080

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 <213> Homo sapiens

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 Met Val Glu  
 1

ttg tta att aat gtg tat att gta ctg aat ttc tgt cag tta agg ggt	163
Leu Leu Ile Asn Val Tyr Ile Val Leu Asn Phe Cys Gln Leu Arg Gly	
5 10 15	
tca ctg ctt tgg tgg aaa ttg gtg gaa att gct agc agg ttc cac gat	211
Ser Leu Leu Trp Trp Lys Leu Val Glu Ile Ala Ser Arg Phe His Asp	
20 25 30 35	
gtt tat ttt ttt ctc cat gtt gta tat cat tac cat ttc aca tac gcg	259
Val Tyr Phe Phe Leu His Val Val Tyr His Tyr His Phe Thr Tyr Ala	
40 45 50	
ttt cta ttt ttc ttc ctc tcc tcc tga tctcc ttaaaaatga atctagagtt	311
Phe Leu Phe Phe Phe Leu Ser Ser *	
55 60	
ggcggcctttt tccccctcct ctttggccag ttccacagtt cagttcttcc tgaaaacagg	371
gatgatgaac ttgtaggac aggacaaatg tgtgtttttc aaaaacttaa ggctgggtgt	431
gaaacacctt ctgtggacaa ggatttgtaa acttctctcc tccctccagc tgcggcccca	491
gcctaactga tagttacttg attcagtgtg ctagacactt aaatagcatc tatgtctctt	551
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aataatgcaa taaaaactag ttgagggttag ctgaggctgg aaatgccttt ttcattgtaa	731
atgattcact tctatatattt tctttctttt tctttttttt tctttgggtt tcatcctgga	791
ttcatccctt gatcttaaat caaaacgtca gatcaatgaa ctatgaacta aagtattttt	851
cttaagccta ttgagtgatt aattttttta aaaatgttta aatgcatatg cttttctttc	911
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tgagtcattt atttccctaa ctactcctc tttcaagtaa caggtggcag atcataaaat	1031
gaattcttta ttgtatctac aactccaca ttctttactg tgtcctacta ctgtatcttg	1091
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ttttgtctcc ccttcaaag tcaactcaaag agtgggactt catcaaaaga aatgaattag	1211
tctctatcac accgaatact aagatttatt tctctgatg gtacatagat ttctctctcc	1271
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ggatcagggt gatgataata cctctaaaaa tatgcaataa taaaacaata gttatgaaag	1451
aaacttgaaa gggttgcaag gtttctccta tcctgttaa aattatcatt tattatctct	1511
ttgtcagtg tagtaaggta acccatgaca gaataatttg agtgatagtt catcatgcag	1571

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aggatatgat caagatatta cctaattggtt ttatcctgaa aaaggtgtat acttttaggg 1631
cactgttaac aatgcgagtg aaaccaagat ggtgcaagtt ccctttgcag atggcgtggg 1691
cacacttgat ttttattatg agtgaatgta atctttctgt attttaccag agttacagca 1751
attacctgaa aagtttccta acattttaat aatggttaggg atttcgtttt ggtttttagtt 1811
gtcctcaaga gacaacaggt tcacagtaat ttccatgatg ttgggtgtgg ctaagctggg 1871
gattggttct gttccccctg ctcccggtga gagaaaagct atatttatac tgcattcttt 1931
ctcaactttc aggtaaaaca aactatgatt taaaaaaga aaaaagaaaa gacaggtact 1991
tttacttcaa agagtgtctt gctacatttt tatttaaacc aaaaatcaaa taaaataagg 2051
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attccaaaaa aaaaaaa 2128

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<210> 246
<211> 3373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (146)..(2254)

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<400> 246

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ccagggctct gggtcacact ccagg atg act tct cgg aac cag ctg gtg cag 172
Met Thr Ser Arg Asn Gln Leu Val Gln
1 5

aag gtg ctg cag gag ctg cag gaa gca gtg gag tgc gaa ggc ctg gag 220
Lys Val Leu Gln Glu Leu Gln Glu Ala Val Glu Cys Glu Gly Leu Glu
10 15 20 25

ggg ctc ata ggt gct tcc ttg gag gcc aag cag gtc ctg tct tcc ttc 268
Gly Leu Ile Gly Ala Ser Leu Glu Ala Lys Gln Val Leu Ser Ser Phe
30 35 40

act ctc ccc acc tgc cgg gag gga ggc cct ggc ctc cag gtg ctg gaa 316
Thr Leu Pro Thr Cys Arg Glu Gly Gly Pro Gly Leu Gln Val Leu Glu
45 50 55

gtg gac tcg gtg gcc ctg agc ctg tat cca gaa gat gct cca cgg aac 364
Val Asp Ser Val Ala Leu Ser Leu Tyr Pro Glu Asp Ala Pro Arg Asn
60 65 70

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atg ctg ccg ctg gtg tgc aag ggg gag ggc agc ctg ctg ttc gag gcg	412
Met Leu Pro Leu Val Cys Lys Gly Glu Gly Ser Leu Leu Phe Glu Ala	
75 80 85	
gcc agc atg ctg ctg tgg ggt gac gca ggc ctc agc ctg gag ctg cgg	460
Ala Ser Met Leu Leu Trp Gly Asp Ala Gly Leu Ser Leu Glu Leu Arg	
90 95 100 105	
gcc cgc acc gtg gta gag atg ctg ctg cac aga cac tac tac ctc cag	508
Ala Arg Thr Val Val Glu Met Leu Leu His Arg His Tyr Tyr Leu Gln	
110 115 120	
ggc atg atc gac tcc aaa gtg atg ctg cag gcc gtg cgc tac tcc cta	556
Gly Met Ile Asp Ser Lys Val Met Leu Gln Ala Val Arg Tyr Ser Leu	
125 130 135	
tgc tct gag gag tcc cct gag atg acc agc ttg ccc ccc gcc acg ctg	604
Cys Ser Glu Glu Ser Pro Glu Met Thr Ser Leu Pro Pro Ala Thr Leu	
140 145 150	
gag gcc atc ttc gat gcc gac gtc aag gcc tcc tgt ttc ccc agc agc	652
Glu Ala Ile Phe Asp Ala Asp Val Lys Ala Ser Cys Phe Pro Ser Ser	
155 160 165	
ttc tcc aac gtg tgg cac ttg tat gct ctc gcc tct gtc ctc cag cgg	700
Phe Ser Asn Val Trp His Leu Tyr Ala Leu Ala Ser Val Leu Gln Arg	
170 175 180 185	
aac atc tac tcc atc tac ccc atg cgc aac ctc aag atc cgg ccc tac	748
Asn Ile Tyr Ser Ile Tyr Pro Met Arg Asn Leu Lys Ile Arg Pro Tyr	
190 195 200	
ttc aac cgt gtc atc cgg ccc cgc cgc tgc gac cac gtg ccc tcc acg	796
Phe Asn Arg Val Ile Arg Pro Arg Arg Cys Asp His Val Pro Ser Thr	
205 210 215	
ctg cac atc atg tgg gct ggc cag ccc ctc acc agc cac ttc ttc cgc	844
Leu His Ile Met Trp Ala Gly Gln Pro Leu Thr Ser His Phe Phe Arg	
220 225 230	
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His Gln Tyr Phe Ala Pro Val Val Gly Leu Glu Glu Val Glu Ala Glu	
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Gly	Glu	Arg	Val	Ile	Ser	Gly	Ser	Tyr	Ser	Phe	Thr	Trp	Ser	Asp	Ala	
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Pro	Pro	Ala	Pro	Pro	Gln	Lys	Pro	Ser	Val	Ile	Gly	Gly	Leu	Gln	Arg	
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Ser	Pro	Pro	Pro	Pro	Asp	Gly	Pro	Leu	Ala	His	Arg	Leu	Ala	Ala	Cys	
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cca tgc ggg gct cgt ttt gga act gca att gct gct gta aaa gac ctc Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala Val Lys Asp Leu 570 575 580	2141
aat ctt gat gga ttt aat gac atc gtg ata gga gct ccg ctg gaa gat Asn Leu Asp Gly Phe Asn Asp Ile Val Ile Gly Ala Pro Leu Glu Asp 585 590 595	2189
gat cac ggg gga gct gtg tac att tat cat gga agt ggc aag act ata Asp His Gly Gly Ala Val Tyr Ile Tyr His Gly Ser Gly Lys Thr Ile 600 605 610	2237
agg aaa gag tat gca caa cgt att cca tca ggt ggg gat ggt aag aca Arg Lys Glu Tyr Ala Gln Arg Ile Pro Ser Gly Gly Asp Gly Lys Thr 615 620 625	2285
ctg aaa ttt ttt ggc cag tct atc cac gga gaa atg gat tta aat ggt	2333



855	860	865	
att gag gct atc caa aaa gac agt tgt gaa tct aat cat aat atc aca Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser Asn His Asn Ile Thr 870 875 880 885			3053
tgt aaa gtt gga tat ccc ttc ctg aga aga gga gag atg gta act ttc Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly Glu Met Val Thr Phe 890 895 900			3101
aaa ata ttg ttt cag ttt aac aca tcc tat ctc atg gaa aat gtg acc Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu Met Glu Asn Val Thr 905 910 915			3149
att tat tta agt gca aca agt gac agc gaa gaa cct cct gaa acc ctt Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro Pro Glu Thr Leu 920 925 930			3197
tct gat aat gta gta aac att tct atc ccg gta aaa tat gaa gtt gga Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val Lys Tyr Glu Val Gly 935 940 945			3245
cta cag ttt tac agc tct gca agt gaa tac cac att tca att gct gcc Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His Ile Ser Ile Ala Ala 950 955 960 965			3293
aat gag aca gtc cct gaa gtt att aat tct act gag gac att gga aat Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr Glu Asp Ile Gly Asn 970 975 980			3341
gaa att aat atc ttc tac ttg att aga aaa agt gga tct ttt cca atg Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser Gly Ser Phe Pro Met 985 990 995			3389
cca gag ctt aag ctg tca att tca ttc ccc aat atg aca tca aat ggt Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn Met Thr Ser Asn Gly 1000 1005 1010			3437
tac cct gtg ctg tac cca act gga ttg tca tct tct gag aat gca aac Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser Ser Glu Asn Ala Asn 1015 1020 1025			3485
tgc aga ccc cat atc ttt gag gat cct ttc agt atc aac tct gga aag Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser Ile Asn Ser Gly Lys 1030 1035 1040 1045			3533
aaa atg act aca tca act gac cat ctc aaa cga ggc aca att ctg gac Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg Gly Thr Ile Leu Asp 1050 1055 1060			3581
tgc aat aca tgt aaa ttt gct acc atc aca tgt aat ctc act tct tct Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys Asn Leu Thr Ser Ser 1065 1070 1075			3629
gac atc agc caa gtc aat gtt tgc ctt atc ttg tgg aaa cca act ttt Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu Trp Lys Pro Thr Phe 1080 1085 1090			3677



ata aaa tca tat ttt tcc agc tta aat ctt act ata agg gga gaa ctt	3725
Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr Ile Arg Gly Glu Leu	
1095 1100 1105	
cgg agt gaa aat gca tct ctg gtt tta agt agc agc aat caa aaa aga	3773
Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser Ser Asn Gln Lys Arg	
1110 1115 1120 1125	
gag ctt gct att caa ata tcc aaa gat ggg cta ccg ggc aga gtg cca	3821
Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu Pro Gly Arg Val Pro	
1130 1135 1140	
tta tgg gtc atc ctg ctg agt gct ttt gcc gga ttg ttg ctg tta atg	3869
Leu Trp Val Ile Leu Leu Ser Ala Phe Ala Gly Leu Leu Leu Leu Met	
1145 1150 1155	
ctg ctc att tta gca ctg tgg aag att gga ttc ttc aaa aga cca ctg	3917
Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly Phe Phe Lys Arg Pro Leu	
1160 1165 1170	
aaa aag aaa atg gag aaa tga aa tattttatga aagaaaataa taacaattat	3970
Lys Lys Lys Met Glu Lys *	
1175 1180	
tcaataatct atcctcaggt ttgcctcaaa tatgtgacaa gaaatgtata attcatgaca	4030
tagtcatgta actatgtaat ccatcaggga ttcattactt ggaaaatgac aggtcatgca	4090
ttatccaaaa acaataccaa aaagacatat ttataaaaat gacaaaaaat attttacata	4150
attactcatt tttgttgagt aagcaaaatt acaaagtgtt tttaaaaaaa cctgtacaaa	4210
tatgtttatg tattaaatca ccatccaaaa tatttaagga atatataaaa agatttttat	4270
gatcatagaa acatctatct tcaaaacaat ataaattaag cttttcccct tgattcctgt	4330
tggatatcca tgttcagcat gacagtcagc actcgtaaat gccaaagaaa gaattacctg	4390
aaaaagatca tttctcccta ttcaaatgag aatattttcc ctcggtagaa tccatataca	4450
atatggattg aaaattaagt cacgaagaat acatttagca tctttgtgtt gggttctata	4510
cctaaaaatt ttccctcccg gcccaag	4537

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (608)..(832)

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ccagccccgt ttccctgaac gactgttggg tgtcccgacg gctcctgtgg ctggcagaaa      120
gagaaagagg ataactga ccaggtttgg gtctggtcag agccccgcc tcttcagggc      180
aggtgctgag ttgtggaaat ttgaggagcc tattttcgtg tttagttttc aaactaagac      240
tgctgcttct gcttctctga cgggcttcag ctgggaacag attaactagg ttgctaaaagg      300
aacaatatatt tcttccgtgc actgaagaca ggcaggaaga caacagataa cgtacctgca      360
gtggagaggt taagctcctg tacggaagcg taattcataa atagataaat ataggaaagg      420
acaacaaaga aaatagggat agaataacgg gcagagaatt tagagatgat gtcaggtgat      480
tagttttctc atctaaaagc ttgaaaatcc tgcattgttg tggagtggtc aagcaggtgg      540
tgaagagggc aaactctttg attctacaat agctgatgag ggaacatgga ctttggagga      600
cagaaaa  atg gtt cgt att gtt ctt aca aag aca aag aga gat gca gca      649
          Met Val Arg Ile Val Leu Thr Lys Thr Lys Arg Asp Ala Ala
          1             5             10

aat tgt tgg act tct cta cta gaa tct gaa tat gca gcg gat cct tgg      697
Asn Cys Trp Thr Ser Leu Leu Glu Ser Glu Tyr Ala Ala Asp Pro Trp
  15             20             25             30

gtg caa gac caa atg cag aga aag ctt aca tta gag aga ttc caa aaa      745
Val Gln Asp Gln Met Gln Arg Lys Leu Thr Leu Glu Arg Phe Gln Lys
          35             40             45

gaa aat cct ggt ttt gac ttc agt gga gca gaa atc tca gga aac tac      793
Glu Asn Pro Gly Phe Asp Phe Ser Gly Ala Glu Ile Ser Gly Asn Tyr
          50             55             60

act aaa ggt gga cca gat ttc tca aac ctt gag aaa taa ctgctttttt      842
Thr Lys Gly Gly Pro Asp Phe Ser Asn Leu Glu Lys  *
          65             70             75

tcctgcattc tgtggatcct agcagatatt gccaaacttaa tcagataaac agattatgta      902
atggaagaaa aatgcggatg cctacagtta acagattgca aaatgtatct taaaatgggt      962
ctaaaaattg cattcaaaca taatttacat aggaaatgta ctgtgggaac tattctatgg     1022
atatatgggt aagttgtttt ggacttgttt ttgctcagca tgaagtttta tatgctgcat     1082
tttactaatt ccatatttaa ccatatgttt aatacaaaag aacattagag tatagatcat     1142
gtgaaatgaa ggggtgccttc ggggaaaatt aactttttct tttgatagta tgatattcac     1202
t                                                                1203

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<210> 251  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (36)..(362)

<400> 251

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                                   Met Thr Pro Ser Arg Leu
                                   1                               5

ccc tgg ttg ctt agc tgg gtc tcg gcc acg gcg tgg aga gcg gca aga   101
Pro Trp Leu Leu Ser Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg
              10                      15                      20

tca ccc ctt ctg tgt cat tct ctg agg aaa aca agt tct tct caa gga   149
Ser Pro Leu Leu Cys His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly
              25                      30                      35

gga aag tct gaa ctt gtc aaa cag tcc ctt aag aag ccg aag tta cca   197
Gly Lys Ser Glu Leu Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro
              40                      45                      50

gaa ggt cgt ttt gat gca cca gag gat tcc cat tta gag aaa gaa cca   245
Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro
              55                      60                      65                      70

ctg gaa aaa ttt cca gat gat gtt aat cca gtg acc aaa gaa aaa ggt   293
Leu Glu Lys Phe Pro Asp Asp Val Asn Pro Val Thr Lys Glu Lys Gly
              75                      80                      85

gga ccc agg ggc cca gaa cct acc cga tat gga gat tgg gaa cga aaa   341
Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys
              90                      95                      100

gga cgc tgt att gat ttt taa gt cgcatttct ttaacttcaa tattgttttc   394
Gly Arg Cys Ile Asp Phe *
              105

tgaatatgta catctgaatt aacttatttc tgattatttt ctttctttat atcctttatg   454

tcgtgtagtt tgtataatgt gtttaaatat atatatatat atatatatat atatatatat   514

atgatggcctt tggaagaaaa tatgctgctg taaattagga aagggagacc agcctgacca   574

atatggagaa atctcgcctt tgctagagat acaaaattag ccaggcgtgg tggcatgcac   634

ctgtaatcag cctcctgagt agctgggatt acagacaccc accattgcgc ctggctaatt   694

tttgtatttt tagtaaagac aaggtttcac catgttagcc aggctgggtct cgaactcctg   754

acctcagttg atccacctgc ctacgcctcc caaagtgctg ggattgcagg tgtgagccac   814

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cacgcccagc ctagaaatga ttcttagagc tgtaggcctt tacttcatca tttttcagtt 874  
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 a 935

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 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 252

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 Met Ser Cys Arg Gly  
 1 5

cgg ggc gcg ggc gga cga tgg aac tcc aca tcc tgg agc acc ggc tgc 103  
 Arg Gly Ala Gly Gly Arg Trp Asn Ser Thr Ser Trp Ser Thr Gly Cys  
 10 15 20

aag ttg cca gcg tgc cca agg aga gta tcc cgc tgt tca cct acg ggc 151  
 Lys Leu Pro Ala Ser Pro Arg Arg Val Ser Arg Cys Ser Pro Thr Gly  
 25 30 35

ctg atc aaa ctt gcc ttc ctg ttc tcc aag acc agg tgc aag ttc ttc 199  
 Leu Ile Lys Leu Ala Phe Leu Phe Ser Lys Thr Arg Cys Lys Phe Phe  
 40 45 50

agt ctg act gag aca cca gag gat tac act atc att gtc gat gag gaa 247  
 Ser Leu Thr Glu Thr Pro Glu Asp Tyr Thr Ile Ile Val Asp Glu Glu  
 55 60 65

gga ttc cta gag ctg ccc tcc tca gag cac ctg agt gtg gcg gat gcc 295  
 Gly Phe Leu Glu Leu Pro Ser Ser Glu His Leu Ser Val Ala Asp Ala  
 70 75 80 85

acc tgg ctg gcc ctg aac gtg gtg tcc ggc ggt ggc agc ttc tcc agc 343  
 Thr Trp Leu Ala Leu Asn Val Val Ser Gly Gly Gly Ser Phe Ser Ser  
 90 95 100

tcc cag cct att ggc atg acc aag atc gcc aag tca gtc atc gcc cca 391  
 Ser Gln Pro Ile Gly Met Thr Lys Ile Ala Lys Ser Val Ile Ala Pro  
 105 110 115

ctg gct gac cag aac ata tcc gtg ttc atg ctg tcc acg tat cag aca 439  
 Leu Ala Asp Gln Asn Ile Ser Val Phe Met Leu Ser Thr Tyr Gln Thr  
 120 125 130

gac ttc atc ctg gtg ctc aag cgg gac ctg ccc ttt gtc acc cac acg 487  
 Asp Phe Ile Leu Val Leu Lys Arg Asp Leu Pro Phe Val Thr His Thr

135	140	145	
ttg tca tca gag ttc acc atc ctg tgg tca gtg gct aga ctg tag cag			535
Leu Ser Ser Glu Phe Thr Ile Leu Trp Ser Val Ala Arg Leu *			
150	155	160	
ccgagaacct cggcatcacc agtggcttcg tgaagcccaa gctggtccag atgccggtca			595
tccaccact gtccagcccg agcaacaggt tctgtgtcac cagcctggac cccgacacgc			655
tgctgtctgt tgccacactc ctcatggatg tcatgtccta cttcaatggg tgaggatata			715
actagaagcc agcagtctac aggctggaag aaggccctca ccagaacca acccttggac			775
ttcagcctcc agaactgtga gaaatacata cctgctgttt gtcagacacc agtctatgga			835
attctgttac agtagcctga actcagacat agcccttttc catttataag gtgggttttac			895
cttatatattt atgtaaaagg tccattttat ttatttttga attgttgatt tttttttaag			955
agacacgtgt ttactatggt acccaggctg gactccaact cctggactat tgatcctcct			1015
gtctccacct cccgagttgc tggaactaca ggctaacagc tctgttttaa agatgagaaa			1075
atgggcccga cgcagtggct cacacctgta atcccagcac ttagggtagc tgagccaggt			1135
ggagccactt gaggtcaggt gttcgagatt agcctggcca acatggcaaa accccgtctc			1195
tactaaaaat acaaaaaaaaa aaaa			1219
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tggggccatg atggtagctg attgctaaat ttacataact cagttcatcg tcacaggagc			120
cctaagaggt tgatacgacc atgagtccat tttcactgag gaaaaccgaa gaaaagaaat			180
tgtaaatggc cagagatgta tggctgggtga	atg gcc ctg tgt gga ggc agg		231
	Met Ala Leu Cys Gly Gly Arg		
	1 5		
gcc aag gtg aat gct cct gct atg cag atg atg cag ccc aga gag ccg			279
Ala Lys Val Asn Ala Pro Ala Met Gln Met Met Gln Pro Arg Glu Pro			
10 15 20			

cag cca cct ctg cga gtc cca cag ctg gaa gga gca ccc agt cct ccc 327  
 Gln Pro Pro Leu Arg Val Pro Gln Leu Glu Gly Ala Pro Ser Pro Pro  
           25                          30                          35

aca cta gcc gga cag gcc cgc agc ctg cac tac tga gctg tcacggagga 377  
 Thr Leu Ala Gly Gln Ala Arg Ser Leu His Tyr \*  
           40                          45                          50

ctctaccaag cccagtgcg gagccacaag tggaggacat cctg 421

<210> 254  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (250)..(516)

<400> 254  
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ccctgcaggt tgggggacag ggaaggggga ataaggcctc gggagaagga agatgagcta 120

ggaggcctgg tgcactacac agctcctttg tgctccagg ccacctgccc aagctgggtgt 180

gcctcccttc taaggctctg tcccactggg cacaggaggc agatccagca gcgtggaatc 240

ccagataac atg tcc cac aga ctc tgg caa cgt cac aga tca cat gga 288  
           Met Ser His Arg Leu Trp Gln Arg His Arg Ser His Gly  
                   1                          5                          10

gag gca agt gca ggc caa cga cat ccg cat ccg ggt cct aca gga gga 336  
 Glu Ala Ser Ala Gly Gln Arg His Pro His Pro Gly Pro Thr Gly Gly  
           15                          20                          25

gaa cgg gcg gct cca atc aat gct gtc caa aat ccg gga agt ggc cca 384  
 Glu Arg Ala Ala Pro Ile Asn Ala Val Gln Asn Pro Gly Ser Gly Pro  
           30                          35                          40                          45

gca ggg tgg cct caa ggt ggg cct gag agg gcg ggc cct tgg gga cca 432  
 Ala Gly Trp Pro Gln Gly Gly Pro Glu Arg Ala Gly Pro Trp Gly Pro  
                           50                          55                          60

gga gga agc ccc tat cca gca gca ggt ctt cag act ctg ccc cgg gaa 480  
 Gly Gly Ser Pro Tyr Pro Ala Ala Gly Leu Gln Thr Leu Pro Arg Glu  
                           65                          70                          75

ctt gtg gag agc cca cct cat cac atg agg cct tag gctg tgcttttgtg 530  
 Leu Val Glu Ser Pro Pro His His Met Arg Pro \*  
                   80                          85

aaacattttt cacatttcca gaaggcgtga ggatgttatg gattcgatgc cttccagttc 590

cataagccct ttgtagctgt cattccttta agtgcagcaa caagcc

636

<210> 255  
 <211> 718  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 255

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caccaccaag cctggactgg aagtgtgttg agccctggg tcaggctggc gagccagctc      120
ggccctgccc acccaggggt ttccgagatc acccctggtg aggcggcgtg ccagtccctt      180
gctttcttac ttgttctgca gagcggggag ctgaggctgc atgagggag actcccgtac      240
cccagcacgg tggaggggtg gatgggggtca cgcctgtgcg acccaggagg tggccagcag      300
aaggaaacag tagtgtccac catggtctgc gtctccccac cacggattgt cttgggtccg      360
gatttgagac atggcagggc cagatgagga caacttgatg acagtttaca gag   atg      416
                                   Met
                                   1

gag gca ggg tgc cag gaa gcc acg ggg gag ccc cca ggg cac tca gca      464
Glu Ala Gly Cys Gln Glu Ala Thr Gly Glu Pro Pro Gly His Ser Ala
                    5                      10                      15

gtc cag gca ggg ctg ggc gtc ctg gca agg agc agg gac ctt ctg ccc      512
Val Gln Ala Gly Leu Gly Val Leu Ala Arg Ser Arg Asp Leu Leu Pro
                20                      25                      30

agg ggt gtg gcc agc ctg tgg gtg ctg tgt gca gga ccc cag gaa cca      560
Arg Gly Val Ala Ser Leu Trp Val Leu Cys Ala Gly Pro Gln Glu Pro
                35                      40                      45

agg ccg cag tct ctt ccc tcg ctc cag cat cct ccc aag gcc acc ctt      608
Arg Pro Gln Ser Leu Pro Ser Leu Gln His Pro Pro Lys Ala Thr Leu
                50                      55                      60                      65

ggc tgc act cag cca gag agc tgg ggc aca ggg acc cca cag gtt tcc      656
Gly Cys Thr Gln Pro Glu Ser Trp Gly Thr Gly Thr Pro Gln Val Ser
                    70                      75                      80

ctg gag gct gtc agg ggc tcc ggt ggg ggc ggg ggg tga gcccgtggg      705
Leu Glu Ala Val Arg Gly Ser Gly Gly Gly Gly Gly *
                    85                      90

ttcactgcac ctc      718
    
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<210> 256  
 <211> 1767  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (251)..(1609)

<400> 256

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gagtgagtgt cgtgggttggg gtgctggacc cagagtgcct accctcgctt gcctgggcct      120
cagtttccac atctgcacaa tgggggtgac catccctgcc ctgctggctg ccaggagcgg      180
ctgtgagtct tcaggcgtgg atgcagcctg ggggaagcca tagggcgctt tcacaggcct      240
ggccttcacc  atg gcg gga ggg aga ccg cat ctg aag agg agt ttc tcc      289
              Met Ala Gly Gly Arg Pro His Leu Lys Arg Ser Phe Ser
              1             5             10

atc atc ccc tgc ttt gtc ttc gtg gag tgc gtg ctg ctg ggc att gtg      337
Ile Ile Pro Cys Phe Val Phe Val Glu Ser Val Leu Leu Gly Ile Val
              15             20             25

atc ctg ctt gct tac cgc ctg gag ttc acg gac acc ttc cct gtg cac      385
Ile Leu Leu Ala Tyr Arg Leu Glu Phe Thr Asp Thr Phe Pro Val His
              30             35             40             45

acc cag gga ttc ttc tgc tat gac agt acc tac gcc aag ccc tac cca      433
Thr Gln Gly Phe Phe Cys Tyr Asp Ser Thr Tyr Ala Lys Pro Tyr Pro
              50             55             60

ggg cct gag gct gcc agc cga gtg cct cct gct ctt gtc tac gca ctg      481
Gly Pro Glu Ala Ala Ser Arg Val Pro Pro Ala Leu Val Tyr Ala Leu
              65             70             75

gtc act gcc ggg ccc acc ctc acg atc ctg ctg gga gag ctg gcg cgt      529
Val Thr Ala Gly Pro Thr Leu Thr Ile Leu Leu Gly Glu Leu Ala Arg
              80             85             90

gcc ttt ttc cct gca cca cct tca gcc gtc cca gtc atc ggg gag agc      577
Ala Phe Phe Pro Ala Pro Pro Ser Ala Val Pro Val Ile Gly Glu Ser
              95             100             105

acc atc gtg tct ggg gcc tgc tgc cgc ttc agc ccc cca gtg cgg agg      625
Thr Ile Val Ser Gly Ala Cys Cys Arg Phe Ser Pro Pro Val Arg Arg
              110             115             120             125

ctg gtc cgc ttc ctg ggg gtc tac tcc ttc ggc ctc ttc acc acg acc      673
Leu Val Arg Phe Leu Gly Val Tyr Ser Phe Gly Leu Phe Thr Thr Thr
              130             135             140
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atc ttc gcc aac gcg ggg cag gtg gtg acc ggc aat ccc acg cca cac Ile Phe Ala Asn Ala Gly Gln Val Val Thr Gly Asn Pro Thr Pro His 145 150 155	721
ttc ctg tcc gtg tgc cgc ccc aac tac acg gcc ctg ggc tgc ctg cca Phe Leu Ser Val Cys Arg Pro Asn Tyr Thr Ala Leu Gly Cys Leu Pro 160 165 170	769
cct tct ccg gat cgg cca ggt ccc gac cgc ttt gtc act gac cag ggt Pro Ser Pro Asp Arg Pro Gly Pro Asp Arg Phe Val Thr Asp Gln Gly 175 180 185	817
gcc tgc gct ggc agt ccc agc ctc gtg gcc gcc gcg cgc cgc gcc ttc Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala Arg Arg Ala Phe 190 195 200 205	865
ccc tgc aag gat gcg gcc ctc tgc gcc tac gcg gtc acc tac aca gcg Pro Cys Lys Asp Ala Ala Leu Cys Ala Tyr Ala Val Thr Tyr Thr Ala 210 215 220	913
atg tac gtg act ctc gtg ttc cgc gtg aag ggc tcc cgc ctg gtc aaa Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys 225 230 235	961
ccc tcg ctc tgc ctg gcc ttg ctg tgc ccg gcc ttc ctg gtg ggc gtg Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val 240 245 250	1009
gtc cgc gtg gcc gag tac cga aac cac tgg tcg gac gtg ctg gct ggc Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly 255 260 265	1057
ttc ctg aca ggg gcg gcc atc gcc acc ttt ttg gtc acc tgc gtt gtg Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val 270 275 280 285	1105
cat aac ttt cag agc cgg cca ccc tct ggc cga agg ctc tct ccc tgg His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp 290 295 300	1153
gag gac ctg ggc caa gcc ccc acc atg gat agc ccc ctc gaa aag tta Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Leu 305 310 315	1201
agt gtg gcg cag gaa ccc gag gtc tgc agg ccg cat tcg aca ccg gca Ser Val Ala Gln Glu Pro Glu Val Cys Arg Pro His Ser Thr Pro Ala 320 325 330	1249
cgg ctc acc cca tcc aag tcg cag aac tgc gcc cgc cgt ggc cac ctg Arg Leu Thr Pro Ser Lys Ser Gln Asn Cys Ala Arg Arg Gly His Leu 335 340 345	1297
atc ccc agc tgt gtc tcc tcc agg gcc cca gcc atg tgt tcg tcg ccc Ile Pro Ser Cys Val Ser Ser Arg Ala Pro Ala Met Cys Ser Ser Pro 350 355 360 365	1345
cgt gtg ccc cgt cct cga ttg agg tct gag ccg acg ccc ttg ccc ctg	1393

Arg Val Pro Arg Pro Arg Leu Arg Ser Glu Pro Thr Pro Leu Pro Leu	
370 375 380	
ccc cta ccc ctg cca gcg ccc acc ccc agc cag ggc ccc tcg cct tcc	1441
Pro Leu Pro Leu Pro Ala Pro Thr Pro Ser Gln Gly Pro Ser Pro Ser	
385 390 395	
tcc cct gga cct ggg ggg cca ggc ggg ggt ggt gga cgt ggc cgg aag	1489
Ser Pro Gly Pro Gly Gly Pro Gly Gly Gly Gly Gly Arg Gly Arg Lys	
400 405 410	
ctg ctg ctg ccc acg ccc ctg ctg cgg gac ctg tac acc ctg agt gga	1537
Leu Leu Leu Pro Thr Pro Leu Leu Arg Asp Leu Tyr Thr Leu Ser Gly	
415 420 425	
ctc tat ccc tcc ccc ttc cac cgg gac aac ttc agc cct tac ctg ttt	1585
Leu Tyr Pro Ser Pro Phe His Arg Asp Asn Phe Ser Pro Tyr Leu Phe	
430 435 440 445	
gcc agc cgt gac cac ctg ctg tga ggcccgacca cccacccaga atctgcccag	1639
Ala Ser Arg Asp His Leu Leu *	
450	
tccccacttc ttccctgcc a cgcgtgtgtg tgcgtgtgcc acgtgagtgc caaagtcccc	1699
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cgctcaggt gcttgggagt cggggactcg aaggacgcaa gtgttgagct cgcgcccttc	180
tcgaagccgt ttgggcggac gctgggggtcc ttcgggctcc gcccagggg gtggggctat	240
atgttcggac aatgaccggc cgtccttgcg gtcccgcgcc ctccccgcc ccggaagccg	300
cggcctcgt gagtgcccag cggcccggcg cccaggcctg gggcaccgcg agtgccgaac	360
cttcggctgg acaccaag atg cct ggc gaa cag cag gca gag gaa gag gag	411
Met Pro Gly Glu Gln Gln Ala Glu Glu Glu Glu	
1 5 10	

gag gaa gag atg cag gag gag atg gtg ctg ctg gtg aag ggt gag gag Glu Glu Glu Met Gln Glu Glu Met Val Leu Leu Val Lys Gly Glu Glu 15 20 25	459
gat gag ggt gag gag aag tat gag gtg gtg aaa ctc aag atc ccc atg Asp Glu Gly Glu Glu Lys Tyr Glu Val Val Lys Leu Lys Ile Pro Met 30 35 40	507
gac aac aag gag gtc ccg ggc gag gcg ccc gcg ccg tcc gcc gac ccg Asp Asn Lys Glu Val Pro Gly Glu Ala Pro Ala Pro Ser Ala Asp Pro 45 50 55	555
gcg cgt ccc cac gcg tgc ccc gac tgc ggc cgc gcc ttc gcg cgc cgc Ala Arg Pro His Ala Cys Pro Asp Cys Gly Arg Ala Phe Ala Arg Arg 60 65 70 75	603
tcc acg ctg gcg aag cac gcg cgc acg cac acg ggc gaa cgg ccc ttc Ser Thr Leu Ala Lys His Ala Arg Thr His Thr Gly Glu Arg Pro Phe 80 85 90	651
ggg tgc acc gag tgc ggg cgg cgc ttc tca cag aag tcg gcg ctg acc Gly Cys Thr Glu Cys Gly Arg Arg Phe Ser Gln Lys Ser Ala Leu Thr 95 100 105	699
aaa cac ggc cgc acg cac acg ggc gag cgg ccc tac gag tgc ccc gag Lys His Gly Arg Thr His Thr Gly Glu Arg Pro Tyr Glu Cys Pro Glu 110 115 120	747
tgc gac aaa cgc ttc tcg gcc gcc tcg aac ctg cgg cag cac cgg cgg Cys Asp Lys Arg Phe Ser Ala Ala Ser Asn Leu Arg Gln His Arg Arg 125 130 135	795
cgg cac acg ggc gag aag ccg tac gca tgc gcg cac tgc ggc cgc cgc Arg His Thr Gly Glu Lys Pro Tyr Ala Cys Ala His Cys Gly Arg Arg 140 145 150 155	843
ttc gcg cag agc tcc aac tac gca cag cac ctg cgc gtg cac acg ggc Phe Ala Gln Ser Ser Asn Tyr Ala Gln His Leu Arg Val His Thr Gly 160 165 170	891
gag aag ccg tac gcg tgc ccg gac tgc gga cgc gcc ttt ggc ggc agc Glu Lys Pro Tyr Ala Cys Pro Asp Cys Gly Arg Ala Phe Gly Gly Ser 175 180 185	939
tcg tgc ctg gcg cgc cac cga cgc acg cac acg ggc gag cgg ccc tac Ser Cys Leu Ala Arg His Arg Arg Thr His Thr Gly Glu Arg Pro Tyr 190 195 200	987
gct tgc gcc gac tgc ggc acg cgc ttc gct cag agc tcg gcg ctg gcc Ala Cys Ala Asp Cys Gly Thr Arg Phe Ala Gln Ser Ser Ala Leu Ala 205 210 215	1035
aag cac cgg cgc gtg cac acg ggc gag aag ccg cac cgc tgc gct gtg Lys His Arg Arg Val His Thr Gly Glu Lys Pro His Arg Cys Ala Val 220 225 230 235	1083

tgt ggc cgt cgc ttc ggc cac cgc tcc aac ctg gcg gag cac gcg cgc Cys Gly Arg Arg Phe Gly His Arg Ser Asn Leu Ala Glu His Ala Arg 240 245 250	1131
acg cac aca ggc gag cgg ccc tac ccc tgc gcc gag tgc ggc cgc cgc Thr His Thr Gly Glu Arg Pro Tyr Pro Cys Ala Glu Cys Gly Arg Arg 255 260 265	1179
ttc cgc cta agc tgc cac ttc att cgc cac cga cgc gcg cac atg cgg Phe Arg Leu Ser Ser His Phe Ile Arg His Arg Arg Ala His Met Arg 270 275 280	1227
cgc cgc ctg tat att tgc gcc ggc tgc ggc agg gac ttc aag ctg ccc Arg Arg Leu Tyr Ile Cys Ala Gly Cys Gly Arg Asp Phe Lys Leu Pro 285 290 295	1275
cct ggc gcc acg gcc gcc act gcc acc gag cgt tgc ccg gag tgt gag Pro Gly Ala Thr Ala Ala Thr Ala Thr Glu Arg Cys Pro Glu Cys Glu 300 305 310 315	1323
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actaaccag gctcctcctc gccccggcct ccgggtctgg gaaattgagg ggacggcagg	1439
cccggtgcc ctggaactgg gagacaggga gaatcccctg ccgggggtccc tggaaacagt	1499
gcccaccca catcactaca ttcctcggc ccgtgttagt gaataaagta ttatatcctc	1559
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ccaaacaaa ccaaaaaaat ctcaaagcga ttggacctag cagctcatgc ctgtaatctc	2279
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<400> 258

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tgagacaggt gttttaatca tcgtttttgc acccag  atg aac aag gag agg gca      114
                                     Met Asn Lys Glu Arg Ala
                                     1               5

ttc agg cat ggc gac ccg cct gag cca cct cca ggg gca aga gat gag      162
Phe Arg His Gly Asp Pro Pro Glu Pro Pro Gly Ala Arg Asp Glu
                10                15                20

cag att tac ttt aga aag gac aac agc atc agc cac tgc cac agc ccc      210
Gln Ile Tyr Phe Arg Lys Asp Asn Ser Ile Ser His Cys His Ser Pro
                25                30                35

ccc cag atc atc tgt act ggc tgt cag aac agt cct gct gaa acg cca      258
Pro Gln Ile Ile Cys Thr Gly Cys Gln Asn Ser Pro Ala Glu Thr Pro
                40                45                50

atc aca cct gtc att cac tgc tct gcc cag gac tct tca gtg ggc tcc      306
Ile Thr Pro Val Ile His Cys Ser Ala Gln Asp Ser Ser Val Gly Ser
                55                60                65                70

cca gcg cta agc att tgg cct gac act cca ggc gcc atg tgc cct ggt      354
Pro Ala Leu Ser Ile Trp Pro Asp Thr Pro Gly Ala Met Cys Pro Gly
                75                80                85

ccc cac cta cct ctc cac tgc aaa ttc tgg cca tac acc cct gca ccc      402
Pro His Leu Pro Leu His Cys Lys Phe Trp Pro Tyr Thr Pro Ala Pro
                90                95                100

cca aac agt gca ctc cca tct cag tcc aca ttc tcc cct tac aac atg      450
Pro Asn Ser Ala Leu Pro Ser Gln Ser Thr Phe Ser Pro Tyr Asn Met
                105                110                115

att cat cca aga cca tgg att cgt ggc ctt aag ttt act tct ggt ctg      498
Ile His Pro Arg Pro Trp Ile Arg Gly Leu Lys Phe Thr Ser Gly Leu
                120                125                130

gac ttc tgt gtc agc tcc aga gta tag ttgtc tcaactgaccc cttcacttgg      550
Asp Phe Cys Val Ser Ser Arg Val *
135                140

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[illegible][illegible][illegible]

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<223> n = a,t,c or g

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acgccc	gc	ctt	tc	gt	ac	gc	gc	ga	att	t	gc	ag	at	ct	t	ccc	ct	gg	ac	ct	cc	ggc	180
tgga	gt	ag	ta	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	238	
atg	gcc	gc	gc	ct	gc	ct	gc	at	gc	ct	c	ac	tt	gc	cc	gc	ag	ct	gc	at	gc	ggg	286
Met	Ala	Ala	Leu	Arg	Arg	Met	Leu	His	Leu	Pro	Ser	Leu	Met	Met	Gly								
1						5										10						15	
acg	tgc	cgc	ccc	ttt	gcg	ggc	tca	ctg	gct	gat	agt	tgc	ctg	gcg	gac							334	
Thr	Cys	Arg	Pro	Phe	Ala	Gly	Ser	Leu	Ala	Asp	Ser	Cys	Leu	Ala	Asp								
			20													25						30	
cgc	tgt	ctc	tgg	gat	cgg	ctg	cat	gcc	cag	cct	cgt	ttg	ggc	act	gtc							382	
Arg	Cys	Leu	Trp	Asp	Arg	Leu	His	Ala	Gln	Pro	Arg	Leu	Gly	Thr	Val								
			35													40						45	
ccc	acc	ttc	gac	tgg	ttc	ttt	gga	tac	gac	gaa	gtc	cag	ggg	ctc	cta							430	
Pro	Thr	Phe	Asp	Trp	Phe	Phe	Gly	Tyr	Asp	Glu	Val	Gln	Gly	Leu	Leu								
			50													55						60	
ctg	cca	ttg	ctg	cag	gag	gca	cag	gct	gcc	agt	cct	ctg	cga	gtg	ctg							478	
Leu	Pro	Leu	Leu	Gln	Glu	Ala	Gln	Ala	Ala	Ser	Pro	Leu	Arg	Val	Leu								
			65													70						80	
gat	gtg	ggc	tgt	ggg	act	tcc	agc	cta	tgt	aca	ggc	ctc	tac	acc	aaa							526	
Asp	Val	Gly	Cys	Gly	Thr	Ser	Ser	Leu	Cys	Thr	Gly	Leu	Tyr	Thr	Lys								
																85						90	
tct	cca	cac	cca	gtg	gat	gtg	ctg	ggg	gtg	gac	ttt	tct	cct	gtg	gct							574	
Ser	Pro	His	Pro	Val	Asp	Val	Leu	Gly	Val	Asp	Phe	Ser	Pro	Val	Ala								
																100						105	
gtg	gcc	cac	atg	aat	agc	ctc	ctg	gag	ggt	ggc	cca	agc	caa	aca	cct							622	
Val	Ala	His	Met	Asn	Ser	Leu	Leu	Glu	Gly	Gly	Pro	Ser	Gln	Thr	Pro								
																115						120	
cta	tgc	cct	gga	cac	cct	gcc	tca	agc	ctc	cac	ttc	atg	cac	gcc	gat							670	
Leu	Cys	Pro	Gly	His	Pro	Ala	Ser	Ser	Leu	His	Phe	Met	His	Ala	Asp								
																130						135	
gct	cag	aac	ctg	ggg	gct	gtg	gct	tct	tca	ggc	tct	ttc	caa	cta	ctg							718	
Ala	Gln	Asn	Leu	Gly	Ala	Val	Ala	Ser	Ser	Gly	Ser	Phe	Gln	Leu	Leu								
																145						150	
ctg	gac	aaa	ggc	aca	tgg	gat	gct	gtt	gcc	cgg	gga	ggt	ctg	cct	agg							766	
Leu	Asp	Lys	Gly	Thr	Trp	Asp	Ala	Val	Ala	Arg	Gly	Gly	Leu	Pro	Arg								
																165						170	
gct	tac	cag	ctt	cta	tca	gaa	tgc	ttg	agg	gtt	cta	aac	cct	cag	ggg							814	
Ala	Tyr	Gln	Leu	Leu	Ser	Glu	Cys	Leu	Arg	Val	Leu	Asn	Pro	Gln	Gly								

180	185	190	
acc ctg att cag ttc tca gat gag gac cct gat	gtg cga ctg ccc tgc	862	
Thr Leu Ile Gln Phe Ser Asp Glu Asp Pro Asp	Val Arg Leu Pro Cys		
195	200	205	
ctg gaa caa ggg tcc tat ggc tgg act gtg act	gtg cag gag cta ggc	910	
Leu Glu Gln Gly Ser Tyr Gly Trp Thr Val Thr	Val Gln Glu Leu Gly		
210	215	220	
ccg ttc agg ggc atc acc tac ttt gct tac ttg	att caa ggc tct cat	958	
Pro Phe Arg Gly Ile Thr Tyr Phe Ala Tyr Leu	Ile Gln Gly Ser His		
225	230	235	
taa agac attttagtag tcctgaccct agtatttctg	tgggcaagga gagggctgaa	1015	
★			
gaactgtctt tgcaagctat ctggctgcaa agtgagaatt	tgagtcctgg cttccacatt	1075	
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ttgaagatcg tgacgtcttg taactagcag tgtgtgcaca	gaatcctact caaggaacgt	180	
cttggcccag cgatgcaaag aactgaagtt tcaagctgga	agagcctgta ttgtcctcac	240	
aatagtatag aagaattcaa gagaggagag agagacagca	ccgaatgaag actgtaaaag	300	



aaaagaagga atgccagaga ttgagaaaat ctgccaagac taggagggta acccagagga 360

aaccgtcttc agggcctgtt tgctggct atg ctt cga gaa cct ggg gat ccc 412  
Met Leu Arg Glu Pro Gly Asp Pro  
1 5

gaa aaa tta ggg gaa ttt ctt cag aaa gac aat atc agc gtg cat tat 460  
Glu Lys Leu Gly Glu Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr  
10 15 20

ttc tgt ctt atc tta tct agt aag ctg cct cag agg ggc cag tcc aac 508  
Phe Cys Leu Ile Leu Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn  
25 30 35 40

aga ggt ttc cat gga ttt ctg cct gaa gac atc aaa aag gag gca gcc 556  
Arg Gly Phe His Gly Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala  
45 50 55

cgg gct tct agg aag atc tgc ttt gtg tgc aag aaa aag gga gct gct 604  
Arg Ala Ser Arg Lys Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala  
60 65 70

atc aac tgc cag aag gat cag tgc ctc aga aac ttc cat ctg cct tgt 652  
Ile Asn Cys Gln Lys Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys  
75 80 85

ggc caa gaa agg ggt tgc ctt tca caa ttt ttt gga gag tac aaa tca 700  
Gly Gln Glu Arg Gly Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser  
90 95 100

ttt tgt gac aaa cat cgc cca aca cag aac atc caa cat ggg cat gtg 748  
Phe Cys Asp Lys His Arg Pro Thr Gln Asn Ile Gln His Gly His Val  
105 110 115 120

ggg gag gaa agc tgc atc tta tgt tgt gaa gac tta tcc caa cag agt 796  
Gly Glu Glu Ser Cys Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser  
125 130 135

gtt gag aac atc cag agc ccg tgt tgt agt caa gcc atc tac cac cgc 844  
Val Glu Asn Ile Gln Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg  
140 145 150

aag tgc ata cag aaa tat gcc cac aca tca gca aag cat ttc ttc aaa 892  
Lys Cys Ile Gln Lys Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys  
155 160 165

tgt cca cag tgt aac aat cga aaa gag ttt cct caa gaa atg ctg aga 940  
Cys Pro Gln Cys Asn Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg  
170 175 180

atg gga att cat att cca gac agg agg tgg tgc ctc att ctg tgt gct 988  
Met Gly Ile His Ile Pro Asp Arg Arg Trp Cys Leu Ile Leu Cys Ala  
185 190 195 200

act gcg gat ccc acg gaa ccc aca gga ctg ctc ctc tct tag atctaac 1037  
Thr Ala Asp Pro Thr Glu Pro Thr Gly Leu Leu Leu Ser \*  
205 210

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<222> (166)..(672)

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gactgtgtcc aaaaagcaag taaaccact tcaagcacac aaatc atg gtg aag 174
Met Val Lys
1
acc aac atg tat cat aat gaa aag gtg aac ttt cat gtt gaa tgt aaa 222
Thr Asn Met Tyr His Asn Glu Lys Val Asn Phe His Val Glu Cys Lys
5 10 15
gac tat gta aaa aag gca aag gta aag atc aac cca gtg caa cag agc 270
Asp Tyr Val Lys Lys Ala Lys Val Lys Ile Asn Pro Val Gln Gln Ser
20 25 30 35
cgg ccc ttg ttg agc cag att cac aca gat gca gca aag gag aac acc 318
Arg Pro Leu Leu Ser Gln Ile His Thr Asp Ala Ala Lys Glu Asn Thr
40 45 50
tgc tac tgt ggt gca gtg gca aag aga caa gag aaa aaa ggg atg gag 366

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Cys Tyr Cys Gly Ala Val Ala Lys Arg Gln Glu Lys Lys Gly Met Glu	
55 60 65	
cct ctt caa ggt cat gcc act ccc gct ttg cct ttt aaa gaa acc cag	414
Pro Leu Gln Gly His Ala Thr Pro Ala Leu Pro Phe Lys Glu Thr Gln	
70 75 80	
gaa cta tta cta agt ccc ctg ccc cag gaa ggt cct ggg tca ctt gca	462
Glu Leu Leu Leu Ser Pro Leu Pro Gln Glu Gly Pro Gly Ser Leu Ala	
85 90 95	
gca gga gag agc agc agt ctt tct gcc agt aca tca gtc tca gat tca	510
Ala Gly Glu Ser Ser Ser Leu Ser Ala Ser Thr Ser Val Ser Asp Ser	
100 105 110 115	
tcc cag aaa aaa gaa gag cac aat tat tct ctt ttt gtc tcc gac aac	558
Ser Gln Lys Lys Glu Glu His Asn Tyr Ser Leu Phe Val Ser Asp Asn	
120 125 130	
ttg ggt gaa cag cca act aaa tgc agt cct gaa gaa gat gag gag gac	606
Leu Gly Glu Gln Pro Thr Lys Cys Ser Pro Glu Glu Asp Glu Glu Asp	
135 140 145	
gag gag gat gtt gat gat gag gac cat gat gaa gga ttc ggc agt gag	654
Glu Glu Asp Val Asp Asp Glu Asp His Asp Glu Gly Phe Gly Ser Glu	
150 155 160	
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His Tyr Ile Ile Ile *	
165	

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tggatgacct cggtgagatg cgcagaaagg tcctggaatc cttgtctgac aagattcaga	180
agaagaagaa aaaaattctg agttctgtgg tggcggaac ccagcgtccc tatgaagagg	240
ctctcctaca gaagatgtgg gaaagccagg acttcctgaa atgcatgcaa aggttcagag	300
aagtgcgtgg gcaaggaagg tgggtggtccc tgtagggaag cagtggatgg gcagtcccca	360

cggcctgtgg gaatgagtca ggcttctcct gatctggcgc tcaggaggtc tctgattctg 420  
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 attggcactg acctaggcct tgcctcatta gccagcaatg ctggctaata acccatttac 540  
 aaccatcacc aaacatcacc tattcagcca ttaaccaccg tgcattcttta ccccttgatt 600  
 cttgttactg cccaccaccc attatcagtg ttaatgaact tcaccatcac tgccttcttg 660  
 aattaatttt cattatcttg cctcttcact gggttttaaat gtgcatgccc ttcactatct 720  
 ctgccagcct ccattcattc ccacgattga gcattccccg ccactttgta acctgtctcc 780  
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 tttgaggaga ac atg cct gta tta agg gcc gag gtg gaa gag ctg caa 1068  
 Met Pro Val Leu Arg Ala Glu Val Glu Glu Leu Gln  
 1 5 10  
 gcc cag acc cgg gaa ccc cga gag gtc ata ttt gag gat gtt ctg ctt 1116  
 Ala Gln Thr Arg Glu Pro Arg Glu Val Ile Phe Glu Asp Val Leu Leu  
 15 20 25  
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 30 35 40  
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 Val Glu Glu Pro Leu Pro Phe \*  
 45 50  
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 ggaatctgca gcaagcattt ccagaatatc tagataaatg gcagaggttag ctctactaga 180  
 gttttaacag agacaaaaca gccttacttc aggag atg cca ttt agg act ttc 233  
 Met Pro Phe Arg Thr Phe  
 1 5  
 aca gct cta ggt aag cta ata tct gac ttc aaa gat tca aag gac ggg 281  
 Thr Ala Leu Gly Lys Leu Ile Ser Asp Phe Lys Asp Ser Lys Asp Gly  
 10 15 20  
 ctg act ctt tac ttt gta gag aca gcg tca cgc tct gtt gtg ctg gct 329  
 Leu Thr Leu Tyr Phe Val Glu Thr Ala Ser Arg Ser Val Leu Ala  
 25 30 35  
 ggt ctt gaa ctc ttg acc tca agt gat cct cca acc tca gcc tcc caa 377  
 Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Thr Ser Ala Ser Gln  
 40 45 50  
 agc act gga att aca ggt gta agc cac ttt tcc cag cct ggg ctg gct 425  
 Ser Thr Gly Ile Thr Gly Val Ser His Phe Ser Gln Pro Gly Leu Ala  
 55 60 65 70  
 ttc ttg tta gag gtc aat gca gtt ggt gac ttt aaa tga atgctaatat 474  
 Phe Leu Leu Glu Val Asn Ala Val Gly Asp Phe Lys \*  
 75 80  
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agagcccagc aacgtttaat caagaatgag aaa atg gaa tgc cca gat gct ctg	174
Met Glu Cys Pro Asp Ala Leu	
1 5	
gct gtg gaa agt aag cca agt cgt aag agc gta tgc atc aac cct ctg	222
Ala Val Glu Ser Lys Pro Ser Arg Lys Ser Val Cys Ile Asn Pro Leu	
10 15 20	
atg tcc ccc aag ctt gcc ctg caa gtg gat gca gat ggg ttt cct gtt	270
Met Ser Pro Lys Leu Ala Leu Gln Val Asp Ala Asp Gly Phe Pro Val	
25 30 35	
aag ccc aag agt act gaa gga atg aag gga agg aag ggg aag cag gtg	318
Lys Pro Lys Ser Thr Glu Gly Met Lys Gly Arg Lys Gly Lys Gln Val	
40 45 50 55	
tct gaa atc ttg cct aaa gca gaa gtt cag agt aaa cgc aag aga aca	366
Ser Glu Ile Leu Pro Lys Ala Glu Val Gln Ser Lys Arg Lys Arg Thr	
60 65 70	
gaa ggc agc agc cct cca gat agt aag aac aag ggg cct acg gtg aaa	414
Glu Gly Ser Ser Pro Pro Asp Ser Lys Asn Lys Gly Pro Thr Val Lys	
75 80 85	
gcc agc aaa gaa aag cat gct gat gga gcc acc aaa acc cct gct gcc	462
Ala Ser Lys Glu Lys His Ala Asp Gly Ala Thr Lys Thr Pro Ala Ala	
90 95 100	
aag agg cca gct gca agg gac aga agc agc caa ccc ccc aaa aag acg	510
Lys Arg Pro Ala Ala Arg Asp Arg Ser Ser Gln Pro Pro Lys Lys Thr	
105 110 115	
tct ttg aaa gag aat aaa gtg aag atc cct aaa aag tcc gct ggg aag	558
Ser Leu Lys Glu Asn Lys Val Lys Ile Pro Lys Lys Ser Ala Gly Lys	
120 125 130 135	
agc tgc cct ccc tcc agg aaa gaa aaa gag aat aca aac aaa agg cct	606
Ser Cys Pro Pro Ser Arg Lys Glu Lys Glu Asn Thr Asn Lys Arg Pro	
140 145 150	
tcc cag tct att gcc tcg gaa aca ctg acg aaa cct gca aaa cag aag	654
Ser Gln Ser Ile Ala Ser Glu Thr Leu Thr Lys Pro Ala Lys Gln Lys	
155 160 165	
ggg gcc ggt gaa tcc tct tca agg cct cag aaa gcc acg aat agg aag	702
Gly Ala Gly Glu Ser Ser Ser Arg Pro Gln Lys Ala Thr Asn Arg Lys	
170 175 180	
cag agt agt gga aag act cgg gcc aga ccc tca acg aaa acc cca gag	750
Gln Ser Ser Gly Lys Thr Arg Ala Arg Pro Ser Thr Lys Thr Pro Glu	
185 190 195	
agc agt gca gct cag aga aag cga aag ctg aag gca aag ctg gac tgt	798
Ser Ser Ala Ala Gln Arg Lys Arg Lys Leu Lys Ala Lys Leu Asp Cys	
200 205 210 215	
tcg cac ggc aaa cgg agg cgg ctg gat gca aag tga ttgg aaagatggta	848

Ser His Gly Lys Arg Arg Arg Leu Asp Ala Lys \*

220

225

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 tcagaaaatg catctcagat ggagaaggga acttgcagag tccttctctg aggctaaggg 1028  
 aagttatata ttatattctg gttgttcctt ggggttttaa cttggaacca agcagttttc 1088  
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 agccgagaag accaccatca tgcacataaa aggagctttt cagcagccac cctgcagcat 1268  
 ctgcccacga acagatgccc ttctttgcaa accccagcag tgaacttccc tctctgtctt 1328  
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 tgcccatggg acaagagata tgcacaagt gttaattttt gtttacaac tctaaaaaat 1568  
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 agagtacttc catattcaaa gaaagccgaa ctattatttc cagtaataga aaggtttaag 1808  
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 ttgagtaatt agcaaaggac agatggttta aaagtagccc agtgtctctg tgagcatccc 1988  
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 cctaacagga gtcactggct caggaccca gggagaaacg ctctccccac ccacgccatg 935  
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 Met  
 1  
 gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc 166  
 Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser  
 5 10 15  
 cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta 214  
 Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu  
 20 25 30  
 gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt 262  
 Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly  
 35 40 45  
 ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg 310  
 Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val  
 50 55 60 65  
 tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag 358  
 Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu  
 70 75 80  
 ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc 406  
 Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val  
 85 90 95

CCDS: CDS: 1-387

atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg	454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val	
100 105 110	
acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag	502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys	
115 120 125	
gtc aca ctg gcg gaa ttc cag gac tac tac agc ggc gtg agt gcc tcc	550
Val Thr Leu Ala Glu Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser	
130 135 140 145	
atg aac acg gat gag gag ttc gtg gcc atg atg acc agt gcc tgg cag	598
Met Asn Thr Asp Glu Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln	
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Leu *	
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ggttatgtgt gcacttcaca cctctgactt ttttcagggt tcctattg atg gtt agg	177
Met Val Arg	
1	

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agc agg att tcg ggg atg aag gcg gca gca gca aga gga ggc tgc gac 225
Ser Arg Ile Ser Gly Met Lys Ala Ala Ala Ala Arg Gly Gly Cys Asp
      5              10              15

tgc gga ccc cag att cgt ccc cct cca cca cac aca acg cca aga cgg 273
Cys Gly Pro Gln Ile Arg Pro Pro Pro Pro His Thr Thr Pro Arg Arg
      20              25              30              35

gcc cca gga ggg cgt gaa gag aag act tcc ttt cct ctc ctc tcg cct 321
Ala Pro Gly Gly Arg Glu Glu Lys Thr Ser Phe Pro Leu Leu Ser Pro
              40              45              50

cct ggc gct ggc cgt atg aag gtg tct ccc aga agc att agc aga gga 369
Pro Gly Ala Gly Arg Met Lys Val Ser Pro Arg Ser Ile Ser Arg Gly
              55              60              65

gcc ctg tgg gag aaa tga ggagtg acccaaaaga aacttgctca aggacagcct 423
Ala Leu Trp Glu Lys *
              70

ccttaaagca gacttccata taccccaacc tgcaaaagaa gactttacgt gaaatgttac 483

ag 485

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tgagttctga cccctggagg agccactgtg gaagcagagc aatcgcc atg gag ttt 176
Met Glu Phe
              1

gtg atg aag cag gct cta gga ggg gcc acc aag gac atg ggg aag atg 224
Val Met Lys Gln Ala Leu Gly Gly Ala Thr Lys Asp Met Gly Lys Met
      5              10              15

ctg ggg ggt gac gag gag aag gac cca gac gcc gcc aag aag gag gag 272
Leu Gly Gly Asp Glu Glu Lys Asp Pro Asp Ala Ala Lys Lys Glu Glu
      20              25              30              35

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gag cgg cag gag gcg ctg cgc cag gcg gag gag gag cgc aag gcc aag	320
Glu Arg Gln Glu Ala Leu Arg Gln Ala Glu Glu Glu Arg Lys Ala Lys	
40 45 50	
tac gcc aag atg gag gcg gag cgc gag gcc gtg cgc cag ggc atc cga	368
Tyr Ala Lys Met Glu Ala Glu Arg Glu Ala Val Arg Gln Gly Ile Arg	
55 60 65	
gac aag tac ggc atc aag aag aag gag gag cgc gag gcc gag gcc cag	416
Asp Lys Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln	
70 75 80	
gcc gcc atg gag gcc aac tcc gag ggg agc ttg acg cgg ccc aag aag	464
Ala Ala Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys	
85 90 95	
gcc atc ccg ccg ggc tgc ggg gac gag gtg gag gag gag gac gag agc	512
Ala Ile Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser	
100 105 110 115	
atc ctg gac acc gtc atc aag tac ctg ccc ggg ccg ctg cat gac atg	560
Ile Leu Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu His Asp Met	
120 125 130	
ctc aag atg tat ccc cgc gcg gga cag ctg ccc cgc gga gcc ggc cat	608
Leu Lys Met Tyr Pro Arg Ala Gly Gln Leu Pro Arg Gly Ala Gly His	
135 140 145	
tga acac tgcaccctcc acaggagccg cagaggccct gaggcaccgg actgcttgga	665
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gaccctgcgc ccctgccag cacctcctcc gtgggcagct cctcggtgtg gggcctgcgg	725
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cggcatccga gccctgttt ctctccatt catgtttatt ttgcatcaca atttggtgaa	845
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gggcttgga ttgaccttca tgaccttaca tagctttaga gaagccataa cgcttgactg	1025
caataactaac gaccgacgcc cctccggaca gagaccaccg cgccctctg cgcccatcg	1085
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<222> (497)..(766)

<400> 270

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ggccactgcc gtgtgtgcca ccctgaactt caagctgccc tgaaccgcgt gcgttttctca      240
gtgtcacgta cagctcggcc tgaccgtttg ccttttagtg ttctcttctt tctcgggtgtc      300
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ctgaactcgg cagctgcgtc ctttttccca tcattctctt tgtcctttgc tagctgtcat      420
ttcttccttc ttggcttcaa ctgcacatcc ctgggtttgt cctaataagg aatttttccc      480
acttgagtag acaagc      atg aga ata tca tta ttt tta tat gtt ata tgt      529
                        Met Arg Ile Ser Leu Phe Leu Tyr Val Ile Cys
                        1          5          10

tat att ttt agc aga gaa aaa agt gga aaa tgt gtg caa act tgc aga      577
Tyr Ile Phe Ser Arg Glu Lys Ser Gly Lys Cys Val Gln Thr Cys Arg
                        15          20          25

agg ccc ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc      625
Arg Pro Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly
                        30          35          40

ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc ccc gga      673
Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly Pro Gly
                        45          50          55

gga ggg tcg tcc ctg tgc cca tgc ggt cag aaa ggc ccc gga gga ggg      721
Gly Gly Ser Ser Leu Cys Pro Cys Gly Gln Lys Gly Pro Gly Gly Gly
                        60          65          70          75

tca tct ctg tgc cca tgc ggt cag gtt ggg gct gag gca ctt tga tca      769
Ser Ser Leu Cys Pro Cys Gly Gln Val Gly Ala Glu Ala Leu *
                        80          85          90

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agagtgagct ccagcctaga tcgtctgggt ttgaatccag ctccatgact gtggccgtgt      889
tgctaattct ctctgagtct cagcttcctt ttctgtaaaag tgggtataat agtagagtct      949
aactgtggg gctgtggtgg gattcattgt gttcacacgt gtgcagggct gagaacaggg      1009
cccaaacag ggtaggcaca atgaagcatg agtcagaata ataatacaga tgacagtttc      1069
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tctatcacta atttgaacat tgcagacagt gcaaagaaga aaattag 1116

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gac cca cgc gtc cgg ttt ccc agc gcg gtg ccc gcc cct cat cct cct 98  
 Asp Pro Arg Val Arg Phe Pro Ser Ala Val Pro Ala Pro His Pro Pro  
 15 20 25

cca gtc tcc ctg ccc tcg ccg act gcc gcc cca ggc tcc gcc atg ggg 146  
 Pro Val Ser Leu Pro Ser Pro Thr Ala Ala Pro Gly Ser Ala Met Gly  
 30 35 40

aat gtg cca tcc gcg gtg aag cac tgc ctg agc tac cag cag ctt ctg 194  
 Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln Leu Leu  
 45 50 55 60

cgg gag cat ctg tgg atc ggg gat tca gtg gca ggg gcg ctg gac ccc 242  
 Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu Asp Pro  
 65 70 75

gcg cag gaa aca tcc cag tta tct gga ctg cct gag ttt gtt aaa ata 290  
 Ala Gln Glu Thr Ser Gln Leu Ser Gly Leu Pro Glu Phe Val Lys Ile  
 80 85 90

gta gaa gtt ggg cct agg gat gga ttg cag aat gaa aag gtt ata gtt 338  
 Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val  
 95 100 105

cct aca gat ata aaa att gaa ttt atc aat cga ctt tcc caa act ggc 386  
 Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly  
 110 115 120

ttg tct gta ata gaa gtg act agc ttt gtg tct tcc aga tgg gta cca 434  
 Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro  
 125 130 135 140

cag gtt gct gct gga gct act gag ata tca gtt ttt gga gct gca tct 482  
 Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser  
 145 150 155

gaa tcc ttt agc aag aag aat att aac tgt tcc att gaa gaa agt atg 530  
 Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met

160	165	170	
gga aaa ttt gag gag gtt gtt aag tct gca aga cac atg aat att cca			578
Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro			
175	180	185	
gca cga ggg tac tta tga aatccc acaaattctg ttttggttaat gtttattggt			632
Ala Arg Gly Tyr Leu *			
190			
aaagcttact caaaaattat ctagagattc ttatatcatt tataaaaata tacatagaat			692
atcatatttc tattttgttt aatcagggtg atcactatat agttacatct cattaacatc			752
actgctgatt attagtgagt atctagcttg tggaatgtgt catgcaattg aaatcagagg			812
tactagcatg caaatctggc attattaact attttattaa cactctagca cccaaatgca			872
gccctcttat ctcagcctac atgtgctgat aagttggtat aaactcaca cagcttttgg			932
aaaagaatca cctaattgtgg ttttcaaatt ttttttaaaa catgactttt tcttcaaaga			992
gtattttatg tagaacttca atagaatata gcagatataa aattgagctg ctctgggaaa			1052
tcattttatc cattctttct cccctcaat ggctgacttt tctacttct ctgggtgatc			1112
ccaaagcacc tccatagtat cttgcagaac actgtttaaa aatacttgat aaattgctta			1172
tagaagataa atataaactt tcagttctct actattttct attatatgtg atttctataa			1232
atttaggagt atcagagata tcaatccctt tctcctcgcc ttgccttttt cttgtggaaa			1292
cttatcagct gttcattcta agagatgttg attacaggac atggaaaata aaaactgacc			1352
caagatccac aaacctaat ttctctctca ggagtttaga aatgggtatac caaacatggg			1412
tacttgtatt gaaagattat gtgattttgt cactgagttc actattttgg ggttcttagg			1472
atggagccac atgcaaacca gtgacaggac agagtagtag aaagcagaaa tggaaaaagg			1532
aggctcctag cggatgatgag aggtatgggg gagggaggag agggaaaaat ctgccttggt			1592
gcttgtctgc ttccaggacc aatagttgcc tcaagtatta taaccaggcc tatgtgctgt			1652
gaaacctata atgcattttt gtgtgtgttt gtttcttaag gaagaatttg tttctaagac			1712
attagctact ttttctatta attttataaa tatggagata tgatgaacac acatcttaac			1772
aagttaaagt gcatagcgat tggtaataga aggttgaaag ctggggatgg atttgggtgc			1832
aggctgtact tcccttagtt gaggtgagca aagttcatgg tagcgggaaa gattcaacag			1892
ttaatgagaa agataagtga gtcaattgtg actgaaaata ttagtgaaat gattggaatt			1952
tcaatcaagg tgttttgggg gaacaattag agttagacta tacctagtaa aatattttgt			2012
tagtttggtt tctatttata ttttctctgt cctccatagt aagtctacat gagtttctaa			2072

aatttgaaat tacttttgta attaagatag atgcatatca tgtaaggact atatgagaaa 2132  
aattttaaatt ccaaggcaat gtacttccaa agacataaaa taaaggatat ttattttttca 2192  
ggcaaaaagtt acaaaaccac aatcaaaaag gagagatata ctattggttt ctcaattcga 2252  
atataaataa gttgtctcaa ttttctttta aataaagaga aagatgaaga ccctatttcta 2312  
cttcaatatg tgtttaaagt gtggagtata agcttttaaag taattctcat tgggaagtta 2372  
aaaagtatgt gactataaga agtaaattgc ttatgtagct tgctcttcaa ataggaaggg 2432  
tttttttagt gttgaaagat ggatgcaaata ataagttgta ggaagtaacc ttttattatc 2492  
ttagctttct gttgtaaaat ggaatagtta atgtaactgg gctaataaaa atcttaaacc 2552  
ctcttaaaaa aaaaaaa 2569

<210> 272  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (64)..(630)

<400> 272  
tttcgtaaat agttgctccg tgggctttcc gcatttcacc ctgctccagg cagcgtggtc 60  
tgt atg gct ccg ccc tgg gca gga gga gaa aga aga ggg cca ggc acc 108  
Met Ala Pro Pro Trp Ala Gly Gly Glu Arg Gly Pro Gly Thr  
1 5 10 15  
acg tgc ctg cac tct ccc tgg atg ctg gag gct gct ccg ccg tgg gca 156  
Thr Cys Leu His Ser Pro Trp Met Leu Glu Ala Ala Pro Pro Trp Ala  
20 25 30  
gga gga gaa gga aga gaa ctg ggt gcc gcc tgc ctg cac tct ctc cgg 204  
Gly Gly Glu Gly Arg Glu Leu Gly Ala Ala Cys Leu His Ser Leu Arg  
35 40 45  
atg ctg gag gct gga ggc agt gag gca gca aca gcg cga ggg cga ggc 252  
Met Leu Glu Ala Gly Gly Ser Glu Ala Ala Thr Ala Arg Gly Arg Gly  
50 55 60  
gac ttt gga gct gcc tca tgc agc gac ctc gcc ttc cgc tgc gcc tcc 300  
Asp Phe Gly Ala Ala Ser Cys Ser Asp Leu Ala Phe Arg Cys Ala Ser  
65 70 75  
tcc cag aac cca aga agc ctg gaa cct gtg gcg tcc agc cct gaa agg 348  
Ser Gln Asn Pro Arg Ser Leu Glu Pro Val Ala Ser Ser Pro Glu Arg  
80 85 90 95



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agg aga cgg caa ccc agc cgc gct ttt gcc tgc act ctc cct gga tgc      396
Arg Arg Arg Gln Pro Ser Arg Ala Phe Ala Cys Thr Leu Pro Gly Cys
                100                      105                      110

tgg agg ctg gag gca gtg acg cag caa cag cgc gag gcg act ttg gag      444
Trp Arg Leu Glu Ala Val Thr Gln Gln Gln Arg Glu Ala Thr Leu Glu
                115                      120                      125

cgg cct cat ata gcg acc tcg cct tcc gct gcg cgt cct ccc aga gcc      492
Arg Pro His Ile Ala Thr Ser Pro Ser Ala Ala Arg Pro Pro Arg Ala
                130                      135                      140

caa gaa gcc cgg aac ctg tgg cat cca tct ctg aaa gga gaa gac ggc      540
Gln Glu Ala Arg Asn Leu Trp His Pro Ser Leu Lys Gly Glu Asp Gly
                145                      150                      155

aac cca gcc gag gca cta ctg ggt tgg ggt ctc cac gac cga gct ggt      588
Asn Pro Ala Glu Ala Leu Leu Gly Trp Gly Leu His Asp Arg Ala Gly
                160                      165                      170                      175

ctc atc aag tgg cgt cca aca agg ggc tca aac ccg ggt tga ggggttg      637
Leu Ile Lys Trp Arg Pro Thr Arg Gly Ser Asn Pro Gly *
                180                      185

ctggagcgcac ggagaacgtg gaactacact ggaggacacc agagtactct taagcaatcc      697

cttggccaaa accagcaact gatttggata ccatcaagac acctgaaatc ttgtcatgag      757

ccagatactg aggaagagat tttgggaaga acccaaggac cccccagttg cagccatgtc      817

aagactgaca ataaggaaga catcagtccc agcaagcaac attcatcggg cacagccacc      877

catgtggggc cagatcaaga agttgacaca gacggcggaa gaaaatctga agaaagcgga      937

tgaccagcta caatgagtaa tctaattgga gctatgatgg ctgtgctcac cattgccatg      997

agtattcccc cagcacctgc tgaaacaaaa aacattatac ttattgggca tatattcctt     1057

ttccaccagt ttcattggcca gtgacatggt tagaccccc agtggaggta tacactaatg     1117

atagcttttg gatacctggt tctacagatg atagaggccc atctcacccc caaaaggagg     1177

gaacattatg aatatttcgt tgggatt                                           1204

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<210> 273  
 <211> 943  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (356)..(610)

<400> 273  
gagaagggat ggcgggcgct ggctgctgag catgctggca ggccccgggac tctgcgttgc 60  
tgccaccctc tcctcagggc cacctcccc tggagccaga ggcaccgtag tcaagagaca 120  
acacgaggag cctccactcc gggcagctgt tcgggttcgt ctcagttgcc aaacggaata 180  
atttcacact ctgataacct gattgttttt taagccttgt ggtattctta attgcccggt 240  
gttagataaa ctgtgattta aagagcacia acccagatag cagacacaca aaacactggc 300  
ttgggaatag caaggagtga cttatttact ttagcaaagc cttttataag gtttt atg 358  
Met  
1  
gct gca cta tca gag tgt cac cca gaa gtc act ctg gga ggt gaa cgc 406  
Ala Ala Leu Ser Glu Cys His Pro Glu Val Thr Leu Gly Gly Glu Arg  
5 10 15  
aca ggg cag gac caa ggt agc acc agg cag aca caa gcc tcc ctg tgg 454  
Thr Gly Gln Asp Gln Gly Ser Thr Arg Gln Thr Gln Ala Ser Leu Trp  
20 25 30  
gga gcc tct ctc atc tgt cgg ggg cct gcg ggc agg gga gag gag gtg 502  
Gly Ala Ser Leu Ile Cys Arg Gly Pro Ala Gly Arg Gly Glu Glu Val  
35 40 45  
ccc cta cag gca agc ctg tgg ggg cgg cac cca gac ctc tgg aga cca 550  
Pro Leu Gln Ala Ser Leu Trp Gly Arg His Pro Asp Leu Trp Arg Pro  
50 55 60 65  
agc acc act gcc acc cag tgc tgg gga gaa ggg atg gag aga atc aaa 598  
Ser Thr Thr Ala Thr Gln Cys Trp Gly Glu Gly Met Glu Arg Ile Lys  
70 75 80  
agc cag cac tag gaa ggctgttgc tctgcatgac ccatggcggg gcaggtggag 653  
Ser Gln His \*  
85  
gggaagccgg acacaggaga gctcctgggg ccagacacgc cacctctgcc aggtgagccc 713  
acgtcctgag ctgcagcctc aggaaccag ggttcttcca agaactccct tcacccaca 773  
tggtcacttc ccagcctcct gaccacact caggccagc tccttccag actgtcatcc 833  
tctttctaga aggaacagg gaccccttg ggtccgggat ggccctgagc tcccctgtgt 893  
gccccacacc ctggcgggtct ttgccccat gtgccctgag tctgatgcct 943

<210> 274  
<211> 803  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> CDS  
 <222> (27) .. (488)

<400> 274

aatttaggtg acactataga agagct atg acg tcg cat gca cgc gta cgt aag	53
Met Thr Ser His Ala Arg Val Arg Lys	
1 5	
ctt gga tcc tct aga gcg gcc gct gtc gtt gtt ctg agg aga aac ctt	101
Leu Gly Ser Ser Arg Ala Ala Val Val Val Leu Arg Arg Asn Leu	
10 15 20 25	
aca agt gta ata aat gtg cga agg ttt tta atc aaa aag gaa tcc ttg	149
Thr Ser Val Ile Asn Val Arg Arg Phe Leu Ile Lys Lys Glu Ser Leu	
30 35 40	
cac aac atc aga gag ttc ata ctg gag aga aac ctt aca agt gta atg	197
His Asn Ile Arg Glu Phe Ile Leu Glu Arg Asn Leu Thr Ser Val Met	
45 50 55	
aat gtg gca agg ttt tta atc aaa aag caa gcc ttg caa aac atc aga	245
Asn Val Ala Arg Phe Leu Ile Lys Lys Gln Ala Leu Gln Asn Ile Arg	
60 65 70	
gag ttc ata ctg cag aga aac ctt aca agt gta atg agt gtg gca aag	293
Glu Phe Ile Leu Gln Arg Asn Leu Thr Ser Val Met Ser Val Ala Lys	
75 80 85	
cct tta ctg gac agt caa cac tta ttc acc atc aag caa tcc atg ggt	341
Pro Leu Leu Asp Ser Gln His Leu Phe Thr Ile Lys Gln Ser Met Gly	
90 95 100 105	
gta ggg aaa ctt tac aaa tgt aat gat tgt cac aaa gtc ttc agt aat	389
Val Gly Lys Leu Tyr Lys Cys Asn Asp Cys His Lys Val Phe Ser Asn	
110 115 120	
gct aca acc att gca aat cat tac aga atc cat att gaa gag aga tct	437
Ala Thr Thr Ile Ala Asn His Tyr Arg Ile His Ile Glu Glu Arg Ser	
125 130 135	
aca agt gta ata aat gtg gca aat ttt tca gac gtc att cat aac ttg	485
Thr Ser Val Ile Asn Val Ala Asn Phe Ser Asp Val Ile His Asn Leu	
140 145 150	
tag ttca tcagtgaact catactggag agaaacctta caaatatcat gactgtgaca	542
*	
aggtcttcag tcaagcttca tcctatgcaa aacatagaat tcatacagga gagaaacctc	602
acaagtgtga tgattgtggc aaagccttta cttcatgttc acacctcatt agacatcaga	662
gaattcatac tggacagatg ccttacaaat gtaaggggtgg caaggtcttc actctgtggg	722
cattccatgc agaacatcag aaaattcatt tttgagataa ttgttcctaaa taaaatgaat	782

<210> 275  
 <211> 1078  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (357)..(713)

<220>  
 <221> misc\_feature  
 <222> (1)...(1078)  
 <223> n = a,t,c or g

<400> 275

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acgccccccc actgagacta cagtccagng ncggcgaant cgagaaaaca cagcaacgag      60
gtgaatgaca tgggagacag acctgggggtc ttttagggac ggaaagcctc agccaagacc      120
cagactccca gggatcatcaa cctcctcggg tcactaacc tccccagtgt ctgtctaccc      180
ctaagtccag agaacacgtc ctctctaggg tcgagccgga atcaatatag gctacaaggg      240
catcagttca ggctgcgcgg aggagagaag gaagtgctga tgtggagtcc tccctcccc      300

ttctccttca cccccaagtg tctcccacga ctgccctccc cgacctctag ctgacc      356
atg gca tca gag gca gaa aaa aca ttc cat cgg ttt gct gcg ttt gga      404
Met Ala Ser Glu Ala Glu Lys Thr Phe His Arg Phe Ala Ala Phe Gly
  1             5             10             15

gaa tca tca agc agt ggc act gaa atg aac aac aag aac ttc tcc aag      452
Glu Ser Ser Ser Ser Gly Thr Glu Met Asn Asn Lys Asn Phe Ser Lys
          20             25             30

ctg tgc aaa gac tgt ggc atc atg gat ggc aag aca gtc acc tcc acg      500
Leu Cys Lys Asp Cys Gly Ile Met Asp Gly Lys Thr Val Thr Ser Thr
          35             40             45

gac gtg gac atc gtg ttc agc aaa gtc aag gcc aag aac gcc cga acc      548
Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala Lys Asn Ala Arg Thr
          50             55             60

atc acg ttt caa cag ttc aaa gag gca gtg aag gaa ctg ggc cag aag      596
Ile Thr Phe Gln Gln Phe Lys Glu Ala Val Lys Glu Leu Gly Gln Lys
          65             70             75             80

cgc ttc aaa ggg aag agt cca gat gaa gtc ctg gag aac att tat gga      644
Arg Phe Lys Gly Lys Ser Pro Asp Glu Val Leu Glu Asn Ile Tyr Gly
          85             90             95

ctc atg gag ggc aaa gac cca gcc acc act ggc gct act ttt ccc tgg      692
Leu Met Glu Gly Lys Asp Pro Ala Thr Thr Gly Ala Thr Phe Pro Trp

```

100	105	110	
tta cct atg caa gaa acc tga aa gtgacccctag acccctccac ctccccaatc			745
Leu Pro Met Gln Glu Thr *			
115			
ccagctacgg ggaggcgggc ctgcatgggtg gttaagatca aggcttttga gtgaaacaga			805
ccaggaattg aatcctgcct ctgcagctta caaactgcac accatctatc tgtttacgaa			865
accactgaaa gcttccttgt ttcattctgtt catgaggata gtatttttta ctcacggcag			925
tatgaggatc cattaagatg tatatcaaga gtttttagac cagtgcccg cacaatgtgga			985
tgctctcgtc tcgcctggac agcacacaca ctccaactcc agtaagactc aactcaaata			1045
tatctcttat acaacttcaa gaaaaaaaaa aaa			1078

<210> 276  
 <211> 724  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (74)..(223)

<400> 276		
aaaaatgaaa catttaccct agtgtctaag tgtctaataa ggaagaactt aaaatgtggg		60
cacctatgta aaa atg tca aaa ttg aaa atg cgg agg ggg cat ctg gaa		109
Met Ser Lys Leu Lys Met Arg Arg Gly His Leu Glu		
1 5 10		
tca aac tgg tgg cct ctc ggt ctg cag tct tat gct cta acc ctg agc		157
Ser Asn Trp Trp Pro Leu Gly Leu Gln Ser Tyr Ala Leu Thr Leu Ser		
15 20 25		
tat acc cct tcc tgc tgc tgt ggg ggt caa tta atg cct ttg act tgt		205
Tyr Thr Pro Ser Cys Cys Cys Gly Gly Gln Leu Met Pro Leu Thr Cys		
30 35 40		
gcg gtc aca ccc aga tga ccagtc acctgtgtgt tgccacttca caatggaagc		259
Ala Val Thr Pro Arg *		
45 50		
tcctaggagc tgccaggctt acctcagtga aaactcattg accttgtgca tagcaagagg		319
cagtccccgc tcctcagata acccccgtgc ctgtgtcttc cctgccttga gtccttagtt		379
atgggcagca ggctggaaaa gcactgccag cagccactag aatggccttg agagtcatcc		439
tcacagtaact gtttatgggtg ggcacatata agagaaactt tgtgtgactg aggtgtctgt		499

tctaaaacac ttaatgacag agttgggcct ggctctcctg gtccagtgtt ccattcaggg 559  
cagattcagc acaactgcag tctaggacaa aagatgattc tttcaacttt tactttcttca 619  
gttaatacaa atgaagaatg ttagagaagg agcaactcca agaaatagtg agaagtgtgt 679  
agctgagtag atttcccaaa agcattaata gggccagtgt tacca 724

<210> 277  
<211> 1007  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (119)..(682)

<400> 277  
tttcgtcagt tcgcggcagt tcgcgcggga gcggggcgcc tgggtggatg ggcgcttggg 60  
cgctgggct gccggacggt gggaacggaa gtcgctgtgg gacgctgagg aagccagg 118  
atg gcg act ccg agc aag aag acg tca act cca agc ccc cag cct tcc 166  
Met Ala Thr Pro Ser Lys Lys Thr Ser Thr Pro Ser Pro Gln Pro Ser  
1 5 10 15  
aag aga gct ctc ccg aga gac cct tcg tcg gag gtc ccg agc aag agg 214  
Lys Arg Ala Leu Pro Arg Asp Pro Ser Ser Glu Val Pro Ser Lys Arg  
20 25 30  
aag aat tcg gcc ccg cag ctg ccg ctg ttg cag tcg tcc ggg cct ttc 262  
Lys Asn Ser Ala Pro Gln Leu Pro Leu Leu Gln Ser Ser Gly Pro Phe  
35 40 45  
gtg gaa ggc tct atc gtc cgc atc tcg atg gag aac ttc cta aca tat 310  
Val Glu Gly Ser Ile Val Arg Ile Ser Met Glu Asn Phe Leu Thr Tyr  
50 55 60  
gat att tgt gaa gta tct cct gga ccc cac ttg aat atg atc gtt gga 358  
Asp Ile Cys Glu Val Ser Pro Gly Pro His Leu Asn Met Ile Val Gly  
65 70 75 80  
gcc aat gga aca ggg aag tcg agc att gtg tgt gcc att tgc ctt ggt 406  
Ala Asn Gly Thr Gly Lys Ser Ser Ile Val Cys Ala Ile Cys Leu Gly  
85 90 95  
tta gct gga aaa cct gct ttc atg gga cga gca gat aag gtt ggg ttt 454  
Leu Ala Gly Lys Pro Ala Phe Met Gly Arg Ala Asp Lys Val Gly Phe  
100 105 110  
ttt gtg aag aga gga tgt tct aga ggc atg gtt gaa att gaa ttg ttc 502  
Phe Val Lys Arg Gly Cys Ser Arg Gly Met Val Glu Ile Glu Leu Phe  
115 120 125  
agg gct tct gga aat ctt gta atc acc cgt gag att gat gtg gca aaa 550

Arg Ala Ser Gly Asn Leu Val Ile Thr Arg Glu Ile Asp Val Ala Lys  
130 135 140

aat cag tcc ttt tgg ttc atc aac aaa aaa tct aca acc cag aaa ata 598  
Asn Gln Ser Phe Trp Phe Ile Asn Lys Lys Ser Thr Thr Gln Lys Ile  
145 150 155 160

gtg gaa gag aaa gtt gca gcc tta aat att cag tgg gga atc ttt gcc 646  
Val Glu Glu Lys Val Ala Ala Leu Asn Ile Gln Trp Gly Ile Phe Ala  
165 170 175

agt ttc tcc tca gga caa gtt gga gga att tgc taa actc agcaaattgg 696  
Ser Phe Ser Ser Gly Gln Val Gly Gly Ile Cys \*  
180 185

actcctcgaa gcaactggaaa gttcaatggg cccccagaaa ttgcgcaata tcctgtgtac 756

tccaaactgt ggagaagaag aacagtcccg acccctgcgc agagaaactg ctgtctctcg 816

cgaaatgggtg tgcccgttc gaggattata cccccgttg gagggcttct agcagggccg 876

cacatattcg agctgccacc cacagcacgc tggacaaaag ctgcgcctc agagacatat 936

tgacgcgag cgcatcacag gcaactccact catgcacagg agccctgcgg cgcggaacgg 996

cgcacacacc g 1007

<210> 278  
<211> 439  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (18)..(131)

<400> 278

cgacgatttc gtccaaa atg gcg gca gcg atg gat gtg gat acc ccg agc 50  
Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser  
1 5 10

ggc acc aac agc ggc gcg ggc aag aag cgc ttt gaa gtg aaa aag gtt 98  
Gly Thr Asn Ser Gly Ala Gly Lys Lys Arg Phe Glu Val Lys Lys Val  
15 20 25

ggg tct cgc cag cgc ctt cct cag gga agc tag agaggcgc ggatctggct 149  
Gly Ser Arg Gln Arg Leu Pro Gln Gly Ser \*  
30 35

ggcaggcccc aggatggtcg aggcgcggag taaagggttt catttcaggg cgttcctggg 209

accgggtacc acgaaaggaa gccggggggc gggctcttaga gttgatcggc gtgacggcgg 269

cccactgttg ggggaagtgt tggtttcgct gtgaggctaa ggggccaatc acagagctgc 329

ttattgagat acgcgggggtt gcgacttggc ggcgggagcc aagcgcttga gctgtcactg 389  
gagtgggttga gaggtggggg aaggacaggg tatggtggag tgggggtgggt 439

<210> 279  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (24)..(1049)

<400> 279  
tttcgtcacg ggccttggtc acc atg tcg gtg ctg gat gcg ctt tgg gag 50  
Met Ser Val Leu Asp Ala Leu Trp Glu  
1 5

gat cgg gat gtc cgt ttc gac ctg tcc gcg cag caa atg aaa aca aga 98  
Asp Arg Asp Val Arg Phe Asp Leu Ser Ala Gln Gln Met Lys Thr Arg  
10 15 20 25

cct gga gaa gtc ctt att gat tgt tta gat tcc att gaa gac acc aaa 146  
Pro Gly Glu Val Leu Ile Asp Cys Leu Asp Ser Ile Glu Asp Thr Lys  
30 35 40

gga aat aat gga gat aga ggt aga ctc ttg gta aca aat tta aga att 194  
Gly Asn Asn Gly Asp Arg Gly Arg Leu Leu Val Thr Asn Leu Arg Ile  
45 50 55

ctc tgg cac tct ttg gca tta tca aga gtc aat gtt tct gtc ggt tac 242  
Leu Trp His Ser Leu Ala Leu Ser Arg Val Asn Val Ser Val Gly Tyr  
60 65 70

aat tgc ata ttg aat att aca aca agg act gct aac tct aaa tta cga 290  
Asn Cys Ile Leu Asn Ile Thr Thr Arg Thr Ala Asn Ser Lys Leu Arg  
75 80 85

ggc caa act gaa gct ctc tat ata cta aca aaa tgt aac agt act cgt 338  
Gly Gln Thr Glu Ala Leu Tyr Ile Leu Thr Lys Cys Asn Ser Thr Arg  
90 95 100 105

ttt gaa ttt ata ttt aca aat ttg gtt cct gga agc cct aga ctt ttt 386  
Phe Glu Phe Ile Phe Thr Asn Leu Val Pro Gly Ser Pro Arg Leu Phe  
110 115 120

act tct gtg atg gca gta cac aga gct tat gaa act tct aaa atg tat 434  
Thr Ser Val Met Ala Val His Arg Ala Tyr Glu Thr Ser Lys Met Tyr  
125 130 135

cgt gat ttt aaa tta aga agt gca cta att cag aac aag caa cta aga 482  
Arg Asp Phe Lys Leu Arg Ser Ala Leu Ile Gln Asn Lys Gln Leu Arg  
140 145 150



ctg ttg cca caa gaa cat gta tat gat aaa ata aat gga gtt tgg aat	530
Leu Leu Pro Gln Glu His Val Tyr Asp Lys Ile Asn Gly Val Trp Asn	
155 160 165	
tta tcc agt gat cag ggc aat tta gga acc ttt ttt att acc aat gtg	578
Leu Ser Ser Asp Gln Gly Asn Leu Gly Thr Phe Phe Ile Thr Asn Val	
170 175 180 185	
aga att gtg tgg cat gca aat atg aat gat agt ttt aat gtc agt ata	626
Arg Ile Val Trp His Ala Asn Met Asn Asp Ser Phe Asn Val Ser Ile	
190 195 200	
cca tat ctg caa att cgt tca ata aag att aga gat tca aaa ttt ggt	674
Pro Tyr Leu Gln Ile Arg Ser Ile Lys Ile Arg Asp Ser Lys Phe Gly	
205 210 215	
tta gct ctt gtc ata gaa agc tct cag cag agt ggt gga tat gtt ctt	722
Leu Ala Leu Val Ile Glu Ser Ser Gln Gln Ser Gly Gly Tyr Val Leu	
220 225 230	
ggc ttt aaa ata gat cct gtg gaa aaa cta caa gaa tca gtt aag gaa	770
Gly Phe Lys Ile Asp Pro Val Glu Lys Leu Gln Glu Ser Val Lys Glu	
235 240 245	
atc aat tca ctt cac aaa gtc tat tct gcc agt ccc ata ttt gga gtt	818
Ile Asn Ser Leu His Lys Val Tyr Ser Ala Ser Pro Ile Phe Gly Val	
250 255 260 265	
gat tat gag atg gaa gaa aag ccc cag ccg ctc gaa gct ctg aca gtc	866
Asp Tyr Glu Met Glu Glu Lys Pro Gln Pro Leu Glu Ala Leu Thr Val	
270 275 280	
gaa caa att caa gat gat gta gaa ata gac tct gat ggt cac acg gat	914
Glu Gln Ile Gln Asp Asp Val Glu Ile Asp Ser Asp Gly His Thr Asp	
285 290 295	
gct ttt gtg gct tat ttt gct gat ggc aat aag caa caa gat cgt gaa	962
Ala Phe Val Ala Tyr Phe Ala Asp Gly Asn Lys Gln Gln Asp Arg Glu	
300 305 310	
cct gta ttt tca gaa gaa ctg ggg ctt gca ata gag aaa ttg aag gat	1010
Pro Val Phe Ser Glu Glu Leu Gly Leu Ala Ile Glu Lys Leu Lys Asp	
315 320 325	
gga ttc acc cta cag gga ctt tgg gaa gta atg agt tga ttgaccttga	1059
Gly Phe Thr Leu Gln Gly Leu Trp Glu Val Met Ser *	
330 335 340	
gttgagatgg atttctatta aagatatctc tagttttaaag atactagtca cctgccataa	1119
gtcatggaat agttttttata ttacagctt ttatatattaa aacttgtaag agttttttta	1179
atgattgagg aaaaagtcac ttagaaaact tcagtttttcg gccagcgcgt cgagggaggg	1239
gccagcgaca catggcctag taaccgtccg gccgcggcgc tggcttaagc catggctgag	1299

ggtagccgga ttcctcaggc ccgggcgctc ctacagcagt gcctgcacgc ccggctgcaa 1359  
 attcgcccag ccgatgggga cgtcgcggcc cagtgggtgg aggtccaaag aggactggtg 1419  
 atctacgtgt gctttttcaa gggagctgat aaagaacttc ttcccaaat ggatctacga 1479  
 ctctggctcc actgattacc ttaaccatat tacatggaat gatgtaaggg agaaacagaa 1539  
 gactcttggt gaacagctcc tgtctttggt gaacagctcc ccagggcctc ctacccgcaa 1599  
 actgcttgct aagaatctag ccatacttta tagtattgga gacacattct ccgttcatga 1659  
 agcaatcgat aaatgtaatg atcttattcg tagcaaagat gattctccaa gttatcttcc 1719  
 cactaagctg taagtgaaac attaaaacag aacagaaaac aaaaaaaaaa aa 1771

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (162)..(1064)

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 cgggtcgacg atttcgttgc gcgttccgga actggtttcc cggaaggatt atgtctgcgc 120  
 cctcgatccg accggaagtt gcacgctgag ccgcggacac c atg cag tcg gat 173  
 Met Gln Ser Asp  
 1  
 gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc ttc aaa 221  
 Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser Phe Lys  
 5 10 15 20  
 ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc ctg act 269  
 Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser Leu Thr  
 25 30 35  
 gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag tat gcc 317  
 Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln Tyr Ala  
 40 45 50  
 act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag gtt ata 365  
 Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys Val Ile  
 55 60 65  
 gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg ctt agt 413  
 Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg Leu Ser  
 70 75 80

aaa aac tat gag aaa gca ctg gag caa ata gat gaa aat ctg att tac	461
Lys Asn Tyr Glu Lys Ala Leu Glu Gln Ile Asp Glu Asn Leu Ile Tyr	
85 90 95 100	
tggtgg ccc cgt ttc att cga cac aaa tgt aag cag aga ttc acc aag atc	509
Trp Pro Arg Phe Ile Arg His Lys Cys Lys Gln Arg Phe Thr Lys Ile	
105 110 115	
acc caa tac cta att cga att aga aaa ctt aca cta aag cga cag agg	557
Thr Gln Tyr Leu Ile Arg Ile Arg Lys Leu Thr Leu Lys Arg Gln Arg	
120 125 130	
aaa ctt gtt cct ttg agt aag aag gtg gag cgt agg gag aaa aga aga	605
Lys Leu Val Pro Leu Ser Lys Lys Val Glu Arg Arg Glu Lys Arg Arg	
135 140 145	
gag gaa aag gca tta ata gct gct cag ctg gac aat gcc att gag aag	653
Glu Glu Lys Ala Leu Ile Ala Ala Gln Leu Asp Asn Ala Ile Glu Lys	
150 155 160	
gaa tta ctg gag aga ctg aaa caa gat acg tat ggc gac atc tac aac	701
Glu Leu Leu Glu Arg Leu Lys Gln Asp Thr Tyr Gly Asp Ile Tyr Asn	
165 170 175 180	
ttc ccc att cat gcc ttc gac aaa gcc ctg gaa caa cag gag gca gag	749
Phe Pro Ile His Ala Phe Asp Lys Ala Leu Glu Gln Gln Glu Ala Glu	
185 190 195	
agt gac tct tca gat act gag gaa aaa gat gat gat gat gat gat gag	797
Ser Asp Ser Ser Asp Thr Glu Glu Lys Asp Asp Asp Asp Asp Asp Glu	
200 205 210	
gaa gat gtg ggg aaa aga gaa ttt gtc gaa gat ggt gag gta gat gag	845
Glu Asp Val Gly Lys Arg Glu Phe Val Glu Asp Gly Glu Val Asp Glu	
215 220 225	
agt gac ata agt gat ttt gag gat atg gat aaa ctg gat gcc agc agt	893
Ser Asp Ile Ser Asp Phe Glu Asp Met Asp Lys Leu Asp Ala Ser Ser	
230 235 240	
gat gaa gat cag gat ggt aaa tcc tcc agt gag gag gag gaa gaa aag	941
Asp Glu Asp Gln Asp Gly Lys Ser Ser Ser Glu Glu Glu Glu Glu Lys	
245 250 255 260	
gcc ctt agt gcg aaa cac aaa ggc aaa atg ccc ttg aga gga cca ctg	989
Ala Leu Ser Ala Lys His Lys Gly Lys Met Pro Leu Arg Gly Pro Leu	
265 270 275	
cag aga aaa cga gcc tat gtg gaa ata gaa tac gag cag gag aca gag	1037
Gln Arg Lys Arg Ala Tyr Val Glu Ile Glu Tyr Glu Gln Glu Thr Glu	
280 285 290	
ccc gtg gcc aaa gcc aaa acc acg tga tttcc ctttcagtca tttataccca	1089
Pro Val Ala Lys Ala Lys Thr *	
295 300	
ggactgaaca tgcagaactg	1109

<210> 281  
 <211> 2018  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (36)..(1520)

<220>  
 <221> misc\_feature  
 <222> (1)...(2018)  
 <223> n = a,t,c or g

<400> 281  
 acagctccca agccacaggc agaagcccca cagag atg gag cag aag gaa ggg 53  
 Met Glu Gln Lys Glu Gly  
 1 5

aag ctc tct gag gat ggg acc acc gtc tcc cca gct gcg gac aac cct 101  
 Lys Leu Ser Glu Asp Gly Thr Thr Val Ser Pro Ala Ala Asp Asn Pro  
 10 15 20

gag atg tca gga ggt gga gcc cct gca gag gag acc aaa ggc aca gct 149  
 Glu Met Ser Gly Gly Gly Ala Pro Ala Glu Glu Thr Lys Gly Thr Ala  
 25 30 35

gga aag gcc atc aat gag ggg cct ccc act gag tca gga aag cag gaa 197  
 Gly Lys Ala Ile Asn Glu Gly Pro Pro Thr Glu Ser Gly Lys Gln Glu  
 40 45 50

aag gca cca gcc gag gac ggc atg tca gca gaa ctc cag ggg gaa gca 245  
 Lys Ala Pro Ala Glu Asp Gly Met Ser Ala Glu Leu Gln Gly Glu Ala  
 55 60 65 70

aat gga tta gat gag gtc aaa gtg gaa tct cag agg gag gct ggt ggg 293  
 Asn Gly Leu Asp Glu Val Lys Val Glu Ser Gln Arg Glu Ala Gly Gly  
 75 80 85

aaa gag gat gct gag gct gaa ctt aaa aag gag gat ggt gag aag gaa 341  
 Lys Glu Asp Ala Glu Ala Glu Leu Lys Lys Glu Asp Gly Glu Lys Glu  
 90 95 100

gag acc act gtg ggt tct cag gag atg act ggc agg aaa gaa gag acc 389  
 Glu Thr Thr Val Gly Ser Gln Glu Met Thr Gly Arg Lys Glu Glu Thr  
 105 110 115

aaa tct gaa ccc aaa gag gct gag gaa aag gag agc acg ctg gcc tct 437  
 Lys Ser Glu Pro Lys Glu Ala Glu Glu Lys Glu Ser Thr Leu Ala Ser  
 120 125 130

gag aag cag aag gct gag gag aaa gag gcc aaa cct gaa tct ggg cag 485  
 Glu Lys Gln Lys Ala Glu Glu Lys Glu Ala Lys Pro Glu Ser Gly Gln

135	140	145	150	
aaa gcc gat gcc aat gac aga gac aag cct gaa cct aag gca aca gtt				533
Lys Ala Asp Ala Asn Asp Arg Asp Lys Pro Glu Pro Lys Ala Thr Val	155	160	165	
gag gag gag gac gcc aag aca gcc tct cag gag gag aca ggc cag agg				581
Glu Glu Glu Asp Ala Lys Thr Ala Ser Gln Glu Glu Thr Gly Gln Arg	170	175	180	
aaa gag tgc agc act gaa ccc aag gag aag gct act gat gaa gag gcc				629
Lys Glu Cys Ser Thr Glu Pro Lys Glu Lys Ala Thr Asp Glu Glu Ala	185	190	195	
aag gct gaa tcg cag aag gct gtt gtg gag gat gag gct aag gct gaa				677
Lys Ala Glu Ser Gln Lys Ala Val Val Glu Asp Glu Ala Lys Ala Glu	200	205	210	
ccc aag gag ccc gat ggg aaa gag gag gcc aaa cat ggt gca aaa gag				725
Pro Lys Glu Pro Asp Gly Lys Glu Glu Ala Lys His Gly Ala Lys Glu	215	220	225	230
gag gct gat gca aaa gag gag gcg gag gat gca gag gag gca gag cca				773
Glu Ala Asp Ala Lys Glu Glu Ala Glu Asp Ala Glu Glu Ala Glu Pro	235	240	245	
ggc agt ccc agc gaa gag cag gag cag gac gtg gaa aaa gag cca gag				821
Gly Ser Pro Ser Glu Glu Gln Glu Gln Asp Val Glu Lys Glu Pro Glu	250	255	260	
gga ggg gca ggg gtg att ccc agc tcc cca gag gag tgg cct gag agc				869
Gly Gly Ala Gly Val Ile Pro Ser Ser Pro Glu Glu Trp Pro Glu Ser	265	270	275	
ccc act ggg gag ggg cac aac ctc agc aca gat ggg ctg ggt cca gac				917
Pro Thr Gly Glu Gly His Asn Leu Ser Thr Asp Gly Leu Gly Pro Asp	280	285	290	
tgt gta gct tcc gga cag acc agt cct tca gcc agt gag tct tca ccc				965
Cys Val Ala Ser Gly Gln Thr Ser Pro Ser Ala Ser Glu Ser Ser Pro	295	300	305	310
agc gac gtg ccc cag agt ccc cct gag tcc cct tcc tca ggg gag aag				1013
Ser Asp Val Pro Gln Ser Pro Pro Glu Ser Pro Ser Ser Gly Glu Lys	315	320	325	
aag gag aag gca cca gag cgc agg gta tca gcc cct gct cgg ccc cgg				1061
Lys Glu Lys Ala Pro Glu Arg Arg Val Ser Ala Pro Ala Arg Pro Arg	330	335	340	
ggg ccc ggg gca cag aac cgc aaa gcc atc gtg gac aag ttt ggc ggg				1109
Gly Pro Gly Ala Gln Asn Arg Lys Ala Ile Val Asp Lys Phe Gly Gly	345	350	355	
gca gct tcc ggc ccc acg gcc ttg ttc cgc aac act aag gca gcc ggg				1157
Ala Ala Ser Gly Pro Thr Ala Leu Phe Arg Asn Thr Lys Ala Ala Gly	360	365	370	

gca gcc att ggt ggt gtc aag aac atg ctc ttg gag tgg tgc cga gcc 1205  
Ala Ala Ile Gly Gly Val Lys Asn Met Leu Leu Glu Trp Cys Arg Ala  
375 380 385 390

atg aca aaa aaa tac gag cat gtg gac atc cag aac ttc tcc tcc agc 1253  
Met Thr Lys Lys Tyr Glu His Val Asp Ile Gln Asn Phe Ser Ser Ser  
395 400 405

tgg agc agt ggt atg gcc ttc tgt gcc ctc atc cac aag ttc ttc cct 1301  
Trp Ser Ser Gly Met Ala Phe Cys Ala Leu Ile His Lys Phe Phe Pro  
410 415 420

gac gcc ttt gac tac gca gag ctg gat ccc gca aag cgc cgg cac aac 1349  
Asp Ala Phe Asp Tyr Ala Glu Leu Asp Pro Ala Lys Arg Arg His Asn  
425 430 435

ttc acc ctg gcc ttc tcc aca gca gag aaa ctg gct gac tgt gct cag 1397  
Phe Thr Leu Ala Phe Ser Thr Ala Glu Lys Leu Ala Asp Cys Ala Gln  
440 445 450

ctg ctg gac gtg gat gac atg gtg cgg ttg gct gtg ccc gac tcc aag 1445  
Leu Leu Asp Val Asp Asp Met Val Arg Leu Ala Val Pro Asp Ser Lys  
455 460 465 470

tgc gtc tac aca tac atc cag gaa ctg tac cgc agc ctt gtg cag aaa 1493  
Cys Val Tyr Thr Tyr Ile Gln Glu Leu Tyr Arg Ser Leu Val Gln Lys  
475 480 485

gga ctg gtg aag acc aag aag aag tga ggagg tgactggctc tgtgggcaga 1545  
Gly Leu Val Lys Thr Lys Lys Lys \*  
490 495

gatgggcagg gtgcccagct cagcagccac ggcccggggg ttcccttctg ctccatggag 1605

gcaccagagc cagggggetta ggcaagggtg tgtggcggtg gttttaactg cattaagagt 1665

acttttgtaa aatcctgtct ggccccctca gtgctctctc ccatacttgg ncccaggaac 1725

ctctgcactc tgggataata aactctggcc cataggggat tcctcacctg ctgaggtctc 1785

aataactgcg caaggtgttt gggaaaggac aatggcctgg tcccaccact aaccagctgt 1845

gtgacacata cagttaacct ctctgggccc cagtttacag tctgaaaggg gataatgaga 1905

gttccaacct tatgaagggtg ttgcaagagt taaacgagat aatgaaatgg gcaaaaagct 1965

ttgcccagtc ctgccactca agtgttcagt aagtggctgc caaaaataaa aaa 2018

<210> 282  
<211> 706  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39) .. (377)

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<400> 282
cgccctccccg ctgaccccg gatctgaggc tgtcagag      atg act ctg gtt ctg      53
                                         Met Thr Leu Val Leu
                                           1              5

tcc atg aat aga ttc tgc gag ccc att gtc tcg gaa gga gct gct gaa      101
Ser Met Asn Arg Phe Cys Glu Pro Ile Val Ser Glu Gly Ala Ala Glu
                10              15              20

att gct ggg tac caa aca cta tgg gag gct gac agc tac gga ggc cca      149
Ile Ala Gly Tyr Gln Thr Leu Trp Glu Ala Asp Ser Tyr Gly Gly Pro
                25              30              35

agc ccc cca ggg cca gca caa gct cct ttg cag gga gac cgg gga gct      197
Ser Pro Pro Gly Pro Ala Gln Ala Pro Leu Gln Gly Asp Arg Gly Ala
                40              45              50

ggt ccc cca ctg gca gct cca ctt ggt gac ttc ctt tct gtg tat cag      245
Gly Pro Pro Leu Ala Ala Pro Leu Gly Asp Phe Leu Ser Val Tyr Gln
                55              60              65

gag cag agc aga gga caa ctt gta gaa gac atg acc att aag aga cat      293
Glu Gln Ser Arg Gly Gln Leu Val Glu Asp Met Thr Ile Lys Arg His
                70              75              80              85

caa ctt cgc aac aaa tat aag aca agg ata caa gga ttc cta tgt gat      341
Gln Leu Arg Asn Lys Tyr Lys Thr Arg Ile Gln Gly Phe Leu Cys Asp
                90              95              100

gca gct agg ttt tta tat cct tct aac aaa tgg tga gcag gagacttttt      391
Ala Ala Arg Phe Leu Tyr Pro Ser Asn Lys Trp *
                105              110

tggaataat tagttgtgaa attccatttt tctgacagcc ccttaaattt gaagttattt      451

catttgtagt taaggttatc acatccctgc caattttact agattttttc agagacaagc      511

attcagcatg gcattagtaa tgatggttta aactaggtgc agaactgtcc catgaagaga      571

agaatgatat cagtatttaa ataataaaag aagagacaat gtatggttta tagtgattca      631

ttttaagatt gctgtatttt gattttgtgg tttaaaataa atgcattaag gatcttttaa      691

gttaaaaaaa aaaaaa                                                    706

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<210> 283  
 <211> 758  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (539) .. (697)

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 aaagtagaaa atttcacact aggatgaaca tactgtattc tctactaggt agcgaagctg 120  
 agtagctgac ctgtgatatc attaggagtt gagctgaaac tacttataaac tgctctagcc 180  
 ccaaccacgc tcaactccta atgatatcac aggtcagcta ctcagcttcg ctacctagta 240  
 gagaatacag tatgttcatc ctagtgtgaa attttctact ttgatttcca ctgttcttat 300  
 acgcattatg tctaagaagc aagaaatgat gacacataat ctaaagaaga aacaatcgat 360  
 agaaaaagac cttatggatc acccaagtgt tggaatttag acaaagactt taaaattcca 420  
 tgaaaaattht tctttatgtht aaagaaaaac gagaggcaga atgattgaga gaatagaaaa 480  
 tttgagcaga gaaaaaaagt aacaaaaatag aaaatctaga actgaaaata tatccgaa 538  
 atg aat aaa ttg ttt tat ttg tta ttt att ttt gta gaa aca gga tct 586  
 Met Asn Lys Leu Phe Tyr Leu Leu Phe Ile Phe Val Glu Thr Gly Ser  
 1 5 10 15  
 cat ggt gtt gcc cag gtt ggt ctt gaa ctc ctg agc tca aga gat cct 634  
 His Gly Val Ala Gln Val Gly Leu Glu Leu Leu Ser Ser Arg Asp Pro  
 20 25 30  
 cct gcc tct gcc tcc caa gct gct ggg att aca ggc atg aac cac tgt 682  
 Pro Ala Ser Ala Ser Gln Ala Ala Gly Ile Thr Gly Met Asn His Cys  
 35 40 45  
 gcc cag ctg aaa tga ataaattgga taggcttaac aaaatggata caacaaaatg 737  
 Ala Gln Leu Lys \*  
 50  
 gatacaacag aaaaaaaaaa a 758

<210> 284  
 <211> 1482  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (939) .. (1475)

<400> 284  
 ccagcctgcc ctcttagtcc ctgacagctg cagtgcagc atctgtgatt gcaaagcatg 60  
 acaatttata tctctcattt catcacacca tctatcagca gacagtcagg ctttaaaaat 120



caatcccaca	ctgactcagt	ccccagcaga	gatggcctct	gacaacagta	tccacactgc		180
aggctggaca	agggccctat	taattttgag	actcagccaa	atttccttct	gaccctaagc		240
tgggtgaatcc	ctgctccttt	gcttttggtt	gggttggtgt	gagctaaggc	tgtgatccca		300
tttgctccta	tggcctccag	gtggcctggg	cctccatgaa	tggggccacat	ggtcatactg		360
aatgcttgat	tacactcaga	cctagcagtc	gtctggggcg	agctggttta	tggatcactt		420
tgtcacaatg	ttccatcctt	ccagggtcccc	atccccgcgg	tgggaaaaca	ttgcttttagg		480
cagtgcctaga	ggacttcagc	aggcattggc	agcttctgga	ttcaggatta	gaacaaagaa		540
ggaggagtca	cagcaaagat	aggaacagaa	ggcagagaga	acagacagat	gggggtgttt		600
gagaaggagg	gcctttgaga	cctcagggag	tgggagacac	tggctcgaga	ataataataa		660
tggcaatttc	tctcatctgt	gttttcaggg	catggactgg	aactccaat	acctctgaca		720
tgggctgagt	caacgtggtc	atgaacatgt	gacaggaggc	agcagaagtt	gcagagaaga		780
gtgaggcacg	tttgaaaaag	gctgaaaaat	gtttctgtcc	aggcaagggt	gtgtgctgaa		840
tgactcaagg	atTTTTTGGT	GcattGaatG	aacAGCGGGA	CattGgacAC	ctGctgatCC		900
atCACCCCgG	GCCCCGGGCAG	GCCCCGTGGAT	GaagAgag	atG gag aag acc agg Met Glu Lys Thr Arg 1                    5			953
cat gag act gtg gag aag cca cac cac cag aaa ccc ctg ccc cat gcg							1001
His Glu Thr Val       Glu Lys Pro His His Gln Lys Pro Leu Pro His Ala							
	10		15		20		
ccg tcc agc cca cac ctg tgg atg cac ggg gga ttg cag gca ggg ctc							1049
Pro Ser Ser Pro His Leu Trp Met His Gly Gly Leu Gln Ala Gly Leu							
	25		30		35		
cca ccg tgg act cag gaa cag gca ggg aag ctg ctg cct cac cag gcg							1097
Pro Pro Trp Thr Gln Glu Gln Ala Gly Lys Leu Leu Pro His Gln Ala							
	40		45		50		
aag ggg cca gga ggg gga ggc gga gag gcc cgt cta gcc cct gcg gct							1145
Lys Gly Pro Gly Gly Gly Gly Gly Glu Ala Arg Leu Ala Pro Ala Ala							
	55		60		65		
gtc acc gtg gtg cct cct cac tgg cca gtg cgg tcg cgc ctc agc ttc							1193
Val Thr Val Val Pro Pro His Trp Pro Val Arg Ser Arg Leu Ser Phe							
	70		75		80		85
gtt aat agg gga ggg ggc cta aga gtt ttc acg tcc agg ctc ggg cag							1241
Val Asn Arg Gly Gly Gly Leu Arg Val Phe Thr Ser Arg Leu Gly Gln							
	90		95		100		
tgg gga ggc agg cag gag tgg ccg ctg gtt ttt cag acc tcc cag gga							1289
Trp Gly Gly Arg Gln Glu Trp Pro Leu Val Phe Gln Thr Ser Gln Gly							
	105		110		115		

ggc cga gga aat ggc ccg tcc tgg agt ggg cgt ggt tct gtc ttc aga	1337
Gly Arg Gly Asn Gly Pro Ser Trp Ser Gly Arg Gly Ser Val Phe Arg	
120 125 130	
tgg atg ctg gag ggt tgg gct gcg tgg gac cct ggg ccc tgc tgc ttc	1385
Trp Met Leu Glu Gly Trp Ala Ala Trp Asp Pro Gly Pro Cys Cys Phe	
135 140 145	
ccg gag gat gcg ctg tcc ggg gct gca cag gtt ggc tgt gtt ttt tgg	1433
Pro Glu Asp Ala Leu Ser Gly Ala Ala Gln Val Gly Cys Val Phe Trp	
150 155 160 165	
atg ctt gtt att ttt ttt ttt ctt ctc ttc act ctg tca tga aactggc	1482
Met Leu Val Ile Phe Phe Phe Leu Leu Phe Thr Leu Ser *	
170 175	

<210> 285  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (392)..(1120)

<400> 285	
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cagacgggtat tttgccgact tgattgccat tgtgagcaat cgcttcacac tctgcccttc	180
tgcccgccat cttgctgtct atttactgga cctgtttatg gaccgctatg acatctctat	240
ccagcagctg catttagttg cgctttcctg cctgcttcta gcaagtaaatttgaagaaaa	300
agaagacagt gtgcctaagc tggagcagct caacagcctg gggtgtatga ctaatatgaa	360
tctagtatta acaaaacaaa atttgctaca t atg gaa cta tta tta tta gaa	412
Met Glu Leu Leu Leu Leu Glu	
1 5	
acc ttt cag tgg aac ctc tgc ctt cca aca gcc gcc cat ttc att gag	460
Thr Phe Gln Trp Asn Leu Cys Leu Pro Thr Ala Ala His Phe Ile Glu	
10 15 20	
tat tat ctc tct gaa gca gta cac gaa aca gat ctt cat gac ggc tgg	508
Tyr Tyr Leu Ser Glu Ala Val His Glu Thr Asp Leu His Asp Gly Trp	
25 30 35	
cca atg att tgc ttg gaa aag act aaa ctc tac atg gcc aaa tat gca	556
Pro Met Ile Cys Leu Glu Lys Thr Lys Leu Tyr Met Ala Lys Tyr Ala	

40	45	50	55	
gat tac ttc ctg gaa gta tct ttg caa gct gct gca tgt gtg gct tct				604
Asp Tyr Phe Leu Glu Val Ser Leu Gln Ala Ala Cys Val Ala Ser				
	60	65	70	
tcg agg att ata ctt cgt ctt tct cca acg tgg cct aca aga cta cat				652
Ser Arg Ile Ile Leu Arg Leu Ser Pro Thr Trp Pro Thr Arg Leu His				
	75	80	85	
cgt ctt act gcc tac tct tgg gat ttc tta gtg cag tgt att gaa cga				700
Arg Leu Thr Ala Tyr Ser Trp Asp Phe Leu Val Gln Cys Ile Glu Arg				
	90	95	100	
ctg ttg atc gct cat gat aat gat gtg aaa gaa gca aac aaa cag aga				748
Leu Leu Ile Ala His Asp Asn Asp Val Lys Glu Ala Asn Lys Gln Arg				
	105	110	115	
ggg caa gca gga cct cag tca gcg caa cta agt gta ttc cag aca gcc				796
Gly Gln Ala Gly Pro Gln Ser Ala Gln Leu Ser Val Phe Gln Thr Ala				
	120	125	130	135
tcc cag cca tca cgg cca gtt cac ttt cag caa cct cag tat ctc cat				844
Ser Gln Pro Ser Arg Pro Val His Phe Gln Gln Pro Gln Tyr Leu His				
	140	145	150	
cag aca cat cag acc tca ctg cag tat cgc cat cct acg tca gaa caa				892
Gln Thr His Gln Thr Ser Leu Gln Tyr Arg His Pro Thr Ser Glu Gln				
	155	160	165	
cca agc tgt cag cag att gta tcg acc aca cac acc tca tct tac aca				940
Pro Ser Cys Gln Gln Ile Val Ser Thr Thr His Thr Ser Ser Tyr Thr				
	170	175	180	
cta cag aca tgt cct gct ggc ttc caa act agt gtt cag ggc ctt ggg				988
Leu Gln Thr Cys Pro Ala Gly Phe Gln Thr Ser Val Gln Gly Leu Gly				
	185	190	195	
cac atg cag act ggt gtt ggg atg tca ctg gca ata cca gta gaa gtt				1036
His Met Gln Thr Gly Val Gly Met Ser Leu Ala Ile Pro Val Glu Val				
	200	205	210	215
aag ccc tgt ctg agt gtt tct tac aac cgg agt tat cag ata aat gaa				1084
Lys Pro Cys Leu Ser Val Ser Tyr Asn Arg Ser Tyr Gln Ile Asn Glu				
	220	225	230	
cat tac cct tgt att act cca tgt ttt gaa agg tga ttat ttgtgaagct				1134
His Tyr Pro Cys Ile Thr Pro Cys Phe Glu Arg *				
	235	240		
gataaccgac ccagactgct ttgtgacatg aagctatggg taagcggtttt gttaaacttct				1194
gttcaaaagg aaagggatct aaatgacatc agaactcttc aggtaccagc accaggaaga				1254
ctgaatatcc tttttaatgc accatgaatc ctgggagact aagcaaatta acagtatgtc				1314
aaattctgtt acaacaaatc cctgtatgac aaaaatgttc aagtcctggc tgatggtcca				1374

aatatttcaa	aaatattcag	tacaacagaa	aatttggaca	gacttcaatt	tgccattttg	1434
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ggaaacactt	aactgtaatg	caacatgcct	tgggaatggt	atagtgtgaa	ctacctttat	1914
aacataggtt	aaaatacgct	tgctaggggtg	tgttttcaaa	tgagaacata	atatagctca	1974
gaatgaagtg	gtagttcctg	tgattcataa	tacatatgta	ggttttgcat	atctcagtgc	2034
aatccatgat	ttatactcag	aatcgacatt	cttaaaaagt	tatttcaagg	gatggcataa	2094
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tcagtagcta	ctttcattgg	attgacccta	caactgccct	gggacatttc	actgtaccag	2334
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tgtgctcctt	tctgggggaa	gaaagatttg	gtggagggaa	gctttctggt	ttaaaaatta	2514
gtaagggtgtg	tcttttttgt	ttttttaaga	tagcacttga	atagaaggga	aaactgcatg	2574
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ttttcctttt	taaagaaggc	tgctaattgg	attttggtag	ttcttacctc	aagaaaactt	2994
gaattatttg	ggggaaagta	ggctcaaaag	agaatatatc	tttcacattc	acattcagaa	3054

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cccagcaacc tggagtccaa ttttcagtat ttttaactacc tcaataatgc tatgaatgta 3114
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<212> DNA
<213> Homo sapiens

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<222> (217)..(510)

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<400> 286

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gaagagccca ggtccctgcc ccagttctac cacagctctc atgccacag ccctgtctgt 180
ctggacacat tactaggcac agactgctga cagggg atg tcc tgg gcg gtt gac 234
Met Ser Trp Ala Val Asp
1 5

ctg cct gtg tgt caa agg aca cct cac tgc agg gtc caa gac aga gtg 282
Leu Pro Val Cys Gln Arg Thr Pro His Cys Arg Val Gln Asp Arg Val
10 15 20

ctc cac tgt ggc ttc ctg gga agc ccg ctg gtg gga gct cct ggg agc 330
Leu His Cys Gly Phe Leu Gly Ser Pro Leu Val Gly Ala Pro Gly Ser
25 30 35

agg aga cag ctg tgc tct ccc cac tcc tcc ctc cgg cct cag cac cca 378
Arg Arg Gln Leu Cys Ser Pro His Ser Ser Leu Arg Pro Gln His Pro
40 45 50

cag gtg gcc tct gct ctc ttg gag gcg aag ctg ctc ccc tct cct cca 426
Gln Val Ala Ser Ala Leu Leu Glu Ala Lys Leu Leu Pro Ser Pro Pro
55 60 65 70

acc tca ttc tct gcc tgc ttc atc cgg ccc cac aca cac acc ggt aat 474
Thr Ser Phe Ser Ala Cys Phe Ile Arg Pro His Thr His Thr Gly Asn

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75	80	85	
ctg tgt tcc ttt ctg cca tta atc ctc ctc atg taa atat tcccaatact			524
Leu Cys Ser Phe Leu Pro Leu Ile Leu Leu Met *			
90	95		
ctttcagtc ccaaagccat aggccacat ctgcttgtgg atcagaaaca tgctggcaga			584
gcgcggtggg actgctgccc cctggccctt aggagtgggg tctggggcgc cctcagaaca			644
acgaca			650

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (120)..(1619)

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atg atg gcg gat gcc aag tat gtc ctc tgc cga tgg gaa aag cga tta	167
Met Met Ala Asp Ala Lys Tyr Val Leu Cys Arg Trp Glu Lys Arg Leu	
1 5 10 15	
tgg cct gcg aag gtt ttg gcc cga acc gcg act tca aca aaa aat aag	215
Trp Pro Ala Lys Val Leu Ala Arg Thr Ala Thr Ser Thr Lys Asn Lys	
20 25 30	
aga aga aag gaa tat ttt cta gct gtg caa atc ctc tcc cta gag gaa	263
Arg Arg Lys Glu Tyr Phe Leu Ala Val Gln Ile Leu Ser Leu Glu Glu	
35 40 45	
aaa att aag gtg aaa agc act gaa gtt gag atc cta gag aag tct caa	311
Lys Ile Lys Val Lys Ser Thr Glu Val Glu Ile Leu Glu Lys Ser Gln	
50 55 60	
att gaa gcc att gct tcc tcg tta gcc tca cag aat gag gtt cct gcg	359
Ile Glu Ala Ile Ala Ser Ser Leu Ala Ser Gln Asn Glu Val Pro Ala	
65 70 75 80	
gca ccc ctg gaa gaa ctg gcc tac aga cgg tcg ctt cgc gtg gct ctg	407
Ala Pro Leu Glu Glu Leu Ala Tyr Arg Arg Ser Leu Arg Val Ala Leu	
85 90 95	
gac gtt ctg agc gag ggc tcg att tgg agt caa gaa agc tct gca ggg	455
Asp Val Leu Ser Glu Gly Ser Ile Trp Ser Gln Glu Ser Ser Ala Gly	
100 105 110	
aca ggt aga gct gac cgg tct ctg cga ggg aag ccc atg gag cat gtc	503



340	345	350	
gcc tct gcg gat gca acc aga tgt ctt cct tgc ccg gat tcc cag aag			1223
Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys			
355	360	365	
ctg gag aaa gag tgc cag tct tcc gaa gag tcc atg ggg tct aat tcc			1271
Leu Glu Lys Glu Cys Gln Ser Ser Glu Glu Ser Met Gly Ser Asn Ser			
370	375	380	
atg cgt tct atc ctg gag gaa gac gag gaa gac gag gag cca cca aga			1319
Met Arg Ser Ile Leu Glu Glu Asp Glu Glu Asp Glu Glu Pro Pro Arg			
385	390	395	400
gtc ctt tta tac cac gaa cca cgt tcg ttt gaa gta gga atg cta gtc			1367
Val Leu Leu Tyr His Glu Pro Arg Ser Phe Glu Val Gly Met Leu Val			
	405	410	415
tgg cat aaa cat aaa aaa tac ccc ttc tgg cca gca gtg gtc aaa agc			1415
Trp His Lys His Lys Lys Tyr Pro Phe Trp Pro Ala Val Val Lys Ser			
	420	425	430
gtc agg cag aga gat aag aaa gca agt gtg cta tac atc gaa gga cac			1463
Val Arg Gln Arg Asp Lys Lys Ala Ser Val Leu Tyr Ile Glu Gly His			
	435	440	445
atg aac ccg aaa atg aaa ggt ttc aca gtg tct ctt aaa agt tta aag			1511
Met Asn Pro Lys Met Lys Gly Phe Thr Val Ser Leu Lys Ser Leu Lys			
	450	455	460
cac ttt gat tgt aaa gag aaa cag acg ctt ctg aat caa gcc agg gag			1559
His Phe Asp Cys Lys Glu Lys Gln Thr Leu Leu Asn Gln Ala Arg Glu			
465	470	475	480
gac ttc aac cag gac atc ggc tgg tgt gct ccc tca tca ccg act aca			1607
Asp Phe Asn Gln Asp Ile Gly Trp Cys Ala Pro Ser Ser Pro Thr Thr			
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ggg tcc ggt tag			1619
Gly Ser Gly *			
500			

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cggcagcagc ctgccagcct gcccagaggag tgctgggacc agcgcgctgc acgccgactg      120

gcacg      atg gcc tcg tct cag ggg aaa aac gag ctg aaa tta gcc gac      167
      Met Ala Ser Ser Gln Gly Lys Asn Glu Leu Lys Leu Ala Asp
            1              5              10

tgg atg gca act ctg ccg gag agc atg cac agc atc ccc ctc acc aat      215
Trp Met Ala Thr Leu Pro Glu Ser Met His Ser Ile Pro Leu Thr Asn
      15              20              25              30

tta gcc att cca ggg tct cat gat tcc ttc agc ttc tac att gat gaa      263
Leu Ala Ile Pro Gly Ser His Asp Ser Phe Ser Phe Tyr Ile Asp Glu
            35              40              45

gcc tct cca gta ggt cct gag cag cca gaa act gtc cag aat ttt gtc      311
Ala Ser Pro Val Gly Pro Glu Gln Pro Glu Thr Val Gln Asn Phe Val
            50              55              60

tct gtg ttt gga act gtg gcc aaa aag ctc atg cgg aaa tgg tta gcc      359
Ser Val Phe Gly Thr Val Ala Lys Lys Leu Met Arg Lys Trp Leu Ala
            65              70              75

act cag aca atg aat ttt act ggc cag cta gga gct gga att cgt tat      407
Thr Gln Thr Met Asn Phe Thr Gly Gln Leu Gly Ala Gly Ile Arg Tyr
            80              85              90

ttt gat ctt cga att tcc acc aag ccc aga gac ccc gac aat gaa ctc      455
Phe Asp Leu Arg Ile Ser Thr Lys Pro Arg Asp Pro Asp Asn Glu Leu
            95              100              105              110

tat ttt gct cat ggt ttg ttc agt gcc aaa gtc aat gaa ggc ctt gag      503
Tyr Phe Ala His Gly Leu Phe Ser Ala Lys Val Asn Glu Gly Leu Glu
            115              120              125

gag atc aat gca ttc ctc aca gat cac cat aag gag gta gtg ttc ttg      551
Glu Ile Asn Ala Phe Leu Thr Asp His His Lys Glu Val Val Phe Leu
            130              135              140

gac ttc aac cac ttc tat ggg atg cag aaa tat cac cat gaa aaa ctg      599
Asp Phe Asn His Phe Tyr Gly Met Gln Lys Tyr His His Glu Lys Leu
            145              150              155

gtc caa atg ctg aaa gac atc tat gga aat aaa atg tgc cca gcg att      647
Val Gln Met Leu Lys Asp Ile Tyr Gly Asn Lys Met Cys Pro Ala Ile
```



Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	16
Income	3500	1500	1000	8000
Health	0.8	0.3	0	1
Smoking	0.2	0.4	0	1
Drinking	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.6	0.4	0	1
Sleep	0.7	0.3	0	1
Work	0.8	0.3	0	1
Family	0.9	0.2	0	1
Friends	0.7	0.4	0	1
Hobbies	0.6	0.5	0	1
Travel	0.4	0.5	0	1
Volunteering	0.3	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.4	0.5	0	1
Environment	0.6	0.4	0	1
Technology	0.7	0.3	0	1
Art	0.5	0.5	0	1
Music	0.6	0.4	0	1
Gardening	0.4	0.5	0	1
Cooking	0.7	0.3	0	1
Reading	0.8	0.2	0	1
Writing	0.5	0.5	0	1
Photography	0.3	0.5	0	1
Video	0.4	0.5	0	1
Video Games	0.2	0.4	0	1
Shopping	0.6	0.4	0	1
Traveling	0.5	0.5	0	1
Learning	0.7	0.3	0	1
Teaching	0.4	0.5	0	1
Researching	0.3	0.5	0	1
Networking	0.6	0.4	0	1
Organizing	0.5	0.5	0	1
Managing	0.7	0.3	0	1
Planning	0.6	0.4	0	1
Executing	0.8	0.2	0	1
Evaluating	0.5	0.5	0	1
Monitoring	0.4	0.5	0	1
Controlling	0.6	0.4	0	1
Communicating	0.7	0.3	0	1
Collaborating	0.5	0.5	0	1
Coordinating	0.6	0.4	0	1
Facilitating	0.4	0.5	0	1
Supporting	0.7	0.3	0	1
Assessing	0.5	0.5	0	1
Analyzing	0.6	0.4	0	1
Interpreting	0.4	0.5	0	1
Presenting	0.7	0.3	0	1
Writing	0.5	0.5	0	1
Editing	0.6	0.4	0	1
Proofreading	0.4	0.5	0	1
Designing	0.7	0.3	0	1
Developing	0.5	0.5	0	1
Testing	0.6	0.4	0	1
Debugging	0.4	0.5	0	1
Deploying	0.7	0.3	0	1
Maintaining	0.5	0.5	0	1
Updating	0.6	0.4	0	1
Archiving	0.4	0.5	0	1
Restoring	0.7	0.3	0	1
Backing up	0.5	0.5	0	1
Recovering	0.6	0.4	0	1
Securing	0.4	0.5	0	1
Encrypting	0.7	0.3	0	1
Decrypting	0.5	0.5	0	1
Authenticating	0.6	0.4	0	1
Authorizing	0.4	0.5	0	1
Accounting	0.7	0.3	0	1
Auditing	0.5	0.5	0	1
Logging	0.6	0.4	0	1
Monitoring	0.4	0.5	0	1
Alerting	0.7	0.3	0	1
Investigating	0.5	0.5	0	1
Reporting	0.6	0.4	0	1
Documenting	0.4	0.5	0	1
Presenting	0.7	0.3	0	1
Reviewing	0.5	0.5	0	1
Revising	0.6	0.4	0	1
Finalizing	0.4	0.5	0	1
Distributing	0.7	0.3	0	1
Archiving	0.5	0.5	0	1
Restoring	0.6	0.4	0	1

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical health	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Emotional health	0.5	0.5	0	1
Behavioral health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Occupational health	0.5	0.5	0	1
Financial health	0.5	0.5	0	1
Family health	0.5	0.5	0	1
Community health	0.5	0.5	0	1
National health	0.5	0.5	0	1
Global health	0.5	0.5	0	1
World health	0.5	0.5	0	1
Universal health	0.5	0.5	0	1
Human health	0.5	0.5	0	1
Planetary health	0.5	0.5	0	1
Ecosystem health	0.5	0.5	0	1
Biodiversity health	0.5	0.5	0	1
Climate health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Natural health	0.5	0.5	0	1
Wildlife health	0.5	0.5	0	1
Marine health	0.5	0.5	0	1
Terrestrial health	0.5	0.5	0	1
Aquatic health	0.5	0.5	0	1
Atmospheric health	0.5	0.5	0	1
Geological health	0.5	0.5	0	1
Hydrological health	0.5	0.5	0	1
Biological health	0.5	0.5	0	1
Chemical health	0.5	0.5	0	1
Physical health	0.5	0.5	0	1
Mathematical health	0.5	0.5	0	1
Scientific health	0.5	0.5	0	1
Technological health	0.5	0.5	0	1
Artistic health	0.5	0.5	0	1
Cultural health	0.5	0.5	0	1
Historical health	0.5	0.5	0	1
Philosophical health	0.5	0.5	0	1
Religious health	0.5	0.5	0	1
Spiritual health	0.5	0.5	0	1
Moral health	0.5	0.5	0	1
Ethical health	0.5	0.5	0	1
Legal health	0.5	0.5	0	1
Political health	0.5	0.5	0	1
Economic health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Cultural health	0.5	0.5	0	1
Historical health	0.5	0.5	0	1
Philosophical health	0.5	0.5	0	1
Religious health	0.5	0.5	0	1
Spiritual health	0.5	0.5	0	1
Moral health	0.5	0.5	0	1
Ethical health	0.5	0.5	0	1
Legal health	0.5	0.5	0	1
Political health	0.5	0.5	0	1
Economic health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Cultural health	0.5	0.5	0	1
Historical health	0.5	0.5	0	1
Philosophical health	0.5	0.5	0	1
Religious health	0.5	0.5	0	1
Spiritual health	0.5	0.5	0	1
Moral health	0.5	0.5	0	1
Ethical health	0.5	0.5	0	1
Legal health	0.5	0.5	0	1
Political health	0.5	0.5	0	1
Economic health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Cultural health	0.5	0.5	0	1
Historical health	0.5	0.5	0	1
Philosophical health	0.5	0.5	0	

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Lys Leu Lys Leu Leu Ser Leu Ser Gln Ser Phe Ser Ser Thr Ala Pro	
185 190 195 200	
tct gac aca gac ctc ggg gag agc tta ggg gcc aac gtg gcc acc aca	795
Ser Asp Thr Asp Leu Gly Glu Ser Leu Gly Ala Asn Val Ala Thr Thr	
205 210 215	
gac tcg gat gag aga gat gat gca tct gtg tgc agt gga ggt gac tcc	843
Asp Ser Asp Glu Arg Asp Asp Ala Ser Val Cys Ser Gly Gly Asp Ser	
220 225 230	
act gat gac ggt ggc tac agg agc agc atg tgg gac cag ggc gac atc	891
Thr Asp Asp Gly Gly Tyr Arg Ser Ser Met Trp Asp Gln Gly Asp Ile	
235 240 245	
ctg gag tct ggg tca ggc act tcc ttg gag gag gca ttg gag gcc cca	939
Leu Glu Ser Gly Ser Gly Thr Ser Leu Glu Glu Ala Leu Glu Ala Pro	
250 255 260	
gcc aca gac ctg gcc agg cct gag ttc tgt tac gag gct gag agc cct	987
Ala Thr Asp Leu Ala Arg Pro Glu Phe Cys Tyr Glu Ala Glu Ser Pro	
265 270 275 280	
gat gag gcc gcc ctg gtg cac gct gcc cat gcc tac agc ttc aca cta	1035
Asp Glu Ala Ala Leu Val His Ala Ala His Ala Tyr Ser Phe Thr Leu	
285 290 295	
gtg tcc cgg aca cct gag cag gtg act gtg cgc ctg ccc cag ggc acc	1083
Val Ser Arg Thr Pro Glu Gln Val Thr Val Arg Leu Pro Gln Gly Thr	
300 305 310	
tgc ctc acc ttc agc ctc ctc tgc acc ctg ggc ttt gac tct gtc agg	1131
Cys Leu Thr Phe Ser Leu Leu Cys Thr Leu Gly Phe Asp Ser Val Arg	
315 320 325	
aag aga atg tct gtg gtt gtg agg cac cca ctg act ggc gag att gtt	1179
Lys Arg Met Ser Val Val Arg His Pro Leu Thr Gly Glu Ile Val	
330 335 340	
gtc tac acc aag ggt gct gac tcg gtc atc atg gac ctg ctg gaa gac	1227
Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Asp Leu Leu Glu Asp	
345 350 355 360	
cca gcc tgc gta cct gac att aat atg gaa aag aag ctg aga aaa atc	1275
Pro Ala Cys Val Pro Asp Ile Asn Met Glu Lys Lys Leu Arg Lys Ile	
365 370 375	
cga gcc cgg acc caa aag cat cta gac ttg tat gca aga gat ggc ctg	1323
Arg Ala Arg Thr Gln Lys His Leu Asp Leu Tyr Ala Arg Asp Gly Leu	
380 385 390	
cgc aca cta tgc att gcc aag aag gtt gta agc gaa gag gac ttc cgg	1371
Arg Thr Leu Cys Ile Ala Lys Lys Val Val Ser Glu Glu Asp Phe Arg	
395 400 405	

aga tgg gcc agt ttc cgg cgt gag gct gag gca tcc ctc gac aac cga	1419
Arg Trp Ala Ser Phe Arg Arg Glu Ala Glu Ala Ser Leu Asp Asn Arg	
410 415 420	
gat gag ctt ctc atg gaa act gca cag cat ctg gag aat caa ctc acc	1467
Asp Glu Leu Leu Met Glu Thr Ala Gln His Leu Glu Asn Gln Leu Thr	
425 430 435 440	
tta ctt gga gcc act ggg atc gaa gac cgg ctg cag gaa gga gtt cca	1515
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro	
445 450 455	
gat acg att gcc act ctg cgg gag gct ggg atc cag ctc tgg gtc ctg	1563
Asp Thr Ile Ala Thr Leu Arg Glu Ala Gly Ile Gln Leu Trp Val Leu	
460 465 470	
act gga gat aag cag gag aca gcg gtc aac att gcc cat tcc tgc aga	1611
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala His Ser Cys Arg	
475 480 485	
ctg tta aat cag acc gac act gtt tat acc atc aat aca gag aat cag	1659
Leu Leu Asn Gln Thr Asp Thr Val Tyr Thr Ile Asn Thr Glu Asn Gln	
490 495 500	
gag acc tgt gaa tcc atc ctc aat tgt gca ttg gaa gag cta aag caa	1707
Glu Thr Cys Glu Ser Ile Leu Asn Cys Ala Leu Glu Glu Leu Lys Gln	
505 510 515 520	
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Phe Arg Glu Leu Gln Lys Pro Asp Arg Lys Leu Phe Gly Phe Arg Leu	
525 530 535	
cct tcc aag aca cca tcc atc acc tca gaa gct gtg gtt cca gaa gct	1803
Pro Ser Lys Thr Pro Ser Ile Thr Ser Glu Ala Val Val Pro Glu Ala	
540 545 550	
gga ttg gtc atc gat ggg aag aca ttg aat gcc atc ttc cag gga aag	1851
Gly Leu Val Ile Asp Gly Lys Thr Leu Asn Ala Ile Phe Gln Gly Lys	
555 560 565	
cta gag aag aag ttt ctg gaa ttg acc cag tat tgt cgg tcc gtc ctg	1899
Leu Glu Lys Lys Phe Leu Glu Leu Thr Gln Tyr Cys Arg Ser Val Leu	
570 575 580	
tgc tgc cgc tcc acg cca ctc cag aag agt atg ata gtc aag ctg gtg	1947
Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met Ile Val Lys Leu Val	
585 590 595 600	
cga gac aag ttg cgc gtc atg acc ctt tcc ata ggt gat gga gca aat	1995
Arg Asp Lys Leu Arg Val Met Thr Leu Ser Ile Gly Asp Gly Ala Asn	
605 610 615	
gat gta agc atg att caa gct gct gat att gga att gga ata tct gga	2043
Asp Val Ser Met Ile Gln Ala Ala Asp Ile Gly Ile Gly Ile Ser Gly	
620 625 630	
cag gaa ggc atg cag gct gtc atg tcc agc gac ttt gcc atc acc cgc	2091

Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ser	Ser	Asp	Phe	Ala	Ile	Thr	Arg	
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ttt	aag	cat	ctc	aag	aag	ttg	ctg	ctc	gtg	cat	ggc	cac	tgg	tgt	tac	2139
Phe	Lys	His	Leu	Lys	Lys	Leu	Leu	Leu	Val	His	Gly	His	Trp	Cys	Tyr	
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tcg	cgc	ctg	gcc	agg	atg	gtg	gtg	tac	tac	ctc	tac	aag	aac	gtg	tgc	2187
Ser	Arg	Leu	Ala	Arg	Met	Val	Val	Tyr	Tyr	Leu	Tyr	Lys	Asn	Val	Cys	
	665				670					675					680	
tac	gtc	aac	ctg	ctc	ttc	tgg	tat	cag	ttc	ttc	tgt	ggc	ttc	tcc	agc	2235
Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly	Phe	Ser	Ser	
				685				690						695		
tcc	acc	atg	att	gat	tac	tgg	cag	atg	ata	ttc	ttc	aat	ctc	ttc	ttt	2283
Ser	Thr	Met	Ile	Asp	Tyr	Trp	Gln	Met	Ile	Phe	Phe	Asn	Leu	Phe	Phe	
			700					705					710			
acc	tcc	ttg	cct	cct	ctt	gtc	ttt	gga	gtc	ctt	gac	aaa	gac	atc	tct	2331
Thr	Ser	Leu	Pro	Pro	Leu	Val	Phe	Gly	Val	Leu	Asp	Lys	Asp	Ile	Ser	
		715					720					725				
gca	gaa	aca	ctc	ctg	gca	ttg	cct	gag	cta	tac	aag	agt	ggc	cag	aac	2379
Ala	Glu	Thr	Leu	Leu	Ala	Leu	Pro	Glu	Leu	Tyr	Lys	Ser	Gly	Gln	Asn	
	730					735					740					
tct	gag	tgc	tat	aac	ctg	tcg	act	ttc	tgg	att	tct	atg	gtg	gat	gca	2427
Ser	Glu	Cys	Tyr	Asn	Leu	Ser	Thr	Phe	Trp	Ile	Ser	Met	Val	Asp	Ala	
	745				750					755					760	
ttc	tac	cag	agc	ctc	atc	tgt	ttc	ttt	atc	cct	tac	ctg	gcc	tat	aag	2475
Phe	Tyr	Gln	Ser	Leu	Ile	Cys	Phe	Phe	Ile	Pro	Tyr	Leu	Ala	Tyr	Lys	
				765					770					775		
ggc	tct	gat	ata	gat	gtc	ttt	acc	ttt	ggg	aca	cca	atc	aac	acc	atc	2523
Gly	Ser	Asp	Ile	Asp	Val	Phe	Thr	Phe	Gly	Thr	Pro	Ile	Asn	Thr	Ile	
			780					785					790			
tcc	ctc	acc	aca	atc	ctt	ttg	cac	cag	gca	atg	gaa	atg	aag	aca	tgg	2571
Ser	Leu	Thr	Thr	Ile	Leu	Leu	His	Gln	Ala	Met	Glu	Met	Lys	Thr	Trp	
		795					800					805				
acc	att	ttc	cac	gga	gtc	gtg	ctc	ctc	ggc	agc	ttc	ctg	atg	tac	ttt	2619
Thr	Ile	Phe	His	Gly	Val	Val	Leu	Leu	Gly	Ser	Phe	Leu	Met	Tyr	Phe	
	810					815					820					
ctg	gta	tcc	ctc	ctg	tac	aat	gcc	acc	tgc	gtc	atc	tgc	aac	agc	ccc	2667
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Ala	Thr	Cys	Val	Ile	Cys	Asn	Ser	Pro	
	825				830					835					840	
acc	aat	ccc	tat	tgg	gtg	atg	gaa	ggc	cag	ctc	tca	aac	ccc	act	ttc	2715
Thr	Asn	Pro	Tyr	Trp	Val	Met	Glu	Gly	Gln	Leu	Ser	Asn	Pro	Thr	Phe	
				845					850					855		
tac	ctc	gtc	tgc	ttt	ctc	aca	cca	gtt	gtt	gct	ctt	ctc	cca	aga	tac	2763
Tyr	Leu	Val	Cys	Phe	Leu	Thr	Pro	Val	Val	Ala	Leu	Leu	Pro	Arg	Tyr	



860	865	870	
ttt ttc ctg tct ctg caa gga act tgt ggg aag tct cta atc tca aaa			2811
Phe Phe Leu Ser Leu Gln Gly Thr Cys Gly Lys Ser Leu Ile Ser Lys			
875	880	885	
gct cag aaa att gac aaa ctc ccc cca gac aaa aga aac ctg gaa atc			2859
Ala Gln Lys Ile Asp Lys Leu Pro Pro Asp Lys Arg Asn Leu Glu Ile			
890	895	900	
cag agt tgg aga agc aga cag agg cct gcc cct gtc ccc gaa gtg gct			2907
Gln Ser Trp Arg Ser Arg Gln Arg Pro Ala Pro Val Pro Glu Val Ala			
905	910	915	920
cga cca act cac cac cca gtg tca tct atc aca gga cag gac ttc agt			2955
Arg Pro Thr His His Pro Val Ser Ser Ile Thr Gly Gln Asp Phe Ser			
	925	930	935
gcc agc acc cca aag agc tct aac cct ccc aag agg aag cat gtg gaa			3003
Ala Ser Thr Pro Lys Ser Ser Asn Pro Pro Lys Arg Lys His Val Glu			
	940	945	950
gag tca gta ctc cac gaa cag aga tgt ggc acg gag tgc atg agg gat			3051
Glu Ser Val Leu His Glu Gln Arg Cys Gly Thr Glu Cys Met Arg Asp			
	955	960	965
gac tca tgc tca ggg gac tcc tca gct caa ctc tca tcc ggg gag cac			3099
Asp Ser Cys Ser Gly Asp Ser Ser Ala Gln Leu Ser Ser Gly Glu His			
	970	975	980
ctg ctg gga cct aac agg ata atg gcc tac tca aga gga cag act gat			3147
Leu Leu Gly Pro Asn Arg Ile Met Ala Tyr Ser Arg Gly Gln Thr Asp			
985	990	995	1000
atg tgc cgg tgc tca aag agg agc agc cat cgc cga tcc cag agt tca			3195
Met Cys Arg Cys Ser Lys Arg Ser Ser His Arg Arg Ser Gln Ser Ser			
	1005	1010	1015
ctg acc ata tga gga gctgcagaaa tctgtacaaa ctcaacagag gccacctagt			3250
Leu Thr Ile *			
1020			
cactgggtcca cataaccctt gacccttct tcttcataga ggaaacaatg tgccagtctt			3310
attctttttct tcaacaacct tgacttccat ggaggaagtg ctggccccaa ggggtctgac			3370
acaaagacgg gaaaccctagt cggcctctag ttttctgctg ctctcaggca gcacatcttg			3430
caaacagttt ggagaaggag gctgtttttg ttgaatcgag ttctcaaadc ggttttagacc			3490
aaagccattc ttctgaccct ctagataagc gtagcctaca acccagtgcc gtaagtttcc			3550
aagattcaag aagtgtatca acccaggcaa tatctcagga tatggaagtt tctgggttta			3610
tttacccttc agtgcccaga gttaaagttt cagaagagac ttgtgcacat aagggttca			3670
tctcaagtgt attgcagtaa tggctgaatc ggggttaaca tcccttccag gcacagcgag			3730

ttggttctgc tttttgctg taagccaaag aaaa

3764

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<220>  
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<400> 292

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gtccaatggc aatttgttca cctctaattt ttataatcat agtttagggg tgtgggctaaa	180
agcacaaact ctggaactag actgctagat atataatctt gggtatgctg tttgattgct	240
ctggtactct gtacctcaat tttcaccagt taaatgcaga ttaggggtgg gtagttgtga	300
ggattaaaat gtatgggtat accttagaaa ggtgccaaat atggctgggt gtggtggctc	360
atg tct gta atc cca acc cct tgg aag gcc gag gcg ggt ggc tca caa	408
Met Ser Val Ile Pro Thr Pro Trp Lys Ala Glu Ala Gly Gly Ser Gln	
1 5 10 15	
ggt cag gag atc aag acc act ctg gcc aac acg gtg aaa cac cgt ctc	456
Gly Gln Glu Ile Lys Thr Thr Leu Ala Asn Thr Val Lys His Arg Leu	
20 25 30	
cac taa aaatacaaaa tacaaaaaat tacaaaaata caaagtacaa aaaatacaaa	512
His *	
aaatacaaaa tactgaaaat actaaaaatt agccgggcat agtggcacgt gcctatagtc	572
ccagctactt gggaatctgc ggacgcgtgg gtcgacccgg gt	614

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<222> (219)..(467)

<400> 293

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cgaagcaggg ttccgagtc attcgaactg ccatctgatc cgctcttatc aatgaagcag      120
ccgatcatgg cggatggggc ccggtgcaag aggcgcaaac aagccaatcc caggaggaaa      180
aacgccttgg agtcagaaat gagcactcgg agcggggag      atg ccc tgc tgc tgc      233
                               Met Pro Cys Cys Cys
                               1                               5

ttg cca ccg gtg cgg ccc gtt tgt aac ttg caa agt ttg ttg ctt ttg      281
Leu Pro Pro Val Arg Pro Val Cys Asn Leu Gln Ser Leu Leu Leu Leu
                               10                               15                               20

ccc ctg att cgg gca gcg ggt cct ggg atg ctc ctg ctt ccc tcc tgc      329
Pro Leu Ile Arg Ala Ala Gly Pro Gly Met Leu Leu Leu Pro Ser Cys
                               25                               30                               35

ctc cca cgg agc ccg gga aga ggg tct gcc tcc cca tcc cgc cac ctt      377
Leu Pro Arg Ser Pro Gly Arg Gly Ser Ala Ser Pro Ser Arg His Leu
                               40                               45                               50

cca gca tca gcc tct gaa aaa tct cac aga gac atg cac gtt gta gca      425
Pro Ala Ser Ala Ser Glu Lys Ser His Arg Asp Met His Val Val Ala
                               55                               60                               65

aaa atc aaa tcc gga aac tgc ttg ttt cag aga aag aaa tga agttgtc      474
Lys Ile Lys Ser Gly Asn Cys Leu Phe Gln Arg Lys Lys *
                               70                               75                               80

ttttaaagaa aaactgaatt aggaggagag aaaagggaaa taggagaaga aaggaaaagt      534
taaatttgat ttttctccag agtttccact aaagggttgg ggacagtgtg aaggagaagg      594
ggagcttttt acaaatacct ttggtctctg aacttcagtg gcaaagaaca gggatcaagt      654
tgaatgttct cagggctttg gacccatagag gagaaacaat cagaagagca gaaatggtta      714
tccctgttta aaataagccc tcactcttta ccacttcctt aaaggagtgg aggtgctggt      774
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<220>  
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 <222> (493)..(735)

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tctcagctgg cctgtcatat aaaacatact gtcattgagc ttaagctccg cttgttctga 180  
ggtttcacct ccatgtgttt cattgggtgca aaagtggatc tcttagttgg tcacttaatt 240  
ctttcttttt cagaaagata ggatgttcac tggatatattt ggtcactctt agaaccttcc 300  
ttcacattgt tttttatggg acccatgaat ggtagcctt tcttttctat tgtagaagga 360  
aataaatagg agtaaaaaga ccattgtagt aaataagttc aaggggaact tgggaccaga 420  
aaccactggt atgtacaaaa aaatggcaaa ttcaataaac tcaaatttaa aataattttt 480  
aaattaacag tt atg ata aat ttt ata ttt tat aca aat aga ttg ctt 528  
Met Ile Asn Phe Ile Phe Tyr Thr Asn Arg Leu Leu  
1 5 10  
aga atg gtt ctc aag aat tat aag aga aat gaa ctc aca gta caa aaa 576  
Arg Met Val Leu Lys Asn Tyr Lys Arg Asn Glu Leu Thr Val Gln Lys  
15 20 25  
ttt tat aat tac tat act tgt gtt ttg ttt ggg ggc tgg gaa atg tat 624  
Phe Tyr Asn Tyr Tyr Thr Cys Val Leu Phe Gly Gly Trp Glu Met Tyr  
30 35 40  
ttt tac att gta gcc aat cat ttt ata ttt gtc aat tta aat ctt atg 672  
Phe Tyr Ile Val Ala Asn His Phe Ile Phe Val Asn Leu Asn Leu Met  
45 50 55 60  
ggg ctt ttt ttt tta tct ctc ttg atg tca gat ttt ata gtc ttt tta 720  
Gly Leu Phe Phe Leu Ser Leu Leu Met Ser Asp Phe Ile Val Phe Leu  
65 70 75  
aat aaa tcc att taa ttaaaacggt aaaaaaaaaa aa 757  
Asn Lys Ser Ile \*  
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<212> DNA  
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aaga atg aaa act ctg ccg ctg ttt gtg tgc atc tgt gca ctg agt gct 169

Met	Lys	Thr	Leu	Pro	Leu	Phe	Val	Cys	Ile	Cys	Ala	Leu	Ser	Ala		
1				5					10					15		
tgc	ttc	tcg	ttc	agt	gaa	ggt	cga	gaa	agg	gat	cat	gaa	cta	cgt	cac	217
Cys	Phe	Ser	Phe	Ser	Glu	Gly	Arg	Glu	Arg	Asp	His	Glu	Leu	Arg	His	
				20					25					30		
aga	agg	cat	cat	cac	caa	tca	ccc	aaa	tct	cac	ttt	gaa	tta	cca	cat	265
Arg	Arg	His	His	His	Gln	Ser	Pro	Lys	Ser	His	Phe	Glu	Leu	Pro	His	
				35					40					45		
tat	cct	gga	ctg	cta	gct	cac	cag	aag	ccg	ttc	att	aga	aag	tcc	tat	313
Tyr	Pro	Gly	Leu	Leu	Ala	His	Gln	Lys	Pro	Phe	Ile	Arg	Lys	Ser	Tyr	
		50					55					60				
aaa	tgt	ctg	cac	aaa	cgc	tgt	agg	cct	aag	ctt	cca	cct	tca	cct	aat	361
Lys	Cys	Leu	His	Lys	Arg	Cys	Arg	Pro	Lys	Leu	Pro	Pro	Ser	Pro	Asn	
	65					70					75					
aac	ccc	ccc	aaa	ttc	cca	aat	cct	cac	cag	cca	cct	aaa	cat	cca	gat	409
Asn	Pro	Pro	Lys	Phe	Pro	Asn	Pro	His	Gln	Pro	Pro	Lys	His	Pro	Asp	
	80				85					90					95	
aaa	aat	agc	agt	gtg	gtc	aac	cct	acc	tta	gtg	gct	aca	acc	caa	att	457
Lys	Asn	Ser	Ser	Val	Val	Asn	Pro	Thr	Leu	Val	Ala	Thr	Thr	Gln	Ile	
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cca	tct	gtg	act	ttc	cca	tca	gct	tcc	acc	aaa	att	act	acc	ctt	cca	505
Pro	Ser	Val	Thr	Phe	Pro	Ser	Ala	Ser	Thr	Lys	Ile	Thr	Thr	Leu	Pro	
			115					120						125		
aat	gtg	act	ttt	ctt	ccc	cag	aat	gcc	acc	acc	ata	tct	tca	aga	gaa	553
Asn	Val	Thr	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Thr	Ile	Ser	Ser	Arg	Glu	
		130					135					140				
aat	gtt	aac	aca	agc	tct	tct	gta	gct	aca	tta	gca	cca	gtg	aat	tcc	601
Asn	Val	Asn	Thr	Ser	Ser	Ser	Val	Ala	Thr	Leu	Ala	Pro	Val	Asn	Ser	
	145					150					155					
cca	gct	cca	caa	gac	acc	aca	gct	gcc	cca	ccc	aca	cct	tct	gca	act	649
Pro	Ala	Pro	Gln	Asp	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Ser	Ala	Thr	
	160				165					170					175	
aca	cca	gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	697
Thr	Pro	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	
				180					185					190		
cca	ccc	aca	cct	tct	gca	act	aca	caa	gct	cca	cca	tct	tcc	tca	gct	745
Pro	Pro	Thr	Pro	Ser	Ala	Thr	Thr	Gln	Ala	Pro	Pro	Ser	Ser	Ser	Ala	
			195					200						205		
cca	cca	gag	acc	aca	gct	gcc	cca	ccc	aca	cct	cct	gca	act	aca	caa	793
Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Thr	Gln	
		210					215					220				
gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	cca	ccc	841
Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	





Lys Val Thr His His Ile Gly Pro Ser Ile Leu Ala Leu Tyr Gln Asn  
70 75 80

gtg gat aag cat cca gac tat gct tga caaat acaaatacgca tccaatatta 469  
Val Asp Lys His Pro Asp Tyr Ala \*  
85 90

acacagaatt tccatggttt acaatagcag tggtaatccc aaatcatcct gtgaacgtct 529  
cctggaatga ctccatagcc acacagaacc acatatggct tcagatagcc atggccctat 589  
ttcacttttg tgctgcacca gctgagacct cagctgtagc aaccctcctc tgtccaccta 649  
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<210> 297  
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<212> DNA  
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1 5 10

aga gta tgg agg acc tca gcc tgg att tgg ggg ccc ttc agg gca gcg 578  
Arg Val Trp Arg Thr Ser Ala Trp Ile Trp Gly Pro Phe Arg Ala Ala  
15 20 25

agt atc tgc agg acc tgg gcc ttg ggg ccc ctt ccc aca gcc agc ctg 626



Ser Ile Cys Arg Thr Trp Ala Leu Gly Pro Leu Pro Thr Ala Ser Leu	
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Gly Arg Pro Gln Thr Ala Ala Pro Pro Val Lys Asn Gln Glu Glu Ile	
45 50 55 60	
ctc ttt tct cca gct tgg cag ggt ccc aag acc tgt caa ggc ggc gca	722
Leu Phe Ser Pro Ala Trp Gln Gly Pro Lys Thr Cys Gln Gly Gly Ala	
65 70 75	
act ggg aaa ggt cgc gga gct gct cac aga gct ggc gga ggc tca acc	770
Thr Gly Lys Gly Arg Gly Ala Ala His Arg Ala Gly Gly Gly Ser Thr	
80 85 90	
tcg atg cct cag ctg tgg atg agg aac cct gtc tcc ccc gaa cac tgg	818
Ser Met Pro Gln Leu Trp Met Arg Asn Pro Val Ser Pro Glu His Trp	
95 100 105	
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Trp Asp Gly Asn Ser Gln Val Gly Ile Gly Asp Tyr Arg Ile Pro Lys	
15 20 25	
gcg atg ctc aca ttc ttg aat gga agt aga att cct gtc act gag aaa	146
Ala Met Leu Thr Phe Leu Asn Gly Ser Arg Ile Pro Val Thr Glu Lys	
30 35 40	
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Ala Pro His Lys Gly Ile Ile Arg Asp Ser Thr Cys Lys Tyr Leu Pro	
45 50 55 60	
gag tgg cag agc tat cag tgc ttt ggg atg gaa tat gca atg atg gtt	242
Glu Trp Gln Ser Tyr Gln Cys Phe Gly Met Glu Tyr Ala Met Met Val	
65 70 75	

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gct ata atg ggc aac ggt tat gtt gat ctt att aat ggc cca cag gat Ala Ile Met Gly Asn Gly Tyr Val Asp Leu Ile Asn Gly Pro Gln Asp 95 100 105	338
cat ggc tgg tgt gct gga tat aca tgc cag aga agg ctg tcc ctg ttt His Gly Trp Cys Ala Gly Tyr Thr Cys Gln Arg Arg Leu Ser Leu Phe 110 115 120	386
cac agc att gtg gct ctg aac aaa tct tat gaa gtt tac ttc act ggc His Ser Ile Val Ala Leu Asn Lys Ser Tyr Glu Val Tyr Phe Thr Gly 125 130 135 140	434
acc agt cct cag aat ctt cga ctg atg ttg ctt aat gtt gat cat aac Thr Ser Pro Gln Asn Leu Arg Leu Met Leu Leu Asn Val Asp His Asn 145 150 155	482
aag gct gtt cta gta gga att ttc ttt tcc aca ctt caa cgt ttg gat Lys Ala Val Leu Val Gly Ile Phe Phe Ser Thr Leu Gln Arg Leu Asp 160 165 170	530
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gcc cag cag aaa cac tgt gaa ctt aat aac cat ctg tac aaa gac caa Ala Gln Gln Lys His Cys Glu Leu Asn Asn His Leu Tyr Lys Asp Gln 190 195 200	626
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gcc ttg ttc cta aag ata cca agt gac aaa atc cgt atc agc aaa ata Ala Leu Phe Leu Lys Ile Pro Ser Asp Lys Ile Arg Ile Ser Lys Ile 270 275 280	866
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ata Ile	gag Glu	att Ile	gga Gly	gac Asp 305	cct Pro	cct Pro	att Ile	cag Gln	ttc Phe 310	ata Ile	agc Ser	aat Asn	ggc Gly	acc Thr 315	aca Thr	962
ggt Gly	cag Gln	atg Met	cag Gln 320	tta Leu	tct Ser	gaa Glu	ctc Leu	cag Gln 325	gaa Glu	att Ile	gct Ala	ggt Gly	tct Ser 330	ctt Leu	gga Gly	1010
caa Gln	gct Ala	gta Val 335	att Ile	tta Leu	gga Gly	aac Asn	atc Ile 340	agt Ser	agt Ser	atc Ile	ctt Leu	gga Gly 345	ttt Phe	aac Asn	att Ile	1058
tcg Ser	tcc Ser	atg Met 350	tct Ser	att Ile	act Thr	aat Asn 355	ccc Pro	ctc Leu	ccc Pro	agc Ser	cca Pro 360	agt Ser	gac Asp	tct Ser	ggg Gly	1106
tgg Trp 365	att Ile	aat Asn	gtg Val	act Thr 370	gcc Ala	cag Gln	cca Pro	gtt Val	gaa Glu	agg Arg 375	tct Ser	gca Ala	ttt Phe	cct Pro	gtt Val 380	1154
cat His	cac His	gtg Val	gcc Ala	ttc Phe 385	gtg Val	tcc Ser	tca Ser	ctc Leu	tta Leu 390	gtg Val	atc Ile	act Thr	cag Gln	ccg Pro 395	gtg Val	1202
gca Ala	gca Ala	cag Gln	cca Pro 400	gga Gly	cag Gln	cca Pro	ttt Phe	cct Pro 405	cag Gln	cag Gln	cct Pro	tcg Ser	gta Val 410	aag Lys	gca Ala	1250
aca Thr	gat Asp	tct Ser 415	gac Asp	ggg Gly	aac Asn	tgt Cys	gta Val 420	tca Ser	gtt Val	gga Gly	att Ile	act Thr 425	gca Ala	cta Leu	act Thr	1298
ttg Leu	agg Arg 430	gcc Ala	ata Ile	ctc Leu	aag Lys	gac Asp 435	tcc Ser	aat Asn	aat Asn	aac Asn	caa Gln 440	gtc Val	aat Asn	ggc Gly	ctt Leu	1346
agt Ser 445	gga Gly	aat Asn	aca Thr	aca Thr 450	att Ile	ccg Pro	ttt Phe	agc Ser	agc Ser	tgt Cys 455	tgg Trp	gcc Ala	aac Asn	tac Tyr	aca Thr 460	1394
gac Asp	ctt Leu	act Thr	ccc Pro	ctt Leu 465	aga Arg	aca Thr	gga Gly	aaa Lys	aat Asn 470	tat Tyr	aag Lys	att Ile	gaa Glu	ttt Phe 475	ata Ile	1442
ctg Leu	gat Asp	aat Asn	gtt Val 480	gtt Val	ggg Gly	gta Val	gaa Glu	tcc Ser 485	aga Arg	act Thr	ttc Phe	agc Ser	ctg Leu 490	ctg Leu	gca Ala	1490
gag Glu	tct Ser	gtc Val 495	tct Ser	agc Ser	agt Ser	ggc Gly	agc Ser 500	agc Ser	agc Ser	agc Ser	agc Ser	aac Asn 505	agc Ser	aaa Lys	gca Ala	1538
tca Ser	act Thr 510	gtg Val	ggt Gly	aca Thr	tat Tyr	gcc Ala 515	cag Gln	ata Ile	atg Met	act Thr 520	gta Val	gta Val	att Ile	agc Ser	tgt Cys	1586
ctg Ser	gtt Glu	gga Glu	aga Glu	atg Glu	tgg Glu	ctc Glu	ttg Glu	gaa Glu	ata Ile	ttt Glu	atg Glu	gct Glu	gca Glu	gtt Glu	tca Glu	1634

Leu Val Gly Arg Met Trp Leu Leu Glu Ile Phe Met Ala Ala Val Ser  
525 530 535 540

act ttg aat ata act tta aga agc tac taa a gtgctgttcc gaagaatagg 1685  
Thr Leu Asn Ile Thr Leu Arg Ser Tyr \*  
545 550

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taaacactaa aatcagattt cttcaaaata taaatttgtt ttgattcttt atatttatat 1865  
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ggtgaggcca tcacttcata cagtgactag caccacctct ggcaatgtca gccccacact 180  
cgcccgcgcc atg gcc tcc atc tcc gag ctt gcc tgt gtc tac ttg gcc 229  
Met Ala Ser Ile Ser Glu Leu Ala Cys Val Tyr Leu Ala  
1 5 10

ctc att ctg cac gat gac gag gtg atc atc atg gag gtt aat atc aat 277  
Leu Ile Leu His Asp Asp Glu Val Ile Ile Met Glu Val Asn Ile Asn  
15 20 25

acc ctc att aaa gca gcc agt gta aat gtt gaa cct ttt ggc ctg gct 325  
Thr Leu Ile Lys Ala Ala Ser Val Asn Val Glu Pro Phe Gly Leu Ala  
30 35 40 45

tgt ttg gaa agg ccc tgg cca acg tca aca ttg gaa gcc tca tct gca 373  
Cys Leu Glu Arg Pro Trp Pro Thr Ser Thr Leu Glu Ala Ser Ser Ala  
50 55 60

atg tag gggctggtgg acctgctcta gcagctggtg ctgcaccagc aggaggtcct 429  
Met \*

gccccctcca ttgctgctgc ttcagctgag gagaagaaaa tgggaagcaaa gaaagaagaa 489

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[illegible]

573

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ggtaagcccg	cctcctccct	cggccggccc	tggggccgtg	tccgcggggc	aactccagcc											180
gaggcctggg	cttctgcctg	caggtgtctg	cgggcgaggcc	cctaggggtac	agccccgattt											240
ggcccc	atg	gtg	ggt	ttc	ggg	gcc	aac	cgg	cgg	gct	ggc	cgc	ctg	ccc		288
	Met	Val	Gly	Phe	Gly	Ala	Asn	Arg	Arg	Ala	Gly	Arg	Leu	Pro		
	1				5					10						
tct	ctc	gtg	ctg	gtg	gtg	ctg	ctg	gtg	gtg	atc	gtc	gtc	ctc	gcc	ttc	336
Ser	Leu	Val	Leu	Val	Val	Leu	Leu	Val	Val	Ile	Val	Val	Leu	Ala	Phe	
15					20					25					30	
aac	tac	tgg	agc	atc	tcc	tcc	cgc	cac	gtc	ctg	ctt	cag	gag	gag	gtg	384
Asn	Tyr	Trp	Ser	Ile	Ser	Ser	Arg	His	Val	Leu	Leu	Gln	Glu	Glu	Val	
				35					40					45		
gcc	gag	ctg	cag	ggc	cag	gtc	cag	cgc	acc	gaa	gtg	gcc	cgc	ggg	cgg	432
Ala	Glu	Leu	Gln	Gly	Gln	Val	Gln	Arg	Thr	Glu	Val	Ala	Arg	Gly	Arg	
			50					55					60			
ctg	gaa	aag	cgc	aat	tcg	gac	ctc	ttg	ctg	ttg	gtg	gac	acg	cac	aag	480
Leu	Glu	Lys	Arg	Asn	Ser	Asp	Leu	Leu	Leu	Leu	Val	Asp	Thr	His	Lys	
		65					70					75				
aaa	cag	atc	gac	cag	aag	gag	gcc	gac	tac	ggc	cgc	ctc	agc	agc	cgg	528
Lys	Gln	Ile	Asp	Gln	Lys	Glu	Ala	Asp	Tyr	Gly	Arg	Leu	Ser	Ser	Arg	
	80					85					90					
ctg	cag	gcc	aga	gag	ggc	ctc	ggg	aag	aga	tgc	gag	gat	gac	aag	gtt	576
Leu	Gln	Ala	Arg	Glu	Gly	Leu	Gly	Lys	Arg	Cys	Glu	Asp	Asp	Lys	Val	
95					100					105					110	
aaa	cta	cag	aac	aac	ata	tcg	tat	cag	atg	gca	gac	ata	cat	cat	tta	624
Lys	Leu	Gln	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Ala	Asp	Ile	His	His	Leu	
				115					120					125		
aag	gag	caa	ctt	gct	gag	ctt	cgt	cag	gaa	ttt	ctt	cga	caa	gaa	gac	672

Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp	
130 135 140	
cag ctt cag gac tat agg aag aac aat act tac ctt gtg aag agg tta	720
Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu	
145 150 155	
gaa tat gaa agt ttt cag tgt gga cag cag atg aag gaa ttg aga gca	768
Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala	
160 165 170	
cag cat gaa gaa aat att aaa aag tta gca gac cag ttt tta gag gaa	816
Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu	
175 180 185 190	
caa aag caa gag acc caa aag att caa tca aat gat gga aag gaa ttg	864
Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu	
195 200 205	
gat ata aac aat caa gta gta cct aaa aat att cca aaa gta gct gag	912
Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu	
210 215 220	
aat gtt gca gat aag aat gaa gaa ccc tca agc aat cat att cca cat	960
Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His	
225 230 235	
ggg aaa gaa caa atc aaa aga ggt ggt gat gca ggg atg cct gga ata	1008
Gly Lys Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile	
240 245 250	
gaa gag aat gac cta gca aaa gtt gat gat ctt ccc cct gct tta agg	1056
Glu Glu Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg	
255 260 265 270	
aag cct cct att tca gtt tct caa cat gaa agt cat caa gca atc tcc	1104
Lys Pro Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser	
275 280 285	
cat ctt cca act gga caa gct ctc tcc cca aat atg cct cca gat tca	1152
His Leu Pro Thr Gly Gln Ala Leu Ser Pro Asn Met Pro Pro Asp Ser	
290 295 300	
cac att aaa cac aat gga aac ccc ggt act tca aaa aca gaa tcc ttc	1200
His Ile Lys His Asn Gly Asn Pro Gly Thr Ser Lys Thr Glu Ser Phe	
305 310 315	
cag tcc tct tca gcg ttt aat tcc agg ctc aaa ctt gga cag tag aac	1248
Gln Ser Ser Ser Ala Phe Asn Ser Arg Leu Lys Leu Gly Gln *	
320 325 330	
ccagaaattc caaacagatt atactaaagg caggttacca aggacagaag ccggggattc	1308
ccataaaatt ggcaccaatg tgaacacaga gagctcgtaa actgggtcct ggaccttggc	1368
agcagcgttc accgacgtcc tcaaaacca gaggacacac tcgaaaacga aaagggggcg	1428

aaccgcaaca cccacggccc ccccgacccg gaagggacga aagacaggggt acaccaggac 1488  
acacaaaatg gcaaaaacaaa ggcaacacgc tccaagaaag aacagccata cacaaaagaa 1548  
caaaagcgcac cacaccaaac aaccccgcac gaaccaacac cacaccaaga catgtcaaca 1608  
aacaagacca cataggagac gacaacgcaa agacaccgat cgagtaaccc caaagccacc 1668  
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tgtcagtgcac tgaggttcgc tgtgacacag aggggttctc ctggagagct atggcac 177  
atg ctc cat att aaa agg caa cat gat gct cgc tcc acc cag agg ccc 225  
Met Leu His Ile Lys Arg Gln His Asp Ala Arg Ser Thr Gln Arg Pro  
1 5 10 15  
cgg tcc ccg cca ttc att ccg ctc ccg gcc gag agt cgc tct agc caa 273  
Arg Ser Pro Pro Phe Ile Pro Leu Pro Ala Glu Ser Arg Ser Ser Gln  
20 25 30  
tca cct tcc agg ctc agg gcg gcc gag gca ggg cct ctg cct ctt cgg 321  
Ser Pro Ser Arg Leu Arg Ala Ala Glu Ala Gly Pro Leu Pro Leu Arg  
35 40 45  
ggg gcc tct ccc tcc ccc tgc ccc tga ttgtg gctgaactgc caccgcttga 373  
Gly Ala Ser Pro Ser Pro Cys Pro \*  
50 55  
tagcaaacca cactcggcac aggaaggaga acagcgcccg cggcacgaaa 423

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<212> DNA  
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<220>  
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 Met Ser Ser Pro  
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 Pro Pro Arg Arg Ser Asn Arg Arg Asn Pro Cys Pro Ser Gly Ile Gln  
 5 10 15 20

gcc aga aac tct ggc tgc ccc cac ctc ccc aat ggt ccc cat caa gta 151  
 Ala Arg Asn Ser Gly Cys Pro His Leu Pro Asn Gly Pro His Gln Val  
 25 30 35

ggt aac atc ctg ctg att tta act cct gtg cag ccc tca aat gca caa 199  
 Gly Asn Ile Leu Leu Ile Leu Thr Pro Val Gln Pro Ser Asn Ala Gln  
 40 45 50

ctg cct ccc att cct gca cag tgc ccc agt tca ggc ctt cac cac ctt 247  
 Leu Pro Pro Ile Pro Ala Gln Cys Pro Ser Ser Gly Leu His His Leu  
 55 60 65

gtt cct ggg cca ctg ccc aag tct ccc ccg act ggt ggc tgg act tct 295  
 Val Pro Gly Pro Leu Pro Lys Ser Pro Pro Thr Gly Gly Trp Thr Ser  
 70 75 80

aat act ttt cca act ccc cac tca tta aat cca tcc ccc tct cat taa 343  
 Asn Thr Phe Pro Thr Pro His Ser Leu Asn Pro Ser Pro Ser His \*  
 85 90 95 100

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caggc 408

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 Met Pro Gln Ser Phe Ser Ala Ile Thr Leu Ser Asn Thr Glu  
 1 5 10

atg aat aat att aat act aat gcc ccg aga aac aaa ctt cca ata aag 158  
 Met Asn Asn Ile Asn Thr Asn Ala Pro Arg Asn Lys Leu Pro Ile Lys  
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gaa ctt ggt aaa gtt tct aaa cat aaa att gcc act aaa aga aca cca	206
Glu Leu Gly Lys Val Ser Lys His Lys Ile Ala Thr Lys Arg Thr Pro	
35 40 45	
cat aaa gaa gat gag gca atg agc tgt tct gaa aat tgt tcg agt gcc	254
His Lys Glu Asp Glu Ala Met Ser Cys Ser Glu Asn Cys Ser Ser Ala	
50 55 60	
cag ggc gac tca ctt cag gat gag tct caa ggg tct cat tct gag tcc	302
Gln Gly Asp Ser Leu Gln Asp Glu Ser Gln Gly Ser His Ser Glu Ser	
65 70 75	
agc tct aat ccc tcc aat cct gaa act ttg cat gca aag gca act gat	350
Ser Ser Asn Pro Ser Asn Pro Glu Thr Leu His Ala Lys Ala Thr Asp	
80 85 90	
tca gtt cta caa ggt tct gaa gga aac aag gtc aag agg aca tcc tgc	398
Ser Val Leu Gln Gly Ser Glu Gly Asn Lys Val Lys Arg Thr Ser Cys	
95 100 105 110	
atg tat ggg gca aac tgc tat agg aag aat cct gtt cat ttt caa cat	446
Met Tyr Gly Ala Asn Cys Tyr Arg Lys Asn Pro Val His Phe Gln His	
115 120 125	
ttt agc cat cct ggt gat agt gat tat gga ggt gta caa atc gtg ggc	494
Phe Ser His Pro Gly Asp Ser Asp Tyr Gly Gly Val Gln Ile Val Gly	
130 135 140	
caa gat gag act gat gac cgg cct gaa tgt ccc tat gga cca tcc tgt	542
Gln Asp Glu Thr Asp Asp Arg Pro Glu Cys Pro Tyr Gly Pro Ser Cys	
145 150 155	
tat agg ttg gaa gtt cag tgt cca gtt gaa aaa cac caa ctc agc tag	590
Tyr Arg Leu Glu Val Gln Cys Pro Val Glu Lys His Gln Leu Ser *	
160 165 170	
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gaaaggatgg aagatttctca aagaaacaac tttccccttc taaggcagat gaaaacctgt	710
acatgtacct aacattttttt ccccttttta aaatataaaa tttcacatta cattttctgc	770
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 atg aag ttc ctt gac ttt gct ttc atc ttg gct ctc aag gtt tcc atg 168  
 Met Lys Phe Leu Asp Phe Ala Phe Ile Leu Ala Leu Lys Val Ser Met  
 1 5 10 15  
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 Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg Ile Ile Val Arg  
 20 25 30  
 atc ggt tat ggg tat ggc cct tat cat tca gtt tca gaa caa cca cta 264  
 Ile Gly Tyr Gly Tyr Gly Pro Tyr His Ser Val Ser Glu Gln Pro Leu  
 35 40 45  
 tac cca caa cca tac caa cca caa tac caa caa tat acc ttt taa tat 312  
 Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr Thr Phe \*  
 50 55 60  
 catcagtaac tgcaggacat gattattgag gcttgattgg ctgatacgac ttctacatcc 372  
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 ctttgcatat gagaaacact atatg 457

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 <212> DNA  
 <213> Homo sapiens

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 <222> (85)..(873)

<400> 305  
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 atgatgaaga ggcagctgca ccgc atg cgg cag ctg gcc cag acg ggc agc 111  
 Met Arg Gln Leu Ala Gln Thr Gly Ser  
 1 5  
 ttg gga cgc acc ccg gag acc gct gag ttc ctg ggt gag gac ctg ctg 159  
 Leu Gly Arg Thr Pro Glu Thr Ala Glu Phe Leu Gly Glu Asp Leu Leu  
 10 15 20 25  
 cag gta gaa cag cgg ctg gag ccg gcc aag cgg gca gcc cac aac atc 207  
 Gln Val Glu Gln Arg Leu Glu Pro Ala Lys Arg Ala Ala His Asn Ile  
 30 35 40  
 cac aag cgg ctg cag gcc tgt ctg cag ggc cag agc ggg gca gac atg 255  
 His Lys Arg Leu Gln Ala Cys Leu Gln Gly Gln Ser Gly Ala Asp Met  
 45 50 55

gac aag cgg gtg aag aag ctt ccc ctc atg gct ctg tcc acc acg atg Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met 60 65 70	303
gct gag agc ctc aag gag ctg gac cct gat tcc agc atg ggg aag gcc Ala Glu Ser Leu Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala 75 80 85	351
ttg gag atg agc tgt gcc atc cag aat cag ctg gcc cgc atc ctg gcc Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala 90 95 100 105	399
gag ttt gag atg acc ctg gag agg gac gtc ctg cag cca ctc agc agg Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg 110 115 120	447
ctg agt gag gag gag ctg cca gcc atc ctc aaa cac aag aaa agc ctc Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu 125 130 135	495
cag aag ctc gtg tcc gac tgg aac aca ctc aag agc agg ctc agt cag Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln 140 145 150	543
gca acc aag aat tca ggc agc agt caa ggc cta gga ggc agc ccg ggt Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly 155 160 165	591
agt cac agc cat acg acc atg gcc aac aag gtg gag acg ctg aag gag Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu 170 175 180 185	639
gag gag gag gag ctg aag agg aaa gtg gag caa tgc agg gac gag tac Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr 190 195 200	687
ttg gct gac ctg tac cac ttt gtt acc aag gag gac tcc tat gcc aac Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn 205 210 215	735
tac ttc att cgt ctc ctg gag att cag gcc gat tac cat cgc agg tca Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser 220 225 230	783
ctg agc tcg ctg gac aca gcc ctg gct gag ctg agg gag aac cac ggc Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly 235 240 245	831
caa gca ggt ggg gac ata ggc ccg gcg ata cca cac ccc tga ccctgcc Gln Ala Gly Gly Asp Ile Gly Pro Ala Ile Pro His Pro * 250 255 260	880
ctgctcgggg cttattgaga agctcgact tcatcctgaa aggtagcagg aagctgtgga	940
tgggttctga gagctaggct caatctgtga tggagaggca gctctggcta ctgtgtggag	1000
ggtggagtga agcgggcagg actagagcca ggcctgtgag gcagaaggag gcaacgggtgg	1060

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cctggactag gacagaggca gtggaggcgg gctgattcga gagatgtgac ggatgatttc 1120
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gccccctgect gactgctcgg ggtgggaagg ccctgggccg ctgatctgtt tcatccctgc 1240
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atctcgacag cgaagtcgac ccgggaatt 1749

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<210> 306
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (55)..(372)

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                                     1

gcg act gga acg cca gag tct caa gcg cgg ttc ggt cag tcc gtg aag  105
Ala Thr Gly Thr Pro Glu Ser Gln Ala Arg Phe Gly Gln Ser Val Lys
      5              10              15

ggg ctt ctc acg gag aag gtg acc acc tgt ggt act gac gta atc gcg  153
Gly Leu Leu Thr Glu Lys Val Thr Thr Cys Gly Thr Asp Val Ile Ala
      20              25              30

ctc acc aag cag gtg ctg aaa ggc tcc cgg agc tcc gag ctg cta ggt  201
Leu Thr Lys Gln Val Leu Lys Gly Ser Arg Ser Ser Glu Leu Leu Gly
      35              40              45

cag gca gct cga aac atg gta ctc cag gaa gat gcc atc ttg cac tca  249
Gln Ala Ala Arg Asn Met Val Leu Gln Glu Asp Ala Ile Leu His Ser
      50              55              60              65

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gaa gat agt tta agg aag atg gca ata ata aca aca cat ctt caa tac	297
Glu Asp Ser Leu Arg Lys Met Ala Ile Ile Thr Thr His Leu Gln Tyr	
70 75 80	
cag caa gaa gct att cag aag aat gtt gaa cag tca tcg gat cta cag	345
Gln Gln Glu Ala Ile Gln Lys Asn Val Glu Gln Ser Ser Asp Leu Gln	
85 90 95	
gac cag ttg aat cat ctg ttg aaa tag aatga catgtaagag tgctgtagga	397
Asp Gln Leu Asn His Leu Leu Lys *	
100 105	
ctcctttgcc taatgctgag gagtaaatac cttacacagc tgtcctctgg gtttggtttt	457
ctattttctt ctccaaaagt taagttagaa aagttcttg	496

<210> 307  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (88)..(840)

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gttccaggat ccaggtgccc aggggtc atg aag ctg gga ctc ctc tgt gct	111
Met Lys Leu Gly Leu Leu Cys Ala	
1 5	
ctg ctc tct ctg ctg gca ggg cat ggc tgg gca gac acc cgt gcc atc	159
Leu Leu Ser Leu Leu Ala Gly His Gly Trp Ala Asp Thr Arg Ala Ile	
10 15 20	
ggg gcc gag gaa tgt cgc ccc aac tcc cag cct tgg cag gcc ggc ctc	207
Gly Ala Glu Glu Cys Arg Pro Asn Ser Gln Pro Trp Gln Ala Gly Leu	
25 30 35 40	
ttc cac ctt act cgg ctc ttc tgt ggg gcg acc ctc atc agt gac cgc	255
Phe His Leu Thr Arg Leu Phe Cys Gly Ala Thr Leu Ile Ser Asp Arg	
45 50 55	
tgg ctg ctc aca gct gcc cac tgc cgc aag ccg tat ctg tgg gtc cgc	303
Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Tyr Leu Trp Val Arg	
60 65 70	
ctt gga gag cac cac ctc tgg aaa tgg gag ggt ccg gag cag ctg ttc	351
Leu Gly Glu His His Leu Trp Lys Trp Glu Gly Pro Glu Gln Leu Phe	
75 80 85	
cgg gtt acg gac ttc ttc ccc cac cct ggc ttc aac aag gac ctc agc	399

Arg	Val	Thr	Asp	Phe	Phe	Pro	His	Pro	Gly	Phe	Asn	Lys	Asp	Leu	Ser		
90						95					100						
gcc	aat	gac	cac	aat	gat	gac	atc	atg	ctg	atc	cgc	ctg	ccc	agg	cag	447	
Ala	Asn	Asp	His	Asn	Asp	Asp	Ile	Met	Leu	Ile	Arg	Leu	Pro	Arg	Gln		
105				110					115						120		
gca	cgt	ctg	agt	cct	gct	gtg	cag	ccc	ctc	aac	ctc	agc	cag	acc	tgt	495	
Ala	Arg	Leu	Ser	Pro	Ala	Val	Gln	Pro	Leu	Asn	Leu	Ser	Gln	Thr	Cys		
				125					130						135		
gtc	tcc	cca	ggc	atg	cag	tgt	ctc	atc	tca	ggc	tgg	ggg	gcc	gtg	tcc	543	
Val	Ser	Pro	Gly	Met	Gln	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ala	Val	Ser		
			140					145							150		
agc	ccc	aag	gcg	ctg	ttt	cca	gtc	aca	ctg	cag	tgt	gcc	aac	atc	agc	591	
Ser	Pro	Lys	Ala	Leu	Phe	Pro	Val	Thr	Leu	Gln	Cys	Ala	Asn	Ile	Ser		
		155					160								165		
atc	ctg	gag	aac	aaa	ctc	tgt	cac	tgg	gca	tac	cct	gga	cac	atc	tgc	639	
Ile	Leu	Glu	Asn	Lys	Leu	Cys	His	Trp	Ala	Tyr	Pro	Gly	His	Ile	Ser		
	170					175						180					
gac	agc	atg	ctc	tgt	gcg	ggc	ctg	tgg	gag	ggg	ggc	cga	ggg	tcc	tgc	687	
Asp	Ser	Met	Leu	Cys	Ala	Gly	Leu	Trp	Glu	Gly	Gly	Arg	Gly	Ser	Cys		
185					190					195					200		
cag	ggg	gac	tct	ggg	ggc	ccc	ctg	gtt	tgc	aat	gga	acc	ttg	gca	ggc	735	
Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Thr	Leu	Ala	Gly		
				205					210						215		
gtg	gtg	tct	ggg	ggg	gct	gag	ccc	tgc	tcc	aga	ccc	cgg	cgc	ccc	gca	783	
Val	Val	Ser	Gly	Gly	Ala	Glu	Pro	Cys	Ser	Arg	Pro	Arg	Arg	Pro	Ala		
			220					225							230		
gtc	tac	acc	agc	gta	tgc	cac	tac	ctt	gac	tgg	atc	caa	gaa	atc	atg	831	
Val	Tyr	Thr	Ser	Val	Cys	His	Tyr	Leu	Asp	Trp	Ile	Gln	Glu	Ile	Met		
		235					240								245		
gag aac tga gcccgcg cgccacgggg gcaccttggg agaccaagag aggccgaagg																887	
Glu Asn *																	
250																	
gcacgggggta ggggggttctc gtaggggtccc agcctcaatg gttcccgccc tggacctcca																947	
gctgccctga ctcccctctg gacactaaga ctccgcccct gaggctccgc cccctcacga																1007	
gggtcaagcaa gacacagtcg cgccccctcg gaacggagca gggacacgcc cttcagagcc																1067	
cgtctctatg acgtcaccga cagccatcac ctcttcttgg gaacagcaca gcctgtgggt																1127	
ccgccccaaag gaaccactta cacaaaatag ctccgcccct cggaactttg cccagtggga																1187	
cttcccctcg ggactccacc ccttgtggcc ccgcctcctt caccagagat ctgcccctc																1247	
gtgatgtcag gggcgagta gctccgcca cgtggagctc gggcggtgta gagctcagcc																1307	

ccttgtggcc ccgctctggg cgtgtgctgg gtttgaatcc tggcggagac ctggggggaa 1367  
attgagggag ggtctggata ccttttagagc caatgcaacg gatgattttt cagtaaacgc 1427  
gggaaacctc a 1438

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<212> DNA  
<213> Homo sapiens

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<222> (110)..(613)

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gccagccctc acctgacttg tctgggtccc tcctggggct aggggatgg atg aga 115  
Met Arg  
1  
agg gct agg ctg gag ctg tca gca gct tct tgg tgc ctg ctg ttt ctc 163  
Arg Ala Arg Leu Glu Leu Ser Ala Ala Ser Trp Cys Leu Leu Phe Leu  
5 10 15  
ttg tct tgt ctg tct tcg gtg tat tgc aat cct gtc ctc tta gca ggc 211  
Leu Ser Cys Leu Ser Ser Val Tyr Cys Asn Pro Val Leu Leu Ala Gly  
20 25 30  
ccc gca gag tca tac ttt ttc tcc ctg gcc ttc cag ctc cct ctc ttc 259  
Pro Ala Glu Ser Tyr Phe Phe Ser Leu Ala Phe Gln Leu Pro Leu Phe  
35 40 45 50  
cac cca gta tgc cca cct ccc tct ccc ttg act acc cca gcc tct gcc 307  
His Pro Val Cys Pro Pro Ser Pro Leu Thr Thr Pro Ala Ser Ala  
55 60 65  
caa tca cgc cct gcc ctc tac cct tca gag gac acc ttg ccg tct gtg 355  
Gln Ser Arg Pro Ala Leu Tyr Pro Ser Glu Asp Thr Leu Pro Ser Val  
70 75 80  
gag ctg gag cta ttc cta tgg tct ctc tgg gtc cac atg acc tta cat 403  
Glu Leu Glu Leu Phe Leu Trp Ser Leu Trp Val His Met Thr Leu His  
85 90 95  
ggc act cct ctc acc ttc tgt cca tcc aac aaa att ctc tgt tcc ttt 451  
Gly Thr Pro Leu Thr Phe Cys Pro Ser Asn Lys Ile Leu Cys Ser Phe  
100 105 110  
gaa gct ctc ttt tca gta agg cct tcc ttg gcc cct aac agg atg gat 499  
Glu Ala Leu Phe Ser Val Arg Pro Ser Leu Ala Pro Asn Arg Met Asp  
115 120 125 130

cac cct ccc ctg agc cct ggt cat tgc ctc tct gtt atg gcc tct cca	547
His Pro Pro Leu Ser Pro Gly His Cys Leu Ser Val Met Ala Ser Pro	
135 140 145	
ttg gta aac gct ctg ccg atg tgt ttc atc ttc cca cta gat cct tgc	595
Leu Val Asn Ala Leu Pro Met Cys Phe Ile Phe Pro Leu Asp Pro Cys	
150 155 160	
gcc cac gca cgc ggc tga atcatc ttacatccc cagaggccct ggtatgtggt	649
Ala His Ala Arg Gly *	
165	
ggacaggcctt gtttctgccg ggcctt	675

<210> 309  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (779)..(952)

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cagtcactta ttcccttcat acctgtcagc cgagagcact gactgcgtga tttccagggt	180
cctttacagc tttagagtat aggggctctg tttttgctgc tcccgaattt ccacctccca	240
tcatccacgc atttcacaga tgcattctgaa tgctcacagt gctctatttg tgcctctctg	300
tttgtccctg ttttttatgt ggatgcgtat cgaccgccat gatagactgc aactccctg	360
tgggcaggag ccatgttcat ttcatTTTTG tgtcccaggc ataatgtagg tgcgctcacc	420
tcattctctc catatcttga acctgtgaat ctcagtggac tcttttcagc agatgaacct	480
gtataagtct ttctgtctt gaaaggacag atgggtggcc cccatcctcc actgagcttc	540
ctgttgaact ccttttgcag gtgacgtcaa aatagaagaa gccctcattc accatatcta	600
ctgttaccct cctcctttcc cctctacttc ccatgaccag ttgttccactg cccctccaca	660
gaacctactt ctgataaatc ccgtgaagaa ttttttattg ccagatccaa attctttggc	720
ctctcacagt gtttgcgtgt gcttgattct cctcattct ggaaactcct ctctctc	778
atg gct ccc atg gga cca gtt gct cct gca gct cct cct gcc cct cac	826
Met Ala Pro Met Gly Pro Val Ala Pro Ala Ala Pro Pro Ala Pro His	
1 5 10 15	
tct gct ctc ctt gga ctc ctc ttt cct ggt att ctc tgc agt tct gtc	874



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Ser Ala Leu Leu Gly Leu Leu Phe Pro Gly Ile Leu Cys Ser Ser Val
      20                      25                      30
ctt cgc tct cag ctc ttt gca ccc ttc ttt ccc tcg ctg aca gct tcg      922
Leu Arg Ser Gln Leu Phe Ala Pro Phe Phe Pro Ser Leu Thr Ala Ser
      35                      40                      45
cgc ata cct gtg gct tca ctg tca cgc taa g gaacattctc tgtggccctg      973
Arg Ile Pro Val Ala Ser Leu Ser Arg *
      50                      55
gcccgctctct cgagcctgag ccccatgatt acaacttctg tctgtacccc acagtacata      1033
accttagcc                                                                1042

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<210> 310
<211> 1333
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (43)..(555)

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Met Arg Leu Pro
1
gct cag ctc ctg ggg ctg cta atg ctc tgg gtc cct gga tcc agt gag      102
Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Glu
5                      10                      15                      20
gat att gtg atg acc cag act cca ctc tcc ctg ccc gtc acc cct gga      150
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
25                      30                      35
gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt      198
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
40                      45                      50
gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag      246
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
55                      60                      65
tct cca cag ctc ctg atc tat acg ctt tcc tat cgg gcc tct gga gtc      294
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
70                      75                      80
cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa      342
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
85                      90                      95                      100
atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa      390

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Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln	
105 110 115	
cgt ata gag ttt cct tgg act ttt ggc cag ggg acc aag ctg gag atc	438
Arg Ile Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
120 125 130	
aaa cga act gtt gct gca cca tct gtc ttc atc ttc ccg cca tct gat	486
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
135 140 145	
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	534
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
150 155 160	
ttc tat ccc aga gag gcc taa gt acagtggaaa gtggtaaacg gcctccaaac	587
Phe Tyr Pro Arg Glu Ala *	
165 170	
tggttaaadc cagtaaagtg tcacagagca agacagtaag gacagcacct acgtactcag	647
cagcaaccag aagctgagca aagttgactt atgagatacc acaagtctag gcctgacgaa	707
gtcaaccatt atggacttgg gctgtgtcca atctgaatat agttatacct gggcagagtg	767
gttaaaagggt atagtgtgtc ccctaaattg tctcctaggt ttcaagctcg tagtcacttg	827
cccaggcttt ttgtcccttg taggtccttt tttcccaatg ggggacctaa gacactaagt	887
gacgggactc tccaaagtta atgattttaa acttaaaatc actctctaag ggatcatcag	947
gagttatgaa gtcgatgact aattgttttt gatacgagta tatctgaaaa tgattgaaag	1007
tgtgaattcc tcatggtagg tgagataaac tagtcgttat agtatctagt agatgaccgg	1067
agcatttata gagtagaagt ccgcatactc ccggataatc taccacgaca catgattaga	1127
ctctcgcgat ggtaaacaga tggatgtaaa ctcaatcgtg ggagtaccga aagaggtggc	1187
tatgatgttg acatgatagg gtctaggatg cgtgatcgtg tgacggaatt gtcaaatacg	1247
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tgaatgagtg acatcttgcg tgtggt	1333

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 <211> 803  
 <212> DNA  
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<220>  
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 <222> (77)..(433)

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 ggggtggtatt cctgcc atg ggt cct ggg ctt ctc cac tgg atg gcc ctt 109  
 Met Gly Pro Gly Leu Leu His Trp Met Ala Leu  
 1 5 10  
 tgt ctc ctt gga aca ggt cat ggg gat gcc atg gtc atc cag aac cca 157  
 Cys Leu Leu Gly Thr Gly His Gly Asp Ala Met Val Ile Gln Asn Pro  
 15 20 25  
 aga tac cag gtt acc cag ttt gga aag cca gtg acc ctg agt tgt tct 205  
 Arg Tyr Gln Val Thr Gln Phe Gly Lys Pro Val Thr Leu Ser Cys Ser  
 30 35 40  
 cag act ttg aac cat aac gtc atg tac tgg tac cag cag aag tca agt 253  
 Gln Thr Leu Asn His Asn Val Met Tyr Trp Tyr Gln Gln Lys Ser Ser  
 45 50 55  
 cag gcc cca aag ctg ctg ttc cac tac tat gac aaa gat ttt aac aat 301  
 Gln Ala Pro Lys Leu Leu Phe His Tyr Tyr Asp Lys Asp Phe Asn Asn  
 60 65 70 75  
 gaa gca gac acc cct gat aac ttc caa tcc agg agg ccg aac act tct 349  
 Glu Ala Asp Thr Pro Asp Asn Phe Gln Ser Arg Arg Pro Asn Thr Ser  
 80 85 90  
 ttc tgc ttt ctt gac atc cgc tca cca ggc ctg ggg gac gca gcc atg 397  
 Phe Cys Phe Leu Asp Ile Arg Ser Pro Gly Leu Gly Asp Ala Ala Met  
 95 100 105  
 tac ctg tgt gcc acc agc gtc cac cgg gac cca tga acac tgaagctttc 447  
 Tyr Leu Cys Ala Thr Ser Val His Arg Asp Pro \*  
 110 115  
 tttggacaag gcaccagact cacagttgta gcatgtgaaa aggtccagag ctctgcagtg 507  
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 ttgtactact tttgagaatg caaagcttaa ctgtggacgg attccaatcc tggccaggca 627  
 ggggttgctgg acactctgag agaagaaagg gttaatccca tgaccatcaa cttccatggg 687  
 atttcagcca tcttgacaa gctaccacac cctcctgccc caaggggagg aggaaatgtg 747  
 gaccatccca tcagaaattg accaaaggac ctgaacaagt ggtccccccc ccccc 803

<210> 312  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (6)..(605)

<400> 312

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Met	Leu	Cys	Arg	Gln	Gln	Leu	Arg	Asn	Leu	Thr	Glu	Asn	Lys			
1					5					10						
gaa	tct	gag	ttg	cag	tgt	ctc	ttt	caa	cag	ata	gaa	agg	cag	gag	cag	95
Glu	Ser	Glu	Leu	Gln	Cys	Leu	Phe	Gln	Gln	Ile	Glu	Arg	Gln	Glu	Gln	
15				20						25					30	
ctt	ctg	gat	gaa	ata	cat	cgt	gag	aag	aga	gat	cta	ctg	gaa	gag	acc	143
Leu	Leu	Asp	Glu	Ile	His	Arg	Glu	Lys	Arg	Asp	Leu	Leu	Glu	Glu	Thr	
				35					40						45	
caa	aga	aaa	gat	gaa	gaa	atg	gga	tct	ctg	cag	gac	cgt	gta	att	gca	191
Gln	Arg	Lys	Asp	Glu	Glu	Met	Gly	Ser	Leu	Gln	Asp	Arg	Val	Ile	Ala	
			50					55					60			
tta	gaa	acg	agt	acc	caa	gtg	gcc	ttg	gac	cat	ctg	gag	tct	gtg	cct	239
Leu	Glu	Thr	Ser	Thr	Gln	Val	Ala	Leu	Asp	His	Leu	Glu	Ser	Val	Pro	
		65					70					75				
gag	aaa	ctg	agc	cta	cta	gaa	gat	ttc	aaa	gac	ttc	aga	gat	tcc	tgc	287
Glu	Lys	Leu	Ser	Leu	Leu	Glu	Asp	Phe	Lys	Asp	Phe	Arg	Asp	Ser	Cys	
	80					85					90					
agt	tca	tct	gag	aga	act	gat	gga	aga	tat	tcc	aaa	tac	agg	gtt	cgc	335
Ser	Ser	Ser	Glu	Arg	Thr	Asp	Gly	Arg	Tyr	Ser	Lys	Tyr	Arg	Val	Arg	
	95				100					105					110	
aga	aat	tct	ctt	cag	cat	cac	caa	gat	gac	acc	aag	tac	aga	acc	aaa	383
Arg	Asn	Ser	Leu	Gln	His	His	Gln	Asp	Asp	Thr	Lys	Tyr	Arg	Thr	Lys	
				115					120						125	
agt	ttc	aaa	ggt	gac	aga	acc	ttt	ctg	gaa	ggt	tcc	cac	act	cgt	ggg	431
Ser	Phe	Lys	Gly	Asp	Arg	Thr	Phe	Leu	Glu	Gly	Ser	His	Thr	Arg	Gly	
			130					135					140			
tta	gat	cac	tca	tcc	tct	tgg	cag	gat	cac	agt	cgc	ttc	ctg	tct	agt	479
Leu	Asp	His	Ser	Ser	Ser	Trp	Gln	Asp	His	Ser	Arg	Phe	Leu	Ser	Ser	
		145					150						155			
cca	aga	ttt	tca	tac	gtg	aac	tca	ttt	acc	aaa	aga	act	ggt	gct	cca	527
Pro	Arg	Phe	Ser	Tyr	Val	Asn	Ser	Phe	Thr	Lys	Arg	Thr	Val	Ala	Pro	
	160					165						170				
gat	tca	gct	tca	aac	aag	gaa	gat	gcc	aca	atg	aat	gga	aca	agt	tca	575
Asp	Ser	Ala	Ser	Asn	Lys	Glu	Asp	Ala	Thr	Met	Asn	Gly	Thr	Ser	Ser	
	175				180					185					190	
caa	ccc	aaa	aaa	gag	gaa	tat	ggg	agc	taa	a	aaagcaa	aatg	taatttg	ttta		626
Gln	Pro	Lys	Lys	Glu	Glu	Tyr	Gly	Ser	*							
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<220>  
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 <222> (714)..(947)

<400> 313

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tcagttgtaa cttattccta tttgtcagca ttcagggttat tagcggctgc tggcgaagtc      180
cttgagaaat aaactgcaca ctggatggtg ggggtagtgt aggaaaatgg aggggaagga      240
agtaaagttt caaattaagc ctgaacagca aagttcccct gagaaggcca cctggattct      300
atcagaaact cgaatgtcca tcttgcaaaa cttccttgcc caaaccaccac ccctggagtc      360
acaaccacc cttgaccaat agattcattt cactgaggga ggcaaagggc tgggtcaatag      420
attcatttca ctgggagagg caaagggctg ggggccagag aggagaagta aaaagccaca      480
catgaagcag caatgcaggc atgcttcttg ctcactctgtg atcaccagga aactcccaga      540
tctgacactg tagtgcattt cactgctgac aagaaggctg ctgccaccag cctgtgaagc      600
aagggttaagg tgagaaggct ggaggtgaga ttctgggcag tctcctgggt gtctacccat      660
ggacctagag gtactttgaa agttttggat atctgggctc tgactgtgca ata   atg      716
                                   Met
                                   1

ggc aac ccc aaa gtc aag gca cat ggc aag aag gtg ctg atc tcc ttc      764
Gly Asn Pro Lys Val Lys Ala His Gly Lys Lys Val Leu Ile Ser Phe
      5              10              15

gga aaa gct gtt atg ctc acg gat gac ctc aaa ggc acc ttt gct aca      812
Gly Lys Ala Val Met Leu Thr Asp Asp Leu Lys Gly Thr Phe Ala Thr
      20              25              30

ctg agt gac ctg cac tgt aac aag ctg cac gtg gac cct gag aac ttc      860
Leu Ser Asp Leu His Cys Asn Lys Leu His Val Asp Pro Glu Asn Phe
      35              40              45

ctg ctc tta ggc aac gtg ata ttg att gtt ttg gca acc cac ttc agc      908
Leu Leu Leu Gly Asn Val Ile Leu Ile Val Leu Ala Thr His Phe Ser
      50              55              60              65

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gag gat ttt acc cta cag ata cag gct tct tgg cag taa ctaacaaatg      957
Glu Asp Phe Thr Leu Gln Ile Gln Ala Ser Trp Gln  *
              70              75

ctgtgggttaa tgctgtagcc cacaagacca ctgagttccc tgtccactat gtttgtacct      1017

atgggtccact atgtttgtac ctatgtccca aaatctcatc tccttttagat gggggagggtt      1077

ggggagaaga gcagtatcct gectgtgat tcagttcctg catgataaaa atagaataaa      1137

gaaatatgct ctctaagaaa      1157


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<212> DNA
<213> Homo sapiens

<220>
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<222> (219)..(479)

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cttggtggtg actttgaagg tagaggctga cagtgagtgg agtatggaca tgtcaccac      180

aaccagatga agagggactc cgagatagcg actcggct      atg cac aca gtc acc      233
                        Met His Thr Val Thr
                        1              5

cac aga gga gga gca ggg aag ggg gaa agt agc ctc tct cag cac atg      281
His Arg Gly Gly Ala Gly Lys Gly Glu Ser Ser Leu Ser Gln His Met
              10              15              20

ata aaa aga cct gga tgg gga ggt gga gca gag gcc ttc act cca tca      329
Ile Lys Arg Pro Gly Trp Gly Gly Gly Ala Glu Ala Phe Thr Pro Ser
              25              30              35

ttt ttt aaa tcc atc ctt caa tat ttt caa gag gaa ggg aaa cca gac      377
Phe Phe Lys Ser Ile Leu Gln Tyr Phe Gln Glu Glu Gly Lys Pro Asp
              40              45              50

agg cca aac cac agc ctt cag tgg ggc ttg act tta gtt cta cgg acc      425
Arg Pro Asn His Ser Leu Gln Trp Gly Leu Thr Leu Val Leu Arg Thr
              55              60              65

tca cca gcc att cca gca gct gaa tgc ctg cca gtt ggt gcc cac acg      473
Ser Pro Ala Ile Pro Ala Ala Glu Cys Leu Pro Val Gly Ala His Thr
              70              75              80              85

cta tga gacccacaa ctgtgtgaga agctgggaac atttcacagg gaaaaagcag      529
Leu  *

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aaatggaggg agtgaaaccc ctacttagtt tctgctgac ctccttgga gaga

583

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<213> Homo sapiens

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cccagagagga aggc atg cgg tgg gcc cta ctg gtg ctt cta gct ttc ctg 110  
Met Arg Trp Ala Leu Val Leu Leu Ala Phe Leu  
1 5 10

tct cct gcc agt cag aaa tct tcc aac ttg gaa ggg aga acg aag tca 158  
Ser Pro Ala Ser Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser  
15 20 25

gtc acc agg cag act ggg tca tct gct gaa atc act tgc gat ctt act 206  
Val Thr Arg Gln Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr  
30 35 40

gta aca aat acc ttc tac atc cac tgg tac cta cac cag gag ggg aag 254  
Val Thr Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys  
45 50 55 60

gcc cca cag cgt ctt ctg tac tat gac gtc tcc act gca agg gat gtg 302  
Ala Pro Gln Arg Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val  
65 70 75

ttg gaa tca gga ctc agt cca gga aag tat tat act cat aca ccc agg 350  
Leu Glu Ser Gly Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg  
80 85 90

agg tgg agc tgg ata ttg ata cta cga aat cta att gaa aat gat tct 398  
Arg Trp Ser Trp Ile Leu Ile Leu Arg Asn Leu Ile Glu Asn Asp Ser  
95 100 105

ggg gtc tat tac tgt gcc acc tgg gac agg cac agt gat tca gac ctg 446  
Gly Val Tyr Tyr Cys Ala Thr Trp Asp Arg His Ser Asp Ser Asp Leu  
110 115 120

tcc tac acc aca ctg aaa atc tgc ctt gtg gct gcc tct ggt tca cag 494  
Ser Tyr Thr Thr Leu Lys Ile Cys Leu Val Ala Ala Ser Gly Ser Gln  
125 130 135 140

gat aga gcc gcc ccc tct cat ttc ctg tca cca aat tta ctg tat tct 542  
Asp Arg Ala Ala Pro Ser His Phe Leu Ser Pro Asn Leu Leu Tyr Ser

145	150	155	
gaa caa gag aaa gac agc tta act cct gat ctc cct cct aat atc aca			590
Glu Gln Glu Lys Asp Ser Leu Thr Pro Asp Leu Pro Pro Asn Ile Thr			
160	165	170	
ctg tcc tgg cag cag ctg cat cct gtt ccc cac ccc tcc ccc aca act			638
Leu Ser Trp Gln Gln Leu His Pro Val Pro His Pro Ser Pro Thr Thr			
175	180	185	
ttc ctg aag atc aag ctg cca tct cca ggc ctc agc taa gcagcctggc			687
Phe Leu Lys Ile Lys Leu Pro Ser Pro Gly Leu Ser *			
190	195	200	
tgagagcaag gttctctcag ctctcctagg acatggggga ggcccactca ctctgcttcc			747
tatgacacac aggtacaact aggggccagc tgtgaagcga gatatttttg acagcaaattg			807
ggaaggggtat ttatactgaa tcatgtatcc actcatggtc cagagatcac agctgagagt			867
ggtgcttatt ccttatgtct ataacaacat aagcaatact ataatgacca ctaaaacact			927
aggc			931
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gaattgaaag tgaggatgac ttgtataaac tggatgaactt ctcccttaaa tatcgagctc			180
accgtttatc ttccagcctc cagatcaagc cctgcagtca ggcgagc atg gag aag			236
		Met Glu Lys	
		1	
gcg agc atg gag gag aca agc acg agg tca gaa ttg gag ctg gca gag			284
Ala Ser Met Glu Glu Thr Ser Thr Arg Ser Glu Leu Glu Leu Ala Glu			
5	10	15	
cag acg gag atg gag gga gaa aag gaa gaa agc ctg gtg gaa ggg gag			332
Gln Thr Glu Met Glu Gly Glu Lys Glu Glu Ser Leu Val Glu Gly Glu			
20	25	30	35
aag gag gaa gag gag gag acc cca ccc tcc ccc tgg gtc atc cac ccc			380
Lys Glu Glu Glu Glu Glu Thr Pro Pro Ser Pro Trp Val Ile His Pro			



	40	45	50	
aat gat gtc ctc aag att ctg gag gcc ttc ttc atg ggt ctg aag aag				428
Asn Asp Val Leu Lys Ile Leu Glu Ala Phe Phe Met Gly Leu Lys Lys				
	55	60	65	
cct agg gac tcg cgg gcc ccg ctg agg gta cag aag aat gtg cgt gac				476
Pro Arg Asp Ser Arg Ala Pro Leu Arg Val Gln Lys Asn Val Arg Asp				
	70	75	80	
aac tcc aag gac tcg gag tac tgg cag gcc ctg acc aca gtg atc cct				524
Asn Ser Lys Asp Ser Glu Tyr Trp Gln Ala Leu Thr Thr Val Ile Pro				
	85	90	95	
tcc tcc aag cag aac ctc tgg gat gcc ctc tac aca gcc ttg gag aag				572
Ser Ser Lys Gln Asn Leu Trp Asp Ala Leu Tyr Thr Ala Leu Glu Lys				
	100	105	110	115
tac cac ctt gtc ctg acc cag agg gcc aag ctg ctg ctg gaa aac agt				620
Tyr His Leu Val Leu Thr Gln Arg Ala Lys Leu Leu Leu Glu Asn Ser				
	120	125	130	
tct ctg gag cag cag aac aca gag ctg cag gcg cta ctg cag cag tat				668
Ser Leu Glu Gln Gln Asn Thr Glu Leu Gln Ala Leu Leu Gln Gln Tyr				
	135	140	145	
ctg aac tcc aag atc aac tct gaa ctg caa gtt cct ccc act cag gtg				716
Leu Asn Ser Lys Ile Asn Ser Glu Leu Gln Val Pro Pro Thr Gln Val				
	150	155	160	
ttg cgg gta ccc aca aaa tga gc tggaccgccca aaggctgatg tgttagggct				769
Leu Arg Val Pro Thr Lys *				
	165	170		
ggcctgatgc tgggtgtctgt gccggagcca gtcatatca cccactgggc cgcacctggg				829
cctgctctct ggattttcca gggctgtctt tatagcctgt cgaaataagg agccagagga				889
gttacctgtg tcctgcatta tgattaaagc cttttaaggt tgaaaaaaaa aaaa				943

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 <212> DNA  
 <213> Homo sapiens

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 <222> (339)..(623)

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cgc ttc ttc cag cag cgc aag agc ctg ctg ctg cac cag cgc ctg cac 99  
 Arg Phe Phe Gln Gln Arg Lys Ser Leu Leu Leu His Gln Arg Leu His  
 10 15 20  
 acc ggc aat ggc cag ggc tgg ccc gcc tgc ccc tac tgc ggc aag gcc 147  
 Thr Gly Asn Gly Gln Gly Trp Pro Ala Cys Pro Tyr Cys Gly Lys Ala  
 25 30 35 40  
 ttc cgc cgg ccc tcg gac ctc ttc cgg cac cag cgc atc cac acc ggt 195  
 Phe Arg Arg Pro Ser Asp Leu Phe Arg His Gln Arg Ile His Thr Gly  
 45 50 55  
 gag cgg ccc tac cag tgc ccc cag tgt ggc cgg acc ttc aac cgc aac 243  
 Glu Arg Pro Tyr Gln Cys Pro Gln Cys Gly Arg Thr Phe Asn Arg Asn  
 60 65 70  
 cac cac ctg gcc gtg cac atg cag acc cac gcc cga ggc cag gtg gcc 291  
 His His Leu Ala Val His Met Gln Thr His Ala Arg Gly Gln Val Gly  
 75 80 85  
 cca cac ttc cct gcc gcc ccc gcc cgc cac ggg agc ctg ccc ctg ccc 339  
 Pro His Phe Pro Ala Ala Pro Ala Arg His Gly Ser Leu Pro Leu Pro  
 90 95 100  
 tgg ccc agc cgg aag gag gag ggc tga cctgg caggagccca cagaggacct 391  
 Trp Pro Ser Arg Lys Glu Glu Gly \*  
 105 110  
 ctggcggggt ctctcccctg tgcctgacgc aggttcttcc ttttctctggg atggagagag 451  
 gtttgtttgtt tttaccatt caaatgggaa gctagctgcc cttctggtga cattgtgtgt 511  
 gaccgggtgc tttctgtttc ctgtttgcac tcttcgctgc cttttctgca ttcctgactt 571  
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 gacctgggat ctgagttttg tgcagagatc tctgcctgc tgtcaccatg agaaacagtg 751  
 gagtggagtg gatggatggc ctgacttgaa gaaagggccc tggaaagttt tctactttgc 811  
 tatattgaaa tataaatccc ttcttataga gactttgaaa tactttctgta aatgtgtgta 871  
 gtagtcaatg gaacttttgc tttagcaaag tcggaaagag tcggcttttc catgtgaggc 931  
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agcagcgaag ctgcgggcg ctggcgggac aggcgcgtga ggccacaaca catgcgtgta	180
tcttgcttgg gctatcttcc ctgctctgcc acgccgggtc tggagaagg gtttcagccc	240
caggacattt actgagagtc ggcgaatatt gggagccgcg atg ttc ccc ctt cgg	295
Met Phe Pro Leu Arg	
1 5	
gcc ctg tgg ttg gtc tgg gcg ctt cta gga gtg gcc gga tca tgc ccg	343
Ala Leu Trp Leu Val Trp Ala Leu Leu Gly Val Ala Gly Ser Cys Pro	
10 15 20	
gag ccg tgc gcc tgc gtg gac aag tac gct cac cag ttc gcg gac tgc	391
Glu Pro Cys Ala Cys Val Asp Lys Tyr Ala His Gln Phe Ala Asp Cys	
25 30 35	
gct tac aaa gag ttg cgt gag gtg ccg gaa gga ctg cct gcc aac gtg	439
Ala Tyr Lys Glu Leu Arg Glu Val Pro Glu Gly Leu Pro Ala Asn Val	
40 45 50	
acg acg ctt agt ctg tcc gcg aac aag atc act gtg ctg cgg cgc ggg	487
Thr Thr Leu Ser Leu Ser Ala Asn Lys Ile Thr Val Leu Arg Arg Gly	
55 60 65	
gcc ttc gcc gac gtc aca cag gtc acg tcg ctg tgg ctg gcg cac aat	535
Ala Phe Ala Asp Val Thr Gln Val Thr Ser Leu Trp Leu Ala His Asn	
70 75 80 85	
gag gtg cgc acc gtg gag cca ggc gca ctg gcc gtg ctg agt cag ctc	583
Glu Val Arg Thr Val Glu Pro Gly Ala Leu Ala Val Leu Ser Gln Leu	
90 95 100	
aag aac ctc gat ctg agc cac aac ttc ata tcc agc ttt ccg tgg agc	631
Lys Asn Leu Asp Leu Ser His Asn Phe Ile Ser Ser Phe Pro Trp Ser	
105 110 115	
gac ctg cgc aac ctg agc gcg ctg cag ctg ctc aaa atg aac cac aac	679
Asp Leu Arg Asn Leu Ser Ala Leu Gln Leu Leu Lys Met Asn His Asn	
120 125 130	
cgc ctg ggc tct ctg ccc cgg gac gca ctc ggt gcg cta ccc gac ctg	727
Arg Leu Gly Ser Leu Pro Arg Asp Ala Leu Gly Ala Leu Pro Asp Leu	
135 140 145	
cgt tcc ctg cgc atc aac aac aac cgg ctg cgt acg ctg gcg cct ggc	775
Arg Ser Leu Arg Ile Asn Asn Asn Arg Leu Arg Thr Leu Ala Pro Gly	
150 155 160 165	

acc	ttc	gac	gcg	ctt	agc	gcg	ctg	tca	cac	ttg	caa	ctc	tat	cac	aat	823
Thr	Phe	Asp	Ala	Leu	Ser	Ala	Leu	Ser	His	Leu	Gln	Leu	Tyr	His	Asn	
				170					175					180		
ccc	ttc	cac	tgc	ggc	tgc	ggc	ctt	gtg	tgg	ctg	cag	gcc	tgg	gcc	gcg	871
Pro	Phe	His	Cys	Gly	Cys	Gly	Leu	Val	Trp	Leu	Gln	Ala	Trp	Ala	Ala	
				185					190					195		
agc	acc	cgg	gtg	tcc	tta	ccc	gag	ccc	gac	tcc	att	gct	tgt	gcc	tcg	919
Ser	Thr	Arg	Val	Ser	Leu	Pro	Glu	Pro	Asp	Ser	Ile	Ala	Cys	Ala	Ser	
				200					205					210		
cct	ccc	gcg	ctg	cag	ggg	gtg	ccg	gtg	tac	cgc	ctg	ccc	gcc	ctg	ccc	967
Pro	Pro	Ala	Leu	Gln	Gly	Val	Pro	Val	Tyr	Arg	Leu	Pro	Ala	Leu	Pro	
				215					220					225		
tgt	gca	ccg	ccc	agc	gtg	cat	ctg	agt	gcc	gag	cca	ccg	ctt	gaa	gca	1015
Cys	Ala	Pro	Pro	Ser	Val	His	Leu	Ser	Ala	Glu	Pro	Pro	Leu	Glu	Ala	
				230					235					240		
ccc	ggc	acc	cca	ctg	cgc	gca	gga	ctg	gcg	ttc	gtg	tta	cac	tgc	atc	1063
Pro	Gly	Thr	Pro	Leu	Arg	Ala	Gly	Leu	Ala	Phe	Val	Leu	His	Cys	Ile	
				250					255					260		
gcc	gac	ggc	cac	cct	acg	cct	cgc	ctg	caa	tgg	caa	ctt	cag	atc	ccc	1111
Ala	Asp	Gly	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	
				265					270					275		
ggt	ggc	acc	gta	gtc	tta	gag	cca	ccg	gtt	ctg	agc	ggg	gag	gac	gac	1159
Gly	Gly	Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	
				280					285					290		
ggg	gtt	ggg	gcg	gag	gaa	gga	gag	gga	gaa	gga	gat	ggg	gat	ttg	ctg	1207
Gly	Val	Gly	Ala	Glu	Glu	Gly	Glu	Gly	Glu	Gly	Asp	Gly	Asp	Leu	Leu	
				295					300					305		
acg	cag	acc	caa	gcc	caa	acg	ccg	act	cca	gca	ccc	gct	tgg	ccg	gcg	1255
Thr	Gln	Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	
				310					315					320		
ccc	cca	gcc	aca	ccg	cgc	ttc	ctg	gcc	ctc	gca	aat	ggc	tcc	ctg	ttg	1303
Pro	Pro	Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	
				330					335					340		
gtg	ccc	ctc	ctg	agt	gcc	aag	gag	gcg	ggc	gtc	tac	act	tgc	cgt	gca	1351
Val	Pro	Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	
				345					350					355		
cac	aat	gag	ctg	ggc	gcc	aac	tct	acg	tca	ata	cgc	gtg	gcg	gtg	gca	1399
His	Asn	Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	
				360					365					370		
gca	acc	ggg	ccc	cca	aaa	cac	gcg	cct	ggc	gcc	ggg	gga	gaa	ccc	gac	1447
Ala	Thr	Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	
				375					380					385		





ctt cac ttc aag ttt gaa aat tat gga gat tca atg tta caa aaa atg	280
Leu His Phe Lys Phe Glu Asn Tyr Gly Asp Ser Met Leu Gln Lys Met	
10 15 20	
aac aaa tta aga gaa gag aat aaa ttt tgt gat gtt aca gtt ctc ata	328
Asn Lys Leu Arg Glu Glu Asn Lys Phe Cys Asp Val Thr Val Leu Ile	
25 30 35	
gat gat att gag gta cag gga cat aaa att gtg ttt gct gca ggt tcc	376
Asp Asp Ile Glu Val Gln Gly His Lys Ile Val Phe Ala Ala Gly Ser	
40 45 50 55	
ccc ttc tta aga gac caa ttt tta ctg aat gat tcc aga gag gtg aaa	424
Pro Phe Leu Arg Asp Gln Phe Leu Leu Asn Asp Ser Arg Glu Val Lys	
60 65 70	
atc tcc ata tta cag agt tcc gaa gtg ggg aga caa ttg ctc tta tcc	472
Ile Ser Ile Leu Gln Ser Ser Glu Val Gly Arg Gln Leu Leu Leu Ser	
75 80 85	
tgt tat agt ggt gtg ctg gaa ttc cct gag atg gaa ctg gta aat tac	520
Cys Tyr Ser Gly Val Leu Glu Phe Pro Glu Met Glu Leu Val Asn Tyr	
90 95 100	
ttg act gct gca agt ttt ctt cag atg agc cac att gta gaa cgg tgc	568
Leu Thr Ala Ala Ser Phe Leu Gln Met Ser His Ile Val Glu Arg Cys	
105 110 115	
aca cag gcc ctg tgg aag ttt ata aag cca aaa caa cca atg gat agt	616
Thr Gln Ala Leu Trp Lys Phe Ile Lys Pro Lys Gln Pro Met Asp Ser	
120 125 130 135	
aaa gag gga tgt gaa cca cag agt gct tct ccc cag tca aaa gaa cag	664
Lys Glu Gly Cys Glu Pro Gln Ser Ala Ser Pro Gln Ser Lys Glu Gln	
140 145 150	
cag gga gat gcc aga ggc tcc cca aag cag gac tca cct tgt att cat	712
Gln Gly Asp Ala Arg Gly Ser Pro Lys Gln Asp Ser Pro Cys Ile His	
155 160 165	
cca tct gaa gac agt atg gat atg gag gac agt gat att cag att gtt	760
Pro Ser Glu Asp Ser Met Asp Met Glu Asp Ser Asp Ile Gln Ile Val	
170 175 180	
aag gta gaa tct att ggg gat gta tca gag gtt aga agt aaa aaa gat	808
Lys Val Glu Ser Ile Gly Asp Val Ser Glu Val Arg Ser Lys Lys Asp	
185 190 195	
cag aac cag ttt att tct tct gaa ccc act gct tta cat tca tca gag	856
Gln Asn Gln Phe Ile Ser Ser Glu Pro Thr Ala Leu His Ser Ser Glu	
200 205 210 215	
ccc cag cac tcc ctg ata aat tca act gtg gaa aac aga gta agt gaa	904
Pro Gln His Ser Leu Ile Asn Ser Thr Val Glu Asn Arg Val Ser Glu	
220 225 230	



ata gaa caa aac cat ctc cac aat tat gcc ctt tct tat aca ggc agt	952
Ile Glu Gln Asn His Leu His Asn Tyr Ala Leu Ser Tyr Thr Gly Ser	
235 240 245	
gat aac atc atc atg gcc tca aaa gat gtc ttt ggc cct aat att cga	1000
Asp Asn Ile Ile Met Ala Ser Lys Asp Val Phe Gly Pro Asn Ile Arg	
250 255 260	
ggg gta gac aaa ggc cta cag tgg cat cac cag tgc cca aag tgt acc	1048
Gly Val Asp Lys Gly Leu Gln Trp His His Gln Cys Pro Lys Cys Thr	
265 270 275	
agg gtg ttt cgt cac ctg gag aac tac gcc aac cat tta aaa atg cac	1096
Arg Val Phe Arg His Leu Glu Asn Tyr Ala Asn His Leu Lys Met His	
280 285 290 295	
aaa ctc ttt atg tgt cta ctc tgc ggc aag act ttc act cag aaa ggc	1144
Lys Leu Phe Met Cys Leu Leu Cys Gly Lys Thr Phe Thr Gln Lys Gly	
300 305 310	
aac ctt cat cga cac atg cgt gtg cat gcc gga att aaa cct ttc cag	1192
Asn Leu His Arg His Met Arg Val His Ala Gly Ile Lys Pro Phe Gln	
315 320 325	
tgt aaa atc tgt ggg aaa acc ttt tct cag aag tgt tcc tta cag gat	1240
Cys Lys Ile Cys Gly Lys Thr Phe Ser Gln Lys Cys Ser Leu Gln Asp	
330 335 340	
cat ctt aac ctt cac agt gga gat aag ccc cat aaa tgt aac tat tgt	1288
His Leu Asn Leu His Ser Gly Asp Lys Pro His Lys Cys Asn Tyr Cys	
345 350 355	
gat atg gtt ttt gca cat aaa cca gtt ttg agg aaa cac ctt aaa cag	1336
Asp Met Val Phe Ala His Lys Pro Val Leu Arg Lys His Leu Lys Gln	
360 365 370 375	
ctg cat ggc aaa aac agc ttt gat aat gcc aat gag aga aat gta caa	1384
Leu His Gly Lys Asn Ser Phe Asp Asn Ala Asn Glu Arg Asn Val Gln	
380 385 390	
gac ctc aca gtg gat ttt gat tct ttt gca tgt aca aca gtc aca gac	1432
Asp Leu Thr Val Asp Phe Asp Ser Phe Ala Cys Thr Thr Val Thr Asp	
395 400 405	
tct aaa ggg tgt cag cca caa ccc gat gca aca cag gtc ctg gat gca	1480
Ser Lys Gly Cys Gln Pro Gln Pro Asp Ala Thr Gln Val Leu Asp Ala	
410 415 420	
ggg aaa ctg gcc caa gct gtc ctg aac tta aga aat gat agt act tgt	1528
Gly Lys Leu Ala Gln Ala Val Leu Asn Leu Arg Asn Asp Ser Thr Cys	
425 430 435	
gtg aat tga gtagggg cttcatgccc acaactcgaa ctgactgaca atgtggcaat	1584
Val Asn *	
440	

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agtcttagtc tttttaggag tgattttgct agtttgactt ctccaaagcc tctgtgtagg 1644
tggtagggag tgagtcaaag cactaataga ccaggcaact taccacttgg agtggatttg 1704
ccttactttt gccctctccc attttctggt ttgagttatt tatcttgtaa agtctgtttt 1764
cctttcccaa ggaataattc cttttgtcta cctaacattg acttatgtct tagactgaca 1824
ctgttttagg cttttcacta ggcacattcc gaaggtaaca acaagttaat aacatcaact 1884
aatctccact aatagaatgc tatgctaaga agaagtgaat aatctttctt aggtagaaaa 1944
taggctggat tttaaggggtg aatattggta ttgactggaa atgtgtgttg aattttggtt 2004
gaccaatgga tattcacact ccatgtcgga ttaagtaaac tgggggccat accattggta 2064
ctgtcctagg aagcgcgata taagaaaata tgccgaactg caacggaccc atacacagat 2124
tattgcacaa aacacacaca ttcaatggca catatcacga agacctatat agagcacctc 2184
gtgaacatat ctattgggag atcatagaga aagtaaaaaa gcgcgtaaac ataattataa 2244
acaacaaagc ggaggtatct gaatagacca gaggaagtag tatacttagg aatagtactg 2304
accaaggaga acacacaagt agagttgaac acatacagag agcagtagca cagaacaaca 2364
agacgatgta gtcgcttaac tttaactact agtctt 2400

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<210> 321
<211> 640
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (167)..(409)

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<400> 321
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gaggagacac ttggatgtag ctcaagtgct gcttaggcag tcctgatctc tcctctcgtc 120
tcttcccagg gagctgaaaa gccagattcg acctggtagc caagca atg tca cag 175
Met Ser Gln
1
cag aag cag caa tct tgg aag cct cca aat gtt ccc aaa tgc tcc cct 223
Gln Lys Gln Gln Ser Trp Lys Pro Pro Asn Val Pro Lys Cys Ser Pro
5 10 15
ccc caa aga tca aac ccc tgc cta gct ccc tac tcg act cct tgt ggt 271
Pro Gln Arg Ser Asn Pro Cys Leu Ala Pro Tyr Ser Thr Pro Cys Gly
20 25 30 35

```

gct ccc cat tca gaa ggt tgt cat tcc agt tcc caa agg cct gag gtt 319  
Ala Pro His Ser Glu Gly Cys His Ser Ser Gln Arg Pro Glu Val  
40 45 50

cag aag cct agg agg gct cgt caa aag ctg cgc tgc cta agt agg ggc 367  
Gln Lys Pro Arg Arg Ala Arg Gln Lys Leu Arg Cys Leu Ser Arg Gly  
55 60 65

aca acc tac cac tgc aaa gag gaa gag tgt gaa ggc gac tga gccaga 416  
Thr Thr Tyr His Cys Lys Glu Glu Glu Cys Glu Gly Asp \*  
70 75 80

agagttgagg cacaggtgca gttactctct cccctgcccc cctttgggta ctaattcccc 476

cttgaaagc caggccctca acctctcatt tggactgaga aacacttcct gatccccagc 536

tctagagaag cgagaactag gctgagccac gctgctactg ctctcttcca ttcacccctt 596

cagctcagca acaataaagc tgctttactt ggaaaaaaaa aaaa 640

<210> 322  
<211> 2906  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (162)..(2906)

<400> 322

ttttattccc gggtcgacga tttgtgcagc tgtcttttcc ggcccccgctg cactctcttt 60

ccgaggcgga gcccccggc tcgcggggat cgcccccgag cgctgcgtcc tgcgggtggg 120

tcacctaacc catttgtggc ttcctctacc tgtgctcagc c atg gcc agc gag 173  
Met Ala Ser Glu  
1

agc tca cct ctg ctg gcc tac cgg ctc ctg ggg gag gag ggg gtt gcc 221  
Ser Ser Pro Leu Leu Ala Tyr Arg Leu Leu Gly Glu Glu Gly Val Ala  
5 10 15 20

ctc cct gcc aat ggg gcc ggg ggt cct gga ggg gcg tct gcc cgg aag 269  
Leu Pro Ala Asn Gly Ala Gly Gly Pro Gly Gly Ala Ser Ala Arg Lys  
25 30 35

ctg tcc acc ttc ctg ggt gtg gtg gtg ccc act gtc ctg tcc atg ttc 317  
Leu Ser Thr Phe Leu Gly Val Val Val Pro Thr Val Leu Ser Met Phe  
40 45 50

agc ata gtt gtt ttt ctg agg att ggg ttc gtg gtg ggt cat gct ggg 365  
Ser Ile Val Val Phe Leu Arg Ile Gly Phe Val Val Gly His Ala Gly  
55 60 65

cta Leu	ctg Leu	cag Gln	gcc Ala	ctg Leu	gcc Ala	atg Met	ctg Leu	ctg Leu	gtt Val	gcc Ala	tac Tyr	ttc Phe	atc Ile	ctg Leu	gca Ala	413
70						75				80						
ctc Leu	acc Thr	gtc Val	ctc Leu	tct Ser	gtc Val	tgt Cys	gcc Ala	atc Ile	gcc Ala	acc Thr	aat Asn	gga Gly	gcc Ala	gtg Val	cag Gln	461
85				90						95				100		
ggg Gly	ggc Gly	gga Gly	gcc Ala	tac Tyr	ttc Phe	atg Met	atc Ile	agc Ser	cgc Arg	aca Thr	ctg Leu	ggg Gly	ccc Pro	gag Glu	gtc Val	509
				105						110				115		
ggg Gly	ggc Gly	agc Ser	att Ile	ggg Gly	ctc Leu	atg Met	ttc Phe	tac Tyr	ctg Leu	gct Ala	aac Asn	gtc Val	tgt Cys	ggc Gly	tgt Cys	557
		120						125				130				
gcc Ala	gtc Val	tcc Ser	ctc Leu	ctg Leu	ggg Gly	ctg Leu	gtg Val	gag Glu	tct Ser	gtg Val	ctt Leu	gat Asp	gtc Val	ttc Phe	ggg Gly	605
		135				140						145				
gcc Ala	gat Asp	gcc Ala	aca Thr	ggg Gly	ccc Pro	agt Ser	ggg Gly	ctc Leu	cgg Arg	gtc Val	ctg Leu	ccc Pro	cag Gln	ggc Gly	tac Tyr	653
150						155				160						
ggc Gly	tgg Trp	aac Asn	ctg Leu	ctg Leu	tat Tyr	ggc Gly	tcc Ser	ctg Leu	ctg Leu	ctg Leu	ggc Gly	ctt Leu	gtg Val	ggt Gly	ggg Gly	701
165				170						175				180		
gtc Val	tgc Cys	acc Thr	ctg Leu	gga Gly	gcc Ala	ggc Gly	ctc Leu	tat Tyr	gcc Ala	cgg Arg	gcc Ala	tca Ser	ttc Phe	ctc Leu	aca Thr	749
				185				190						195		
ttc Phe	ctg Leu	ctg Leu	gtc Val	tct Ser	ggc Gly	tcc Ser	ctg Leu	gcc Ala	tct Ser	gtg Val	ctc Leu	atc Ile	agt Ser	ttt Phe	gtg Val	797
		200						205				210				
gct Ala	gtg Val	ggg Gly	ccg Pro	agg Arg	gac Asp	atc Ile	cgc Arg	ttg Leu	act Thr	cct Pro	agg Arg	cct Pro	ggc Gly	ccc Pro	aat Asn	845
		215				220				225						
ggc Gly	tcc Ser	tcc Ser	ctg Leu	ccg Pro	ccc Pro	cgg Arg	ttt Phe	ggc Gly	cac His	ttc Phe	acc Thr	ggc Gly	ttc Phe	aac Asn	agc Ser	893
230						235				240						
agt Ser	acc Thr	ctg Leu	aag Lys	gac Asp	aac Asn	ttg Leu	ggc Gly	gct Ala	ggc Gly	tat Tyr	gct Ala	gag Glu	gac Asp	tac Tyr	acc Thr	941
245				250						255				260		
acg Thr	gga Gly	gcc Ala	gtg Val	atg Met	aat Asn	ttt Phe	gcc Ala	aac Asn	gtc Val	ttt Phe	gct Ala	gtc Val	ctc Leu	ttt Phe	aac Asn	989
				265				270						275		
ggc Gly	tgt Cys	aca Thr	ggc Gly	atc Ile	atg Met	gct Ala	ggg Gly	gcc Ala	aac Asn	atg Met	tca Ser	ggg Gly	gag Glu	ctg Leu	aag Lys	1037
		280				285						290				
gac	ccc	agc	cgg	gcg	atc	cct	ctg	ggc	acg	atc	gtc	gcc	gtc	gcc	tac	1085



520	525	530	
cag ctg ctg ctc ctg gtg ggg aac ccc cgg ggc gcc ctg cct ctg ctg Gln Leu Leu Leu Leu Val Gly Asn Pro Arg Gly Ala Leu Pro Leu Leu 535 540 545			1805
cgg ttg gcc aac cag ctt aag aag ggg ggg ctg tat gtg ctg ggc cac Arg Leu Ala Asn Gln Leu Lys Lys Gly Gly Leu Tyr Val Leu Gly His 550 555 560			1853
gtc acc ctg gga gac ctc gac tcc ctg ccc tcg gac cct gta cag ccg Val Thr Leu Gly Asp Leu Asp Ser Leu Pro Ser Asp Pro Val Gln Pro 565 570 575 580			1901
cag tat ggg gca tgg ctc agc ctg gtg gac cgt gcc cag gtg aag gct Gln Tyr Gly Ala Trp Leu Ser Leu Val Asp Arg Ala Gln Val Lys Ala 585 590 595			1949
ttt gtg gat cta acc ttc tca ccc tcc gtg cgc cag ggg gct cag cat Phe Val Asp Leu Thr Phe Ser Pro Ser Val Arg Gln Gly Ala Gln His 600 605 610			1997
ctg ctg cga atc tcc ggc ctc ggt ggc atg aag ccc aac acg ttg gtc Leu Leu Arg Ile Ser Gly Leu Gly Gly Met Lys Pro Asn Thr Leu Val 615 620 625			2045
cta ggt ttc tac gat gac gct cca ccg cag gac cat ttc ctg acg gac Leu Gly Phe Tyr Asp Asp Ala Pro Pro Gln Asp His Phe Leu Thr Asp 630 635 640			2093
ccg gct ttc tct gag cct gca gac agc acc agg gag ggc agt tcc cca Pro Ala Phe Ser Glu Pro Ala Asp Ser Thr Arg Glu Gly Ser Ser Pro 645 650 655 660			2141
gct ctg agc acc ctg ttc cct cct ccc cgg gct cct ggg agc ccc cgg Ala Leu Ser Thr Leu Phe Pro Pro Pro Arg Ala Pro Gly Ser Pro Arg 665 670 675			2189
gcc ctc aat ccc cag gac tat gtg gcc acg gtg gcc gac gcc ctc aag Ala Leu Asn Pro Gln Asp Tyr Val Ala Thr Val Ala Asp Ala Leu Lys 680 685 690			2237
atg aac aag aat gtg gtg ctg gcc cgg gcc agc ggg gcc ttg ccc cct Met Asn Lys Asn Val Val Leu Ala Arg Ala Ser Gly Ala Leu Pro Pro 695 700 705			2285
gag cgg ctg agc cgg ggg tct ggg ggc acc tct cag ttg cac cat gtg Glu Arg Leu Ser Arg Gly Ser Gly Gly Thr Ser Gln Leu His His Val 710 715 720			2333
gac gtg tgg ccc ctc aac ttg ttg cgg ccc cgg ggt ggg ccc ggc tat Asp Val Trp Pro Leu Asn Leu Leu Arg Pro Arg Gly Gly Pro Gly Tyr 725 730 735 740			2381
gtg gat gtc tgc ggc ctc ttc ctg ctg cag atg gca acc atc ttg ggc Val Asp Val Cys Gly Leu Phe Leu Leu Gln Met Ala Thr Ile Leu Gly 745 750 755			2429

atg gtg ccc gct tgg cat agc gcc cgg ctc cgg atc ttc ctg tgc ctg	2477
Met Val Pro Ala Trp His Ser Ala Arg Leu Arg Ile Phe Leu Cys Leu	
760 765 770	
ggg cct cgg gag gcg cct ggg gcg gcc gag ggg cgg ctg cgg gca ctg	2525
Gly Pro Arg Glu Ala Pro Gly Ala Ala Glu Gly Arg Leu Arg Ala Leu	
775 780 785	
ctg agc caa ctg agg atc cgg gct gag gtg cag gag gtg gtg tgg ggc	2573
Leu Ser Gln Leu Arg Ile Arg Ala Glu Val Gln Glu Val Val Trp Gly	
790 795 800	
gag ggg gcc ggg gct ggg gaa ccc gag gcg gag gag gaa ggg gac ttt	2621
Glu Gly Ala Gly Ala Gly Glu Pro Glu Ala Glu Glu Glu Gly Asp Phe	
805 810 815 820	
gtg aac agt ggg cgg gga gac gca gag gca gag gcc ctg gca cgc agc	2669
Val Asn Ser Gly Arg Gly Asp Ala Glu Ala Glu Ala Leu Ala Arg Ser	
825 830 835	
gcc aac gcc ctg gtt cgg gcc cag cag ggg cgc ggc aca gga gga ggg	2717
Ala Asn Ala Leu Val Arg Ala Gln Gln Gly Arg Gly Thr Gly Gly Gly	
840 845 850	
ccg ggt ggg ccg gag ggt ggg gat gct gag ggc ccc atc aca gcc ctc	2765
Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu Gly Pro Ile Thr Ala Leu	
855 860 865	
acc ttc ctg tac ttg cct cgg ccg cca gcc gat ccc gcc cga tac ccc	2813
Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala Asp Pro Ala Arg Tyr Pro	
870 875 880	
cgc tac ctg gcg cta ctg gag act cta acc cga gac ctg ggc ccc acg	2861
Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr Arg Asp Leu Gly Pro Thr	
885 890 895 900	
ctg ctg gtt cat ggg gtc act cca gtc acc tgc act gat ctg tga	2906
Leu Leu Val His Gly Val Thr Pro Val Thr Cys Thr Asp Leu *	
905 910 915	

<210> 323  
 <211> 607  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (78)..(416)

<400> 323

actagcgtgg ttccagtgtc gtcacgcgtg ctaaaaaagg gggtttcccg tgacaggccc 60





gat ttg ctg ata tta aca ata gat ttt aat ctc ttg tta ata ata tac	156
Asp Leu Leu Ile Leu Thr Ile Asp Phe Asn Leu Leu Leu Ile Ile Tyr	
15 20 25	
ctt gca aac tac ttt tct cag tct gtg gct tat ctt ttc att tct tta	204
Leu Ala Asn Tyr Phe Ser Gln Ser Val Ala Tyr Leu Phe Ile Ser Leu	
30 35 40	
tgg gtt ttc ttt ggc atg agg gta caa gtt tta ctt tta atg aag taa	252
Trp Val Phe Phe Gly Met Arg Val Gln Val Leu Leu Leu Met Lys *	
45 50 55 60	
aatatgtaac ttacattac agtttgtgct tatttgtatt acttatgaaa catttcctta	312
cccagaagtc atgaaggtat tctcctctat ttccttctag aagtttggct cttcagattt	372
ccaatgttcc tgaaattaac ttctatgtag ggtgaggtag caaccaatt ttattttctt	432
ccatataatc acttgaccta gcaaaatata attgcctatt ctttcccca tgatctacaa	492
tgccatattt agt	505

<210> 325  
 <211> 670  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (232) .. (624)

<400> 325	
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aggtcataac acatccagac tccttaagag aaagcctttc tgttttgga acttttcaaa	120
gccagggact tgtccagccc aacctcccca ttgctcctag ctccctgaggc tcaggacccc	180
tggcttctgt cctccctgct cagggctctg cagcgttgcc tctgctcagc c atg ctc	237
Met Leu	
1	
ctg ctg ctc gtc cca gtg ctc gag gtg att ttt act ctg gga gga acc	285
Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly Gly Thr	
5 10 15	
aga gcc cag tgc gtg acc cag ctt gac agc cac gtc tct gtc tct gaa	333
Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val Ser Glu	
20 25 30	
gga acc ccg gtg ctg ctg agg tgc aac tac tca tct tct tat tca cca	381
Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr Ser Pro	
35 40 45 50	

tct ctc ttc tgg tat gtg caa cac ccc aac aaa gga ctc cag ctt ctc	429
Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln Leu Leu	
55 60 65	
ctg aag tac aca tca gcg gcc acc ctg gtt aaa ggc atc aac ggt ttt	477
Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn Gly Phe	
70 75 80	
gag gct gaa ttt aag aag agt gaa acc tcc ttc cac ctg acg aaa ccc	525
Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr Lys Pro	
85 90 95	
tca gcc cat atg agc gac gcg gct gag tac ttc tgt gtt gtg agt gac	573
Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val Ser Asp	
100 105 110	
aca gtg ctt gag act gca gga gag ctg aac aca agc ctc ctg aga tgc	621
Thr Val Leu Glu Thr Ala Gly Glu Leu Asn Thr Ser Leu Leu Arg Cys	
115 120 125 130	
tga gactttctgt gactcaagaa ctcgaccttg aagtctgttt tataat	670
*	

<210> 326  
 <211> 794  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
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<400> 326	
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accacagtc tgtgtgactg ctgtgtgatt ggttttcaga cattagcttt aataggaatc	120
ataggagaag ggacatgggt gctactgcaa ggggtttttt tgtttaggga gaacgcactg	180
tggaactcaa attccgggt atg cac tca acc tcg gca aag gca cct cgc tgt	232
Met His Ser Thr Ser Ala Lys Ala Pro Arg Cys	
1 5 10	
tgg tca cac ccc gtg agt ttt tgt ggt tta cta att gtc ctc tct gga	280
Trp Ser His Pro Val Ser Phe Cys Gly Leu Leu Ile Val Leu Ser Gly	
15 20 25	



cag ctc aat aga gcc agc cag tat att tcc ctg ctc atc aga gac tcc	343
Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser	
85 90 95 100	
aag ctc agt gat tca gcc acc tac ctc tgt gtg gtg aac att cgc cca	391
Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Ile Arg Pro	
105 110 115	
gga aac aca cct ttg gga ctg gaa caa gac ttc agg tca cgc tcg ata	439
Gly Asn Thr Pro Leu Gly Leu Glu Gln Asp Phe Arg Ser Arg Ser Ile	
120 125 130	
tcc aga acc ctg acc ctg ccg tgt acc agc tga gagactct aaatccagt	490
Ser Arg Thr Leu Thr Leu Pro Cys Thr Ser *	
135 140	
acaatgctgt cgaccta	507

<210> 328  
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 <212> DNA  
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<220>  
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aggaagggcc atttccaaaa gccctgtgct gacacagggt tgctggttcc tcttcaagag	120
cccactctct ggggtggggc catatctcca gcagaggtgg gctggaaagg acccccccaa	180
tcccgccgc cgtgagctta gctggagcc atg gcc tct gca ccc atc tcg atg	233
Met Ala Ser Ala Pro Ile Ser Met	
1 5	
ctt gcg atg ctc ttc aca ttg agt ggg ctg aga gct cag tca gtg gct	281
Leu Ala Met Leu Phe Thr Leu Ser Gly Leu Arg Ala Gln Ser Val Ala	
10 15 20	
cag ccg gaa gat cag gtc aac gtt gct gaa ggg aat cct ctg act gtg	329
Gln Pro Glu Asp Gln Val Asn Val Ala Glu Gly Asn Pro Leu Thr Val	
25 30 35 40	
aaa tgc acc tat tca gtc tct gga aac cct tat ctt ttt tgg tat gtt	377
Lys Cys Thr Tyr Ser Val Ser Gly Asn Pro Tyr Leu Phe Trp Tyr Val	
45 50 55	
caa tac ccc aac cga ggc ctc cag ttc ctt ctg aaa tac atc aca ggg	425
Gln Tyr Pro Asn Arg Gly Leu Gln Phe Leu Leu Lys Tyr Ile Thr Gly	
60 65 70	

gat aac ctg gtt aaa ggc agc tat ggc ttt gaa gct gaa ttt aac aag	473
Asp Asn Leu Val Lys Gly Ser Tyr Gly Phe Glu Ala Glu Phe Asn Lys	
75 80 85	
agc caa acc tcc ttc cac ctg aag aaa cca tct gcc ctt gtg agc gac	521
Ser Gln Thr Ser Phe His Leu Lys Lys Pro Ser Ala Leu Val Ser Asp	
90 95 100	
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Ser Ala Leu Tyr Phe Cys Ala Val Arg Glu Val Ile Leu Thr Gly Gly	
105 110 115 120	
gga aac aaa ctc acc ttt ggg aca ggc act cag cta aaa gtg gaa ctc	617
Gly Asn Lys Leu Thr Phe Gly Thr Gly Thr Gln Leu Lys Val Glu Leu	
125 130 135	
aat atc cag aac cct gac cct gcc gtg tac cag ctg aga gac tct aaa	665
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys	
140 145 150	
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Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr	
155 160 165	
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Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr	
170 175 180	
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Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala	
185 190 195 200	
tgg agc aac aaa tct gac ttt gca tgt gca aac gcc ttc aac aac agc	857
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser	
205 210 215	
att att cca gaa gac acc ttc ttc ccc agc cca gaa agt tcc tgt gat	905
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp	
220 225 230	
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Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe	
235 240 245	
caa aac ctg tca gtg att ggg ttc cga atc ctc ctc ctg aaa gtg gcc	1001
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala	
250 255 260	
ggg ttt aat ctg ctc atg acg ctg cgg ctg tgg tcc agc tga	1043
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser *	
265 270 275	

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ggt cca gtg aat gct ggt ggt gtc act cag acc cca aaa ttc cgc atc	96
Gly Pro Val Asn Ala Gly Gly Val Thr Gln Thr Pro Lys Phe Arg Ile	
20 25 30	
ctg aag ata gga cag agc atg aca ctg cag tgt gcc cag gat atg aac	144
Leu Lys Ile Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn	
35 40 45	
cat aac tac atg tac tgg tat cga caa gac cca ggc atg ggg ctg aag	192
His Asn Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys	
50 55 60	
ctg att tat tat tca gtt ggt gct ggt atc act gac aaa gga gaa gtc	240
Leu Ile Tyr Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val	
65 70 75 80	
ccg aat ggc tac aac gtc tcc aga tca acc aca gag gat ttc ccg ctc	288
Pro Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu	
85 90 95	
agg ctg gag ttg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc	336
Arg Leu Glu Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala	
100 105 110	
agc agt agg ggt ggg gcc ggg ctc aat gag cag ttc ttc ggg cca ggg	384
Ser Ser Arg Gly Gly Ala Gly Leu Asn Glu Gln Phe Phe Gly Pro Gly	
115 120 125	
aca cgg ctc acc gtg cta gag gac ctg aaa aac gtg ttc cca ccc gag	432
Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu	
130 135 140	
gtc gct gtg ttt gag cca tca gaa gca gag atc tcc cac acc caa aag	480
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys	
145 150 155 160	
gcc aca ctg gta tgc ctg gcc aca ggc ttc tac ccc gac cac gtg gag	528
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu	
165 170 175	
ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt ggg gtc agc aca	576
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr	
180 185 190	

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gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat gac tcc aga tac      624
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
      195                      200                      205

tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc tgg cag aac ccc      672
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
      210                      215                      220

cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg ctc tcg gag aat      720
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
      225                      230                      235                      240

gac gag tgg acc cag gat agg gcc aaa cct gtc acc cag atc gtc agc      768
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
      245                      250                      255

gcc gag gcc tgg ggt aga gca ggt gag tgg ggc ctg ggg aga tgc ctg      816
Ala Glu Ala Trp Gly Arg Ala Gly Glu Trp Gly Leu Gly Arg Cys Leu
      260                      265                      270

gag gag att agg tga gaccagctac cagggaaaat ggaaagatcc aggtagcggg      871
Glu Glu Ile Arg *
      275

caagactata tccagaagaa agccagagtg gacaagggtgg gatgatcaag gttcacaggg      931

tcagcaaagc acggtgtgca cttccccac caagaagcat atagggtgaa tggagcacct      991

caagctcatt cttccttcag atcctgacac cttagagcta agctttt      1037

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ggcgaaaccc cttctctttt tcttttttta aaatttttta gttagaaatg aaaaaaagaa      180

agaagtctag gttttctgaa acaagcactg tcttggtgct accttttttc atgtgtggac      240

acatagaaag cgaggatatt tgtacagcac cttgaaacaa ataagcagga ggtgatgtc      299
atg agc ctt agc cct gca ggg acc aga cta ggc ctt ctg aag ctg agg      347
Met Ser Leu Ser Pro Ala Gly Thr Arg Leu Gly Leu Leu Lys Leu Arg
      1              5              10              15

tgg tcc ttg tcc cca cac ctt gta acc cat ttc cag ccc atg ggt gtc      395

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Trp	Ser	Leu	Ser	Pro	His	Leu	Val	Thr	His	Phe	Gln	Pro	Met	Gly	Val		
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agt	tgg	gaa	att	cta	cac	aag	atc	cta	gta	gat	gta	att	aca	tat	aat		443
Ser	Trp	Glu	Ile	Leu	His	Lys	Ile	Leu	Val	Asp	Val	Ile	Thr	Tyr	Asn		
		35					40					45					
tca	atg	gtt	ttt	gat	gat	ggg	gtt	tta	aaa	tca	agt	tat	tca	ata	ggg		491
Ser	Met	Val	Phe	Asp	Asp	Gly	Val	Leu	Lys	Ser	Ser	Tyr	Ser	Ile	Gly		
		50				55					60						
ggg	gtg	cag	tgg	ctc	acg	cct	gta	att	cca	gca	ctt	tgg	gag	gcc	gag		539
Gly	Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu		
		65			70				75					80			
gag	ggc	aga	tca	caa	ggg	cgg	gag	ttc	aag	acc	agc	ctg	acc	aac	atg		587
Glu	Gly	Arg	Ser	Gln	Gly	Arg	Glu	Phe	Lys	Thr	Ser	Leu	Thr	Asn	Met		
			85				90					95					
gta	aaa	ctc	cgt	ctc	tac	taa	aa	attcaaaaaat	tagccggccg	tggtggtgga							640
Val	Lys	Leu	Arg	Leu	Tyr	*											
			100														
catctgtaat	cccagctact	tagggggctg	aggcaggaga	atcgcttgaa	cggggggcagg												700
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tgtgacccgc	atacctaccg	gccccgaccc	cgaaccgcgt	ggcgtccgcc	cgagccctgg												180
cgtctgtggg	tctctgtctg	ctgccgtgc	tcgcagagcc	caggaaactc	tgccccgcagc												240
tt	atg	acg	gtc	att	aac	cag	ttt	ctg	acc	aag	gac	aag	gac	acc	tac		287
	Met	Thr	Val	Ile	Asn	Gln	Phe	Leu	Thr	Lys	Asp	Lys	Asp	Thr	Tyr		
	1				5				10					15			



atg gac act gtc aac aga tac cac ctc acg gag ccg gaa aga aac aca 335  
Met Asp Thr Val Asn Arg Tyr His Leu Thr Glu Pro Glu Arg Asn Thr  
20 25 30

tcc tct aaa ctc aag gac tgc gtg acc gac aca atg acc ccc gag gag 383  
Ser Ser Lys Leu Lys Asp Cys Val Thr Asp Thr Met Thr Pro Glu Glu  
35 40 45

aca gag gcc gtc gtg cag caa ctg gaa gaa atc aac aac cag tgt gcc 431  
Thr Glu Ala Val Val Gln Gln Leu Glu Glu Ile Asn Asn Gln Cys Ala  
50 55 60

gac acg ata ctg aag taa caccat ccataggcac ctcggttcc tgtccaggct 485  
Asp Thr Ile Leu Lys \*  
65

gcctgtccca accatgagaa tctgggcca gggccccacc ctccctagct cccgccctgc 545

tgctgcctct actctctctc ctgctgtgct gattggggca agcctgggaa cggctgcccc 605

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ccaaaaaaaaa aaaa 679

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aagggccaca agatgaccaa gaacatgagc aagcccaggc acagctgccg ccgcgggcgc 180

ctgaccaaac accaaattc atg tgg gac atg atc cga gag gtg tgt ggt ttc 232  
Met Trp Asp Met Ile Arg Glu Val Cys Gly Phe  
1 5 10

gcc ccg tat gag cgg cac gcc atg gtg tta ctc aag gtc tcc aag gac 280  
Ala Pro Tyr Glu Arg His Ala Met Val Leu Leu Lys Val Ser Lys Asp  
15 20 25

aaa cgg gcc ctc aag ttc atc aag aaa aga gtg ggg aca cac atc cgc 328  
Lys Arg Ala Leu Lys Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg  
30 35 40

act aag agg agg cag gag gag ctg agc aat gtc cca gcc atc atg agg 376  
Thr Lys Arg Arg Gln Glu Glu Leu Ser Asn Val Pro Ala Ile Met Arg

45	50	55	
aaa gct gat gcc aag aaa gac tga gccccctgtc ctgccctctc tctgaaataa			430
Lys Ala Asp Ala Lys Lys Asp *			
60	65		

agaacacctt gacag	445
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aatgtcctgg ctgacctaa ggacgacaga agattgggga agagggggta tcaggaagaa	180
atgggtttca gttcagttta acaaacatct attgtgtgtt cactggggcca ggccagtgtt	240
aggtgctagg gagacagagg tgaagagcct gccctctagc agctgacagc ctggcaaaaa	300
aataagacag aataaggtag accctgattt tggaacctga agaccaaagt gcaagattag	360
ctctgtact tccatctgtg gaccattggg caggtatctc tgggccttca cttactcttt	420
gtgaaatgag gacaggggca atccctaccc taccaagtca ttgggagtga agacatgatg	480
acacggtgat tgtgaaaaga ttttgtcaat cgcaccagca ttaaggggtgc ccatctccag	540
gttccccag gcctcaaggc tccaaggcc tgagtgggca ggtagcacc aggtatagac	600
cttcacgtg cagcaccag gacacagcca gc atg aac tgg gca ttt ctg cag	653
	Met Asn Trp Ala Phe Leu Gln
	1 5
ggc ctg ctg agt ggc gtg aac aag tac tcc aca gtg ctg agc cgc atc	701
Gly Leu Leu Ser Gly Val Asn Lys Tyr Ser Thr Val Leu Ser Arg Ile	
10 15 20	
tgg ctg tct gtg gtg ttc atc ttt cgt gtg ctg gtg tac gtg gtg gca	749
Trp Leu Ser Val Val Phe Ile Phe Arg Val Leu Val Tyr Val Val Ala	
25 30 35	
gcg gag gag gtg tgg gac gat gag cag aag gac ttt gtc tgc aac acc	797
Ala Glu Glu Val Trp Asp Asp Glu Gln Lys Asp Phe Val Cys Asn Thr	
40 45 50 55	

aag cag ccc ggc tgc ccc aac gtc tgc tat gac gag ttc ttc ccc gtg	845
Lys Gln Pro Gly Cys Pro Asn Val Cys Tyr Asp Glu Phe Phe Pro Val	
60 65 70	
tcc cac gtg cgc ctc tgg gcc cta cag ctc atc ctg gtc acg tgc ccc	893
Ser His Val Arg Leu Trp Ala Leu Gln Leu Ile Leu Val Thr Cys Pro	
75 80 85	
tca ctg ctc gtg gtc atg cac gtg gcc tac cgc gag gaa cgc gag cgc	941
Ser Leu Leu Val Val Met His Val Ala Tyr Arg Glu Glu Arg Glu Arg	
90 95 100	
aag cac cac ctg aaa cac ggg ccc aat gcc ccg tcc ctg tac gac aac	989
Lys His His Leu Lys His Gly Pro Asn Ala Pro Ser Leu Tyr Asp Asn	
105 110 115	
ctg agc aag aag cgg ggc gga ctg tgg tgg acg tac ttg ctg agc ctc	1037
Leu Ser Lys Lys Arg Gly Gly Leu Trp Trp Thr Tyr Leu Leu Ser Leu	
120 125 130 135	
atc ttc aag gcc gcc gtg gat gct ggc ttc ctc tat atc ttc cac cgc	1085
Ile Phe Lys Ala Val Asp Ala Gly Phe Leu Tyr Ile Phe His Arg	
140 145 150	
ctc tac aag gat tat gac atg ccc cgc gtg gtg gcc tgc tcc gtg gag	1133
Leu Tyr Lys Asp Tyr Asp Met Pro Arg Val Val Ala Cys Ser Val Glu	
155 160 165	
cct tgc ccc cac act gtg gac tgt tac atc tcc cgg ccc acg gag aag	1181
Pro Cys Pro His Thr Val Asp Cys Tyr Ile Ser Arg Pro Thr Glu Lys	
170 175 180	
aag gtc ttc acc tac ttc atg gtg acc aca gct gcc atc tgc atc ctg	1229
Lys Val Phe Thr Tyr Phe Met Val Thr Thr Ala Ala Ile Cys Ile Leu	
185 190 195	
ctc aac ctc agt gaa gtc ttc tac ctg gtg ggc aag agg tgc atg gag	1277
Leu Asn Leu Ser Glu Val Phe Tyr Leu Val Gly Lys Arg Cys Met Glu	
200 205 210 215	
atc ttc ggc ccc agg cac cgg cgg cct cgg tgc cgg gaa tgc cta ccc	1325
Ile Phe Gly Pro Arg His Arg Arg Pro Arg Cys Arg Glu Cys Leu Pro	
220 225 230	
gat acg tgc cca cca tat gtc ctc tcc cag gga ggg cac cct gag gat	1373
Asp Thr Cys Pro Pro Tyr Val Leu Ser Gln Gly Gly His Pro Glu Asp	
235 240 245	
ggg aac tct gtc cta atg aag gct ggg tcg gcc cca gtg gat gca ggt	1421
Gly Asn Ser Val Leu Met Lys Ala Gly Ser Ala Pro Val Asp Ala Gly	
250 255 260	
ggg tat cca taa cct gcgagatcag cagataagat caacaggtcc cccccacatg	1476
Gly Tyr Pro *	
265	
aggccacca ggaaaaaagg caggggcagt ggcaccccttg ccgtagcagg gtggtgagga	1536

gggtggctgt gggggctcag gaagctcgcc caggggccaa tgtgggaggt tgggggtagt 1596  
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 Ala Leu Arg Ser Cys Ser Val Pro Thr Gly Pro Ala Thr Thr Phe Cys  
 5 10 15 20  
 tca ttt gat aaa agc tgc cgc tgt gga gtc tgc cta ccc agc acc tgc 151  
 Ser Phe Asp Lys Ser Cys Arg Cys Gly Val Cys Leu Pro Ser Thr Cys  
 25 30 35  
 cca cat gag atc agc ctc ctt cag ccc atc tgc tgt gac acc tgc ccc 199  
 Pro His Glu Ile Ser Leu Leu Gln Pro Ile Cys Cys Asp Thr Cys Pro  
 40 45 50  
 cca ccc tgc tgc aag cct gat acc tat gtg cca act tgc tgg ctg ctc 247  
 Pro Pro Cys Cys Lys Pro Asp Thr Tyr Val Pro Thr Cys Trp Leu Leu  
 55 60 65  
 aac aac tgt cac ccg act ccc gga ctg agt ggg atc aac ctg acc acc 295  
 Asn Asn Cys His Pro Thr Pro Gly Leu Ser Gly Ile Asn Leu Thr Thr  
 70 75 80  
 tat gtt cag cct ggc tgt gag agt ccc tgt gag ccc cgc tgt taa cca 343  
 Tyr Val Gln Pro Gly Cys Glu Ser Pro Cys Glu Pro Arg Cys \*  
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Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr Gly Phe
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gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg gcc gac      148
Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu Ala Asp
                  30                      35                      40

cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga ggc atc      196
Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly Gly Ile
                  45                      50                      55

ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc acg gtg      244
Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe Thr Val
                  60                      65                      70

cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct gac aag      292
Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala Asp Lys
                  75                      80                      85                      90

att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc tac aga      340
Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly Tyr Arg
                  95                      100                      105

ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc aat atc      388
Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser Asn Ile
                  110                      115                      120

acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac ccc gtg      436
Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp Pro Val
                  125                      130                      135

ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc ttg ggg      484
Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu Leu Gly
                  140                      145                      150

tcc cct ggc ctg cag ctg ttc aac gtc cac cca tgg ctc ggg gcc ctg      532
Ser Pro Gly Leu Gln Leu Phe Asn Val His Pro Trp Leu Gly Ala Leu
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175 180 185	
att ctg agg acc ctc ctg gag gcg cgg agg ccc cac gtg tgc ccg ggg	628
Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys Pro Gly	
190 195 200	
gac ccc gtg tgc agc tat gtg gac gcc ctg atc cag cag gga cag ggg	676
Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly Gln Gly	
205 210 215	
gat gac ccc gag ggc ctg ttt gct gag gcc aac gcg gtg gcc tgc acc	724
Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala Cys Thr	
220 225 230	
ctg gac atg gtc atg gcc ggg acg gag acg acc tcg gcc acg ctg cag	772
Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr Leu Gln	
235 240 245 250	
tgg gcc gca ctt ctg atg ggc cgg cac ccg gac gtg cag ggc cgg gtg	820
Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly Arg Val	
255 260 265	
cag gag gag cta gac cgc gtg ctg ggc cct ggg cgg act ccc cgg ctg	868
Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro Arg Leu	
270 275 280	
gag gac cag cag gct ctg ccc tac aca agc gcc gtg ctc cac gag gtg	916
Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His Glu Val	
285 290 295	
cag cgg ttc atc acg ctc ctg cgg cac gtg ccc cgc tgc acc gcg gcc	964
Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr Ala Ala	
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gac aca cag ctg ggc ggc ttc ctg ctc ccc aag ggc acg ccc gtg att	1012
Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro Val Ile	
315 320 325 330	
ccc ctg ctg acc tcg gtg ctc ctg gat gag aca cag tgg cag acc cca	1060
Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln Thr Pro	
335 340 345	
ggc cag ttc aac ccc ggc cat ttc ctg gac gcg aat ggg cac ttt gtg	1108
Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His Phe Val	
350 355 360	
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Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Gln Gln Pro Ser Gly	
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Pro Gly Trp Gly Gly Thr Ser Arg Ala Pro Gly Val Gly Arg Pro Gln	
380 385 390	
ctc cgc ctg ccg cct ctg cac cca cct cct gat ctc agg ttc tga agg	1252

Leu Arg Leu Pro Pro Leu His Pro Pro Pro Asp Leu Arg Phe \*  
 395 400 405

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Met Phe Thr  
1

ttg tcg ttt aaa aaa caa tca aac gac att agc agt ttt aca aca ttt 163  
Leu Ser Phe Lys Lys Gln Ser Asn Asp Ile Ser Ser Phe Thr Thr Phe  
5 10 15

tcc ttt cca gtt aaa act gta tac cgt tac cat ttt ccc atc ata ctc 211  
Ser Phe Pro Val Lys Thr Val Tyr Arg Tyr His Phe Pro Ile Ile Leu  
20 25 30 35

ttc acc tac gat act gtt tta agt ggc tgt ata gat ttc cac ttt cac 259  
Phe Thr Tyr Asp Thr Val Leu Ser Gly Cys Ile Asp Phe His Phe His  
40 45 50

aac aga att agc aga ttc cca aaa ctt gaa tat tta att tta aaa aaa 307  
Asn Arg Ile Ser Arg Phe Pro Lys Leu Glu Tyr Leu Ile Leu Lys Lys  
55 60 65

att ctt aat aac tga tattaaattt atatacgcaa atctgacaca ttacttcctt 362  
Ile Leu Asn Asn \*  
70

aggataaatt cctgtacgca cagtctttcc attttaagcc tattatacta tgaaggagtc 422

tgaatcaaca tctaagagct ccgagagttc aacaccagcc tgggccatat tgtgagaaca 482

cgtctctaca gacgatcaaa aaattagctt ggtgtggtgg cgcgcgcttg tgatctcagc 542

taccaggag gctgaggtgg gaggatcact taagcccggg aggtcgaggc tgctgtgagc 602

cgtgagccac tgatcatacc actgcactcc agtctgggca acagagcgat cctgtttcag 662

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Met Glu Tyr  
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aag ggc tac ctg gta tct gta gat ggc tat atg aac atg cag ctt gca 584  
Lys Gly Tyr Leu Val Ser Val Asp Gly Tyr Met Asn Met Gln Leu Ala  
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Asp Thr Glu Phe Ile Asn Glu Ala Leu Pro Gly His Leu Gly Glu Val  
20 25 30 35  
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Ser Ile Arg Cys Asn Asn Val Leu Tyr Ile Arg Asp Val Glu Glu Glu  
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Met Asn Thr Gln Ser Thr Pro Ser  
1 5  
aat aat gtt cat acc tca tta agc cat gtt cag aat gga gca cct ttt 158

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cca	gca	gct	ttt	cca	aag	gac	aat	atc	cat	ttc	aag	cct	ata	aat	aca	206
Pro	Ala	Ala	Phe	Pro	Lys	Asp	Asn	Ile	His	Phe	Lys	Pro	Ile	Asn	Thr	
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aat	ctt	gat	agg	gca	aat	gaa	ttg	gca	aaa	aca	gac	att	ttg	agt	cta	254
Asn	Leu	Asp	Arg	Ala	Asn	Glu	Leu	Ala	Lys	Thr	Asp	Ile	Leu	Ser	Leu	
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aca	agt	caa	aac	aag	acc	ttt	gat	ccc	aag	aaa	gaa	aat	ccc	att	gtg	302
Thr	Ser	Gln	Asn	Lys	Thr	Phe	Asp	Pro	Lys	Lys	Glu	Asn	Pro	Ile	Val	
		60					65					70				
tta	ctt	agt	gac	ttt	tac	tat	gga	cag	cat	aaa	gga	gaa	ggg	cag	ccg	350
Leu	Leu	Ser	Asp	Phe	Tyr	Tyr	Gly	Gln	His	Lys	Gly	Glu	Gly	Gln	Pro	
	75					80					85					
gaa	cag	aag	act	cac	acc	acc	ttt	aaa	tgc	ctc	agc	tgc	gtg	aaa	gtt	398
Glu	Gln	Lys	Thr	His	Thr	Thr	Phe	Lys	Cys	Leu	Ser	Cys	Val	Lys	Val	
90				95						100				105		
cta	aaa	aat	gtt	aag	ttt	atg	aat	cac	gtg	aag	cat	cat	ttg	gaa	ttt	446
Leu	Lys	Asn	Val	Lys	Phe	Met	Asn	His	Val	Lys	His	His	Leu	Glu	Phe	
				110					115					120		
gag	aag	cag	agg	aac	gac	agc	tgg	gaa	aac	cac	acc	acc	tgc	cag	cac	494
Glu	Lys	Gln	Arg	Asn	Asp	Ser	Trp	Glu	Asn	His	Thr	Thr	Cys	Gln	His	
			125					130					135			
tgc	cac	cgg	agt	ctt	ccc	act	ccc	ttc	cag	cta	cag	tgt	cac	atc	gaa	542
Cys	His	Arg	Ser	Leu	Pro	Thr	Pro	Phe	Gln	Leu	Gln	Cys	His	Ile	Glu	
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Asn	Val	His	Thr	Ala	Gln	Glu	Pro	Ser	Thr	Val	Cys	Lys	Ile	Cys	Glu	
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Leu	Ser	Phe	Glu	Thr	Asp	Gln	Val	Leu	Leu	Gln	His	Met	Lys	Asp	His	
170					175					180					185	
cat	aag	cct	ggc	gaa	atg	ccc	tat	gtg	tgc	cag	gtt	tgc	cat	tat	aga	686
His	Lys	Pro	Gly	Glu	Met	Pro	Tyr	Val	Cys	Gln	Val	Cys	His	Tyr	Arg	
			190						195					200		
tcg	tcg	gtc	ttt	gct	gat	gta	gaa	aca	cat	ttt	aga	acg	tgc	cat	gaa	734
Ser	Ser	Val	Phe	Ala	Asp	Val	Glu	Thr	His	Phe	Arg	Thr	Cys	His	Glu	
			205					210					215			
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Asn	Thr	Lys	Asn	Leu	Leu	Cys	Pro	Phe	Cys	Leu	Lys	Ile	Phe	Lys	Thr	
		220					225					230				
gca	aca	cca	tac	atg	tgt	cat	tat	agg	ggc	cac	tgg	gga	aag	agt	gca	830
Ala	Thr	Pro	Tyr	Met	Cys	His	Tyr	Arg	Gly	His	Trp	Gly	Lys	Ser	Ala	

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His Gln Cys Ser Lys Cys Arg Leu Gln Phe Leu Thr Phe Lys Glu Lys			
250	255	260	265
atg gag cac aag acc cag tgt cat caa atg ttt aag aag cct aag caa			926
Met Glu His Lys Thr Gln Cys His Gln Met Phe Lys Lys Pro Lys Gln			
	270	275	280
cta gaa gga tta cct cct gaa aca aaa gtt act att caa gtg tca ctg			974
Leu Glu Gly Leu Pro Pro Glu Thr Lys Val Thr Ile Gln Val Ser Leu			
	285	290	295
gaa cct ctt cag cca gga tca gtg gat gta gca tcc ata act gtg agc			1022
Glu Pro Leu Gln Pro Gly Ser Val Asp Val Ala Ser Ile Thr Val Ser			
	300	305	310
aca tct gac tct gaa cca tca ctc ccc agg tct aaa agc aaa att tca			1070
Thr Ser Asp Ser Glu Pro Ser Leu Pro Arg Ser Lys Ser Lys Ile Ser			
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Lys Lys Ser His *			
330			
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		atg cct tct	114
		Met Pro Ser	
		1	
gca tcc tgt gat aca cta ctg gat gac atc gaa gat atc gtg tct cag			162
Ala Ser Cys Asp Thr Leu Leu Asp Asp Ile Glu Asp Ile Val Ser Gln			
5	10	15	
gaa gat tca aaa cca caa gat agg cat ttt gta aga aag gat gtt gtc			210
Glu Asp Ser Lys Pro Gln Asp Arg His Phe Val Arg Lys Asp Val Val			

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ccg aag gta cga agg cga aat acc caa aaa tat ttg caa gag gaa gaa				258
Pro Lys Val Arg Arg Arg Asn Thr Gln Lys Tyr Leu Gln Glu Glu	40	45	50	
aac agt cca cca agt gac agc act att cca ggc ata cag aaa att tgg				306
Asn Ser Pro Pro Ser Asp Ser Thr Ile Pro Gly Ile Gln Lys Ile Trp	55	60	65	
ata cga aca tgg ggt tgt tct cat aat aat tca gat gga gaa tat atg				354
Ile Arg Thr Trp Gly Cys Ser His Asn Asn Ser Asp Gly Glu Tyr Met	70	75	80	
gct gga cag cta gct gct tat ggc tat aaa att aca gaa aat gca tcc				402
Ala Gly Gln Leu Ala Ala Tyr Gly Tyr Lys Ile Thr Glu Asn Ala Ser	85	90	95	
gat gca gat tta tgg ctc ctg aac agt tgc act gta aaa aac cca gct				450
Asp Ala Asp Leu Trp Leu Leu Asn Ser Cys Thr Val Lys Asn Pro Ala	100	105	110	115
gaa gac cac ttt aga aac tca att aaa aaa gct caa gag gag aac aag				498
Glu Asp His Phe Arg Asn Ser Ile Lys Lys Ala Gln Glu Glu Asn Lys	120	125	130	
aaa atc gta ctg gct gga tgc gtt cct caa gcc cag cct cgc cag gac				546
Lys Ile Val Leu Ala Gly Cys Val Pro Gln Ala Gln Pro Arg Gln Asp	135	140	145	
tac ctt aag gga ctg agt atc att ggg gtt cag cag ata gat cgt gtg				594
Tyr Leu Lys Gly Leu Ser Ile Ile Gly Val Gln Gln Ile Asp Arg Val	150	155	160	
gta gaa gtt gtg gag gag aca att aaa ggt cac tct gtg aga ctg ctg				642
Val Glu Val Val Glu Glu Thr Ile Lys Gly His Ser Val Arg Leu Leu	165	170	175	
ggg cag aaa aag gat aat gga agg cgg ctt ggg gga gca cga ttg gat				690
Gly Gln Lys Lys Asp Asn Gly Arg Arg Leu Gly Gly Ala Arg Leu Asp	180	185	190	195
ttg ccg aag att agg aag aat cca ctg ata gaa atc att tcc atc aat				738
Leu Pro Lys Ile Arg Lys Asn Pro Leu Ile Glu Ile Ile Ser Ile Asn	200	205	210	
acc ggg tgt ctc aat gct tgt acc tac tgc aaa act aaa cac gcc aga				786
Thr Gly Cys Leu Asn Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg	215	220	225	
gga aat ttg gcc agt tat cca att gat gaa cta gta gat aga gcc aaa				834
Gly Asn Leu Ala Ser Tyr Pro Ile Asp Glu Leu Val Asp Arg Ala Lys	230	235	240	
caa tct ttt caa gag ggt gtt tgt gag ata tgg ttg acc agt gaa gac				882
Gln Ser Phe Gln Glu Gly Val Cys Glu Ile Trp Leu Thr Ser Glu Asp	245	250	255	

acg ggg gct tat ggc aga gat att ggc acc aat ctc ccc aca ctc ctg	930
Thr Gly Ala Tyr Gly Arg Asp Ile Gly Thr Asn Leu Pro Thr Leu Leu	
260 265 270 275	
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Trp Lys Leu Val Glu Val Ile Pro Glu Gly Ala Met Leu Arg Leu Gly	
280 285 290	
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Met Thr Asn Pro Pro Tyr Ile Leu Glu His Leu Glu Glu Met Ala Lys	
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Ile Leu Asn His Pro Arg Val Tyr Ala Phe Leu His Ile Pro Val Gln	
310 315 320	
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Gln Asp Phe Gln Glu Thr Val Lys Leu Val Glu Glu Tyr Lys Phe Pro	
375 380 385	
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Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly Thr Pro Ala Ala	
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Lys Met Glu Gln Val Pro Ala Gln Val Lys Lys Gln Arg Thr Lys Asp	
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Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr Asp His Lys Ile Gly	
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Tyr Val Ala His Asn Gln Phe Tyr Glu Gln Val Leu Val Pro Lys Asn	
455 460 465	
cct gcg ttc atg ggg aag atg gtt gaa gtg gac atc tat gaa tca ggc	1554
Pro Ala Phe Met Gly Lys Met Val Glu Val Asp Ile Tyr Glu Ser Gly	
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aaa cat ttt atg aaa ggg cag cca gta tct gat gcc aaa gtg tac acg	1602
Lys His Phe Met Lys Gly Gln Pro Val Ser Asp Ala Lys Val Tyr Thr	
485 490 495	
ccc tcc atc agc aaa ccg cta gca aag gga gaa gtc tca ggt ttg aca	1650
Pro Ser Ile Ser Lys Pro Leu Ala Lys Gly Glu Val Ser Gly Leu Thr	
500 505 510 515	
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Lys Asp Phe Arg Asn Gly Leu Gly Asn Gln Leu Ser Ser Gly Ser His	
520 525 530	
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Thr Ser Ala Ala Ser Gln Cys Asp Ser Ala Ser Ser Arg Met Val Leu	
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Pro Met Pro Arg Leu His Gln Asp Cys Ala Leu Arg Met Ser Val Gly	
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• • •

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cac ctc ctg cag ttc ctc tcg tgc ctg gag aat ggg ctg ctc cca cat His Leu Leu Gln Phe Leu Ser Cys Leu Glu Asn Gly Leu Leu Pro His 175 180 185	816
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aga tgg gac act act ctc ccc acg cca agc ccg aag gag cag ccc ccc Arg Trp Asp Thr Thr Leu Pro Thr Pro Ser Pro Lys Glu Gln Pro Pro 290 295 300	1152
agt aat gtc tgg gat ctc ccc gtc ccc agg ggc tgg gtg cca gcc acc Ser Asn Val Trp Asp Leu Pro Val Pro Arg Gly Trp Val Pro Ala Thr 305 310 315	1200
tct gcc atg ttg tca att gag ttc tgg tcc caa ggg aga tgg agg cag Ser Ala Met Leu Ser Ile Glu Phe Trp Ser Gln Gly Arg Trp Arg Gln 320 325 330	1248
gaa ggg aga tgg agg cag agg gat tga tgccc tcctgctgtc cagcctccac Glu Gly Arg Trp Arg Gln Arg Asp *	1300
t	1301

<210> 341  
<211> 723  
<212> DNA



<213> Homo sapiens

<220>

<221> CDS

<222> (101)..(637)

<400> 341

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tttcgtgtca tcgcggctta tcgttacaag acttggctgc caaattacca aactgggtga      60
aaggagcgtc acacgattaa gtatcgtgtc acataatagg  atg aca aag ttt tta      115
                                         Met Thr Lys Phe Leu
                                         1           5

att gtt tca gat aca cat ggt gat cgt gag atc att gct gat att ttt      163
Ile Val Ser Asp Thr His Gly Asp Arg Glu Ile Ile Ala Asp Ile Phe
                        10                        15                        20

gac aaa tgg cgg gat agc gtt gcc ggc att ttt tac aat ggg gat tct      211
Asp Lys Trp Arg Asp Ser Val Ala Gly Ile Phe Tyr Asn Gly Asp Ser
                        25                        30                        35

gaa tta gcg gct gat gac aca gta ttt gat ggc gta tcc act gtg att      259
Glu Leu Ala Ala Asp Asp Thr Val Phe Asp Gly Val Ser Thr Val Ile
                        40                        45                        50

ggc aat atg gat gat gat cct gat ttc gtg gcc gca agg gcg aca acg      307
Gly Asn Met Asp Asp Asp Pro Asp Phe Val Ala Ala Arg Ala Thr Thr
                        55                        60                        65

att gat ggg att act ttt ttc caa acg cac gga cat ctc tat gac gcg      355
Ile Asp Gly Ile Thr Phe Phe Gln Thr His Gly His Leu Tyr Asp Ala
                        70                        75                        80                        85

acc caa ttt aac gct tgg gcg aac cta aaa tta atg gcc gtg gca gca      403
Thr Gln Phe Asn Ala Trp Ala Asn Leu Lys Leu Met Ala Val Ala Ala
                        90                        95                        100

cag gaa gct aac gca cag gtc gcc ctc ttt ggg cat acc cat ctg gaa      451
Gln Glu Ala Asn Ala Gln Val Ala Leu Phe Gly His Thr His Leu Glu
                        105                        110                        115

ggg gcg gtt gtg ttt gat gat atc ttg ttt att aat cca ggt tca atc      499
Gly Ala Val Val Phe Asp Asp Ile Leu Phe Ile Asn Pro Gly Ser Ile
                        120                        125                        130

cgg ctg cct aaa ggg cca cat gcc aac tta ggt ggt act tat gct gtg      547
Arg Leu Pro Lys Gly Pro His Ala Asn Leu Gly Gly Thr Tyr Ala Val
                        135                        140                        145

ttg gat gtg acg gag acg agc tat gac gtg aga ttt tat aat cgt cag      595
Leu Asp Val Thr Glu Thr Ser Tyr Asp Val Arg Phe Tyr Asn Arg Gln
                        150                        155                        160                        165

cat caa cca ttg cca caa ctc acg gta cag gtc gca cgt taa gtgaccc      644
His Gln Pro Leu Pro Gln Leu Thr Val Gln Val Ala Arg *
                        170                        175
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gtactgattt gcaggcaata aatgtggtaa aatggtagtt atggcaaatg aaaaacacca 704  
caatttaatc aatggtatg 723

<210> 342  
<211> 637  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (364)..(543)

<400> 342  
tgcgaggggtg gaatgggata aagcgcaaaa agccctggca ctggcgagc gtctggtcag 60  
tggcgctgcc ctcgatcact ctgcccctct gggtgccctgt cacctcatta gtgcagttac 120  
tcctgggacc aagaccagga aatctaacca ataagcaatg gtaacagtga ctcagtgtc 180  
agtccgccct cagtggcccg agtccgaggt gggcatcatg gcaccagttt acatctcgga 240  
aagggaggct cagagaggtc aagtcacttg cctaagggtca cccagggact gcttagctgg 300  
ctaggatgag aaccagcctg ctccaacgcc ccctcgtgga acagttgcga gcctaggaat 360  
taa atg ttc cct ccc cca ggc tat gcc aat gag gtg ggc gag gct ttc 408  
Met Phe Pro Pro Pro Gly Tyr Ala Asn Glu Val Gly Glu Ala Phe  
1 5 10 15  
cgc tct ctt gtg cca gcg gcg gtg gtg tgg ctg agc tat ggc gtg gcc 456  
Arg Ser Leu Val Pro Ala Ala Val Val Trp Leu Ser Tyr Gly Val Ala  
20 25 30  
agc tcc tac gtg ctg gcg gat gcc att gac aaa ggc aag aag gct gga 504  
Ser Ser Tyr Val Leu Ala Asp Ala Ile Asp Lys Gly Lys Lys Ala Gly  
35 40 45  
gag gtg agt gtt agc cta ttt tcc aac ccc caa ccc tag ctctcctctt 553  
Glu Val Ser Val Ser Leu Phe Ser Asn Pro Gln Pro \*  
50 55 60  
gtgtggctca gtccacagcc tggcatgtga taaagtcctt gtgggacact ccagtcctta 613  
caacttgcct agtgcagtcc ataa 637

<210> 343  
<211> 998  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> CDS  
 <222> (7)..(399)

<400> 343

aagaag	atg agt ttt aac aga ctc ctt tct gta aaa ctg aat gat gga	48
	Met Ser Phe Asn Arg Leu Leu Ser Val Lys Leu Asn Asp Gly	
	1 5 10	
aag ttc atg cct att ctg ggg ttt ggc acc tct gtt gct agg aag gtt	96	
Lys Phe Met Pro Ile Leu Gly Phe Gly Thr Ser Val Ala Arg Lys Val		
15 20 25 30		
gct atg agt aat gta gaa gaa gcc gtc cag gta gca att gat gta ggc	144	
Ala Met Ser Asn Val Glu Glu Ala Val Gln Val Ala Ile Asp Val Gly		
35 40 45		
tac cgc cat att gac tca gct tat aca cac ctg aat gaa gaa ggc atc	192	
Tyr Arg His Ile Asp Ser Ala Tyr Thr His Leu Asn Glu Glu Gly Ile		
50 55 60		
ggg cag gcc atc cga aag aag att gcc aac ggc act gtg aag aga aaa	240	
Gly Gln Ala Ile Arg Lys Lys Ile Ala Asn Gly Thr Val Lys Arg Lys		
65 70 75		
gat ata ttc tat acc aca aag gtg tgg ggc acc ttt tcc cgc cca gaa	288	
Asp Ile Phe Tyr Thr Thr Lys Val Trp Gly Thr Phe Ser Arg Pro Glu		
80 85 90		
ttg gtc caa aga ggc ctt gaa atg tca ctg aag aaa ctt cag ctg agc	336	
Leu Val Gln Arg Gly Leu Glu Met Ser Leu Lys Lys Leu Gln Leu Ser		
95 100 105 110		
tac atg gat ctt tac ctt ttt cat ttc cca gta cct ttg cag cct ggg	384	
Tyr Met Asp Leu Tyr Leu Phe His Phe Pro Val Pro Leu Gln Pro Gly		
115 120 125		
agg agc ttt tgc tga cggatgcaca gggaaagatc atgtttgaca cagtgggtct	439	
Arg Ser Phe Cys *		
130		
ctgcagcaca tgggagagtt ttactcctgt tgccaaggct ggagtacagt ggcacgatct	499	
cggctcactg caacctccgc ctcccagggt caagcatgta cctctgcctc ccacatagct	559	
gggaatacag gtggaatata acccttacct caaccaaagc aaactcctgg agtactgtaa	619	
gtccaaggac attgtcatga ctgcatattc tgccttgggg tctgactcag acaaagactg	679	
gtaatcatct tcataaagtt attttgttta ttttttttag gtgggggtct cattctgtca	739	
tccaggctgg agtgcagggg cacaatcaca gcttgttgca ggcttgacct tccaggctca	799	
agtcaggatc ttcctccta gacctcctaa gtagctggga ctacaggagt gcaccaccat	859	
gcctggctaa ttgtttatct tcatttttgt agagacaggg tctcactacg ttaccaagc	919	

cagtcttgaa ttcttgggct caagtgatcc tcccaccttg gcctcccaaa gtgctgggat 979  
tagaggtgta agccacggt 998

<210> 344  
<211> 478  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (188)..(376)

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actgctgctg tggagctcag catcaagtac ttccaggaga agcttcagca ggacctagag 180  
gcagagc atg gta gag gta gag gat aca gcc ctc ata cca ccg tgc tgt 229  
Met Val Glu Val Glu Asp Thr Ala Leu Ile Pro Pro Cys Cys  
1 5 10  
atg tcc atc ttt caa gtc ctg gtg gtg ccc gca gag ttt gaa ggg aag 277  
Met Ser Ile Phe Gln Val Leu Val Val Pro Ala Glu Phe Glu Gly Lys  
15 20 25 30  
cca ctg ctt cag aga tac cag gtg gta aat gca tgc cta gtg gaa gtg 325  
Pro Leu Leu Gln Arg Tyr Gln Val Val Asn Ala Cys Leu Val Glu Val  
35 40 45  
tgc tcc tct gca tct atg cct ttg agc aga aag cct ttg agt ccc aat 373  
Cys Ser Ser Ala Ser Met Pro Leu Ser Arg Lys Pro Leu Ser Pro Asn  
50 55 60  
tag tggg cccatgagtg gccaaaatga gggactggga cctgtatagc cgttaaacta 430  
\*

taaatcaggg ccaaaaagga aagataaatt ataagtttaa agaaaatg 478

<210> 345  
<211> 459  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (201)..(368)

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<400> 345
cagtagtcta atctgagttc tctggataat gacttcctgt cattaattat caacatgact      60
tttatacaaaa ttaagaaatc tatgggcgtg tgctcttggg ctgctctctg gccagcaccc      120
tctcctgtgt cacctctctt gtgtccacag tctaaccat ctcttcattt ccctcaacct      180
caggtggagc ctccacaaaa      atg cag att ttt cca aaa atc ctt aca ggg      230
                        Met Gln Ile Phe Pro Lys Ile Leu Thr Gly
                        1              5              10

acg atc atc acc cta gag gtt gaa ccc ttg gat aca aca gaa aaa tgt      278
Thr Ile Ile Thr Leu Glu Val Glu Pro Leu Asp Thr Thr Glu Lys Cys
                        15              20              25

aaa ggc caa tat cag gat aag gaa cga att cct cct gat cag caa aga      326
Lys Gly Gln Tyr Gln Asp Lys Glu Arg Ile Pro Pro Asp Gln Gln Arg
                        30              35              40

caa gtg act gga agc tgg caa gta act gga aga tgg aca taa cttctc      375
Gln Val Thr Gly Ser Trp Gln Val Thr Gly Arg Trp Thr  *
                        45              50              55

tgactacaac attcaaaagg aatttactct ttttatgttg tgttgagact tcatggtagt      435
gctaaaacta ggaagaaatc ttac      459

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<210> 346
<211> 1867
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)..(1835)

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<400> 346
atctgcag atg tta aca tac ctt aac att agc cga aat ctt tta tca aca      50
      Met Leu Thr Tyr Leu Asn Ile Ser Arg Asn Leu Leu Ser Thr
      1              5              10

ttg cca aaa tac cta ttt gat ctt ccc ctt aaa gtt ttg gtc gtc agt      98
Leu Pro Lys Tyr Leu Phe Asp Leu Pro Leu Lys Val Leu Val Val Ser
      15              20              25              30

aat aat aaa ctg gta tcc att cca gaa gaa att ggg aag tta aaa gat      146
Asn Asn Lys Leu Val Ser Ile Pro Glu Glu Ile Gly Lys Leu Lys Asp
      35              40              45

tta atg gaa ttg gat att agc tgc aat gag att caa gtc ctt ccc caa      194
Leu Met Glu Leu Asp Ile Ser Cys Asn Glu Ile Gln Val Leu Pro Gln
      50              55              60

caa atg gga aaa tta cat tca ctt aga gag cta aat ata aga aga aat      242

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Gln Met Gly Lys Leu His Ser Leu Arg Glu Leu Asn Ile Arg Arg Asn	
65 70 75	
aat ctt cat gtt ttg cca gat gaa tta gga gac ctt ccc tta gtc aag	290
Asn Leu His Val Leu Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Lys	
80 85 90	
ctg gat ttc tct tgt aat aaa gtg acc gaa att cca gtt tgt tac aga	338
Leu Asp Phe Ser Cys Asn Lys Val Thr Glu Ile Pro Val Cys Tyr Arg	
95 100 105 110	
aag ctg cat cat tta caa gta ata att ttg gat aac aat cca ttg caa	386
Lys Leu His His Leu Gln Val Ile Ile Leu Asp Asn Asn Pro Leu Gln	
115 120 125	
gta cca cca gca cag ata tgt tta aag ggt aag gtg cac ata ttt aag	434
Val Pro Pro Ala Gln Ile Cys Leu Lys Gly Lys Val His Ile Phe Lys	
130 135 140	
tac tta aat att caa gca tgt tgc aga atg gat aag aaa cca gat tcc	482
Tyr Leu Asn Ile Gln Ala Cys Cys Arg Met Asp Lys Lys Pro Asp Ser	
145 150 155	
ctg gat ctt cca tca ttg agt aaa cga atg ccc tca cag cct ctc aca	530
Leu Asp Leu Pro Ser Leu Ser Lys Arg Met Pro Ser Gln Pro Leu Thr	
160 165 170	
gac agt atg gaa gat ttt tat cca aat aaa aat cat ggc cct gac tct	578
Asp Ser Met Glu Asp Phe Tyr Pro Asn Lys Asn His Gly Pro Asp Ser	
175 180 185 190	
gga att gga agt gat aat gga gag aaa cga tta tcc aca aca gaa cca	626
Gly Ile Gly Ser Asp Asn Gly Glu Lys Arg Leu Ser Thr Thr Glu Pro	
195 200 205	
tca gat gat gac aca gtc agc ctt cat tct caa gtc tca gaa tca aat	674
Ser Asp Asp Asp Thr Val Ser Leu His Ser Gln Val Ser Glu Ser Asn	
210 215 220	
aga gag cag aca tca aga aat gac agt cac ata ata gga agt aag act	722
Arg Glu Gln Thr Ser Arg Asn Asp Ser His Ile Ile Gly Ser Lys Thr	
225 230 235	
gat tct cag aaa gac cag gag gta tat gat ttt gtt gac ccc aac aca	770
Asp Ser Gln Lys Asp Gln Glu Val Tyr Asp Phe Val Asp Pro Asn Thr	
240 245 250	
gaa gat gta gca gtt cct gaa cag gga aat gca cat att gga tca ttt	818
Glu Asp Val Ala Val Pro Glu Gln Gly Asn Ala His Ile Gly Ser Phe	
255 260 265 270	
gta tca ttc ttt aag gga aaa gaa aaa tgt tct gaa aaa tct cgg aaa	866
Val Ser Phe Phe Lys Gly Lys Glu Lys Cys Ser Glu Lys Ser Arg Lys	
275 280 285	
aat gaa gaa tta gga gat gaa aaa aga ctt gag aaa gaa cag tta ctg	914
Asn Glu Glu Leu Gly Asp Glu Lys Arg Leu Glu Lys Glu Gln Leu Leu	

290	295	300	
gca gag gaa gag gat gat gat ttg aag gaa gta act gat ttg agg aaa			962
Ala Glu Glu Glu Asp Asp Asp Leu Lys Glu Val Thr Asp Leu Arg Lys			
305	310	315	
ata gct gct cag tta ttg cag caa gaa cag aag aac agg att ctt aat			1010
Ile Ala Ala Gln Leu Leu Gln Gln Glu Gln Lys Asn Arg Ile Leu Asn			
320	325	330	
cat tca act tct gtg atg aga aac aag cca aaa caa act gtg gaa tgt			1058
His Ser Thr Ser Val Met Arg Asn Lys Pro Lys Gln Thr Val Glu Cys			
335	340	345	350
gaa aag agt gtc tca gca gat gaa gtt aat tca cca tta tca ccc ctc			1106
Glu Lys Ser Val Ser Ala Asp Glu Val Asn Ser Pro Leu Ser Pro Leu			
355	360	365	
acc tgg cag ccc tta gaa aat cag aag gat caa ata gat gaa caa ccg			1154
Thr Trp Gln Pro Leu Glu Asn Gln Lys Asp Gln Ile Asp Glu Gln Pro			
370	375	380	
tgg cca gaa tct cac cct ata atc tgg cag agt gaa gaa agg agg cgg			1202
Trp Pro Glu Ser His Pro Ile Ile Trp Gln Ser Glu Glu Arg Arg Arg			
385	390	395	
agc aaa cag att aga aaa gaa tat ttc aag tat aaa tca atg agg aag			1250
Ser Lys Gln Ile Arg Lys Glu Tyr Phe Lys Tyr Lys Ser Met Arg Lys			
400	405	410	
agt tca agt ggc aat gaa aat gat gag caa gac agt gat aat gct aat			1298
Ser Ser Ser Gly Asn Glu Asn Asp Glu Gln Asp Ser Asp Asn Ala Asn			
415	420	425	430
atg tca aca caa tct cca gta tca tct gag gaa tat gac aga act gat			1346
Met Ser Thr Gln Ser Pro Val Ser Ser Glu Glu Tyr Asp Arg Thr Asp			
435	440	445	
ggt ttt tca cac agt ccc ttt ggc ttg aag cct aga tca gct ttt agc			1394
Gly Phe Ser His Ser Pro Phe Gly Leu Lys Pro Arg Ser Ala Phe Ser			
450	455	460	
cgc tca tct cgc caa gaa tat ggg gca gca gat cca gga ttt aca atg			1442
Arg Ser Ser Arg Gln Glu Tyr Gly Ala Ala Asp Pro Gly Phe Thr Met			
465	470	475	
aga aga aag atg gaa cat tta cgg gaa gag cga gag caa ata cga caa			1490
Arg Arg Lys Met Glu His Leu Arg Glu Glu Arg Glu Gln Ile Arg Gln			
480	485	490	
ctt cgc aac aat ctt gaa tcc agg tta aaa gta att ttg cct gat gac			1538
Leu Arg Asn Asn Leu Glu Ser Arg Leu Lys Val Ile Leu Pro Asp Asp			
495	500	505	510
att gga gct gca ctg atg gat ggg gtt gtt ctt tgc cat tta gcc aat			1586
Ile Gly Ala Ala Leu Met Asp Gly Val Val Leu Cys His Leu Ala Asn			
515	520	525	

cat ata agg cca cgt tct gtt gct agt att cat gta cca tca cca gca	1634
His Ile Arg Pro Arg Ser Val Ala Ser Ile His Val Pro Ser Pro Ala	
530 535 540	
gtg ccc aaa ctg agc atg gca aaa tgt cga aga aat gta gaa aat ttt	1682
Val Pro Lys Leu Ser Met Ala Lys Cys Arg Arg Asn Val Glu Asn Phe	
545 550 555	
ctt gat gct tgt aaa aag ttg ggt gtc tca cag gaa aga ctt tgt ttg	1730
Leu Asp Ala Cys Lys Lys Leu Gly Val Ser Gln Glu Arg Leu Cys Leu	
560 565 570	
cct cat cat att ttg gaa gaa cga gga ctt gtg aaa gtt ggt gtc aca	1778
Pro His His Ile Leu Glu Glu Arg Gly Leu Val Lys Val Gly Val Thr	
575 580 585 590	
gtt cag gcg ctc ctt gaa tta cca aca acc aag gca tct cag ctt tct	1826
Val Gln Ala Leu Leu Glu Leu Pro Thr Thr Lys Ala Ser Gln Leu Ser	
595 600 605	
gtg gct taa tataacattt taaaattcta aaaaaaaaaa aa	1867
Val Ala *	

<210> 347  
 <211> 527  
 <212> DNA  
 <213> Homo sapiens  
  
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 <221> CDS  
 <222> (133)..(336)

<400> 347	
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tacataactc ttttatctgc agttttgggg gagtccaatt ccaccatttt ttatgtctgt	120
tactgtcatt ca atg tgg att gct tcc tta tgt ttc att att ttg gat	168
Met Trp Ile Ala Ser Leu Cys Phe Ile Ile Leu Asp	
1 5 10	
tgt gag ctc atc ttt tgt agg gtg tta gct aca gaa atc cta tgc tgc	216
Cys Glu Leu Ile Phe Cys Arg Val Leu Ala Thr Glu Ile Leu Cys Cys	
15 20 25	
agg gtt gag att tgt ccc tat ttg ctt ctg tat tac tgc cta agg acc	264
Arg Val Glu Ile Cys Pro Tyr Leu Leu Leu Tyr Tyr Cys Leu Arg Thr	
30 35 40	
aac ttt gct cat tta aaa tat att tat ata agc tca aag att aaa gct	312
Asn Phe Ala His Leu Lys Tyr Ile Tyr Ile Ser Ser Lys Ile Lys Ala	



45	50	55	60	
gac tgt ggg gag gtc tat ggc taa aaattttcaa gggagatttc ttccccctaa				366
Asp Cys Gly Glu Val Tyr Gly *				
65				
tctggctaag atgggcagat toccattgtc ttcctgtgcc agtgtgcaga tatcatctag				426
tatactcttt cactgcaagc atggctcttc gagggctctg gctctatgac gaagtcttca				486
gttccaaatc ttcattctgt gccagcctaa cgcctttgtt t				527

<210> 348  
 <211> 2112  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (410)..(868)

<400> 348

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gcaaattcac tgcctcctcc catgcacgtg gtagagagta ccagtatcaa catggccctg	120
ttttctgcta aaaccagatt ttgaggaatc agagaccccc aacactactc actcagtagc	180
tagcagcccc ttcctttcaa ctgggagtgt tattagaatg aaaagtaatt agttagaagg	240
gcatacatct cagtggcatg agcattgtgg aatatccttt cctaggcaca tttgtccact	300
aagggaacag cctcagaaac tgggtacagca atgggtgaga tgagatcctg gagagagaac	360
acagccatcc cctatagaaa ggcacagctt ttgggcttct ctggcctga	415
	atg cct Met Pro 1
tct ggg gta ttt cca tat gca aca gcc cag agt cat agc ctt ggg caa	463
Ser Gly Val Phe Pro Tyr Ala Thr Ala Gln Ser His Ser Leu Gly Gln	
5 10 15	
cca cac ata gag gtt tcc ttc tca ctt cag aca cat aca tca ctt tca	511
Pro His Ile Glu Val Ser Phe Ser Leu Gln Thr His Thr Ser Leu Ser	
20 25 30	
cac cac ttg ggg atg gaa ata cct aca aga gtg aag gtc aag ggc cct	559
His His Leu Gly Met Glu Ile Pro Thr Arg Val Lys Val Lys Gly Pro	
35 40 45 50	
ccc cag gca tct cat tca tta ctc agc ttc ctt cct gac caa gtc tgc	607
Pro Gln Ala Ser His Ser Leu Leu Ser Phe Leu Pro Asp Gln Val Cys	
55 60 65	

caa cca atg gcc agc tat gcg cct cat cct cat tgc ttc tgc ctc cac	655
Gln Pro Met Ala Ser Tyr Ala Pro His Pro His Cys Phe Cys Leu His	
70 75 80	
gta aat gaa acc aaa ggc ctc agc ata tcc tgg gag gac tgg ggg ctg	703
Val Asn Glu Thr Lys Gly Leu Ser Ile Ser Trp Glu Asp Trp Gly Leu	
85 90 95	
tta cct aat ggt cct ctc tgt ccc att ata ggt gca agg cac ccc atc	751
Leu Pro Asn Gly Pro Leu Cys Pro Ile Ile Gly Ala Arg His Pro Ile	
100 105 110	
cac aca ttt gca cca cta ctc caa gat agt att ttt ctt ttc aca caa	799
His Thr Phe Ala Pro Leu Leu Gln Asp Ser Ile Phe Leu Phe Thr Gln	
115 120 125 130	
tct ctt tac agc aga atc cag agt tgg gtt gta gtt tac ctt cct gga	847
Ser Leu Tyr Ser Arg Ile Gln Ser Trp Val Val Val Tyr Leu Pro Gly	
135 140 145	
aag ctc att atc ttt gtt tga at taacatttca gcatggaact aactgggcgg	900
Lys Leu Ile Ile Phe Val *	
150	
aggaaggatc gttatacgtc ttcagaaagt tctcattgcc ccagctgcct agtactatac	960
aagaagctct actttgatgg cagatctaag aaggctatag gcctttgttt gtaggaagca	1020
gtgtcattac attcaagctt cacttctctg attggcttcc aacctgagg attcaaagag	1080
aatccaaggt tctgcctatg tctgatgaca taaggaaaac ttggcttcct ctgctcaagg	1140
ttcccctctg ctcatccctc ctcatcaga catcctccac cataccagtg tttagaagca	1200
aaacatgaag ggctagcgcc accaggatag ttagcagaaa tattgtctgt aaagctaggc	1260
aggtgagccc agaagaatgg tcccagagaa agcagactgg ctccaataga tatcaggcag	1320
caatcccaat aaattctgac atgtccttgg caatggaagc ctgggttgga gatcctgagg	1380
cagctgtgcc tactgttccc cacctcagaa gcttcctgcc cagagagcca gcagccttgg	1440
gatactaatag aggatgcaac tggcttattg gtatgaaata gaaggtggct ttgtaggggc	1500
aagcaggcaa agagtactat ccacatggca ggcagggtgc tttgtgtctg gaaagctttg	1560
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gcaactctgc ctctgttccc ttgcattctg tttgggtgcc ctttagtttc ctagtaaattg	1680
ctccttttga aaaactccaa ccttgtctta tttaacttgg gggaagggga ttctccaatg	1740
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aggaaacatt ctgatcagac cttgggaaaa gctggtgccg agagagggag aggccagggtg	1860
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gagacctgcc cttgatgtgt gttgctgctg aagcaccctc ccagccagtg agttggacat 1980  
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Gln Ala Val Gln Ala Val His Leu Glu Ser Asp Ala Phe Leu Val Cys  
15 20 25  
ctc aac cac gct ctg agc aca gag aag gag gaa gta atg ggg ctg tgc 147  
Leu Asn His Ala Leu Ser Thr Glu Lys Glu Glu Val Met Gly Leu Cys  
30 35 40  
ata ggg gag ttg aac gat gat aca agg agt gac tcc aaa ttt gca tat 195  
Ile Gly Glu Leu Asn Asp Asp Thr Arg Ser Asp Ser Lys Phe Ala Tyr  
45 50 55  
act gga act gaa atg cgc aca gtt gct gaa aag gtt gat gcc gtc aga 243  
Thr Gly Thr Glu Met Arg Thr Val Ala Glu Lys Val Asp Ala Val Arg  
60 65 70 75  
att gtt cac att cat tct gtc atc atc tta cga cgt tct gat aag agg 291  
Ile Val His Ile His Ser Val Ile Ile Leu Arg Arg Ser Asp Lys Arg  
80 85 90  
aag gac cga gta gaa att tct cca gag cag ctg tct gca gct tca aca 339  
Lys Asp Arg Val Glu Ile Ser Pro Glu Gln Leu Ser Ala Ala Ser Thr  
95 100 105  
gag gca gag agg ttg gct gaa ctg aca ggc cgc ccc atg aga gtt gtg 387  
Glu Ala Glu Arg Leu Ala Glu Leu Thr Gly Arg Pro Met Arg Val Val

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ggc tgg tat cat tcc cat cct cat ata act gtt tgg cct tca cat gtt			435
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Asp Val Arg Thr Gln Ala Met Tyr Gln Met Met Asp Gln Gly Phe Val			
140	145	150	155
gga ctt att ttt tcc tgt ttc ata gaa gat aag aac acg aag act ggc			531
Gly Leu Ile Phe Ser Cys Phe Ile Glu Asp Lys Asn Thr Lys Thr Gly			
	160	165	170
cgg gta ctc tac act tgc ttc caa tcc ata cag gcc caa aag agt tca			579
Arg Val Leu Tyr Thr Cys Phe Gln Ser Ile Gln Ala Gln Lys Ser Ser			
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Glu Ser Leu His Gly Pro Arg Asp Phe Trp Ser Ser Ser Gln His Ile			
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	205	210	215
cca atc cat att gta cct cat gtc act atc tgg aaa gtg tgc ctt gaa			723
Pro Ile His Ile Val Pro His Val Thr Ile Trp Lys Val Cys Leu Glu			
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Ser Ala Val Glu Leu Pro Lys Ile Leu Cys Gln Glu Glu Gln Asp Ala			
	240	245	250
tat agg agg atc cac agc ctt aca cat ctg gac tca gta acc aag atc			819
Tyr Arg Arg Ile His Ser Leu Thr His Leu Asp Ser Val Thr Lys Ile			
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cat aat ggc tca gtg ttt acc aag aat ctg tgc agt cag atg tcg gca			867
His Asn Gly Ser Val Phe Thr Lys Asn Leu Cys Ser Gln Met Ser Ala			
	270	275	280
gtc agc ggg cct ctc cta cag tgg ttg gag gac aga ctg gag caa aac			915
Val Ser Gly Pro Leu Leu Gln Trp Leu Glu Asp Arg Leu Glu Gln Asn			
	285	290	295
caa cag cat ttg cag gaa tta caa caa gaa aag gaa gag ctt atg caa			963
Gln Gln His Leu Gln Glu Leu Gln Gln Glu Lys Glu Glu Leu Met Gln			
	300	305	310
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Glu Leu Ser Ser Leu Glu *			
	320		
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tttacctgac ttcaagactt actataaagc tatagtaatc aagatagatg gtattggcag			1136

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 tctgagccga tgtaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct 172  
 Met Phe Ala Pro Ala Val Met Arg Ala  
 1 5  
 ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg atg gat 220  
 Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Met Asp  
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 cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct tta gag tcg 268  
 Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser  
 30 35 40  
 gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg aag aat att 316  
 Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile  
 45 50 55  
 cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa gga aga aat 364  
 Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn  
 60 65 70  
 cca gaa agc ctt aag act aag aca act tga c tctgctgatt ctttttttcct 415  
 Pro Glu Ser Leu Lys Thr Lys Thr Thr \*  
 75 80  
 tttttttttt ttaaaaaaaaa aa 437

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<400> 351

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Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10          15          20          25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc      147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
          30          35          40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg      195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
          45          50          55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac      243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
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agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc      291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
          75          80          85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat      339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
          90          95          100          105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct      387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
          110          115          120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt      435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
          125          130          135

ccc aat aag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg      483
Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly
          140          145          150

act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag      531
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys
          155          160          165

gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc      579
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu
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ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac	675
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His	
205 210 215	
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg	723
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val	
220 225 230	
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta	771
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val	
235 240 245	
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc	819
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro	
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tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc	867
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro	
270 275 280	
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga	915
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly	
285 290 295	
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc	963
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser	
300 305 310	
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act	1011
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr	
315 320 325	
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg	1059
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu	
330 335 340 345	
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc	1107
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile	
350 355 360	
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Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
365 370 375	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1203
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
380 385 390	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1253
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
395 400 405	

gatcccatcc atcagctccc tttttttttt cccttgaact gttctggcct cagaccaact 1313  
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Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn  
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30 35 40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg 195  
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg  
45 50 55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac 243  
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp  
60 65 70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc 291  
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val  
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ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat 339  
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn  
90 95 100 105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct 387  
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro  
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ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt 435  
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val  
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ccc aat aag gta gtg gaa gaa agc agg aga agt aga aaa cgg ccc tgt 483  
Pro Asn Lys Val Val Glu Glu Ser Arg Arg Ser Arg Lys Arg Pro Cys



140	145	150	
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act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys 170 175 180 185			579
gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu 190 195 200			627
ttc aca ctg cag tgc gag cta atg gtg acc cca gcc cgg gga gga gat Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp 205 210 215			675
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His 220 225 230			723
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val 235 240 245			771
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val 250 255 260 265			819
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro 270 275 280			867
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro 285 290 295			915
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly 300 305 310			963
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser 315 320 325			1011
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr 330 335 340 345			1059
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu 350 355 360			1107
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ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa	1203
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
380 385 390	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1251
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395 400 405	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1301
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
410 415 420	
gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact	1361
ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca	1421
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Val Val Ala Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly	
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Pro Tyr Phe Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu	
30 35 40 45	
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Tyr Phe Asn Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr	
50 55 60	
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Gly Gly Thr Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala	
65 70 75	
ccc gag tcc tac gta caa tgt cac gct ccc acc agc agc gcc tat gag	288
Pro Glu Ser Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu	
80 85 90	
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Phe Val Thr Trp Leu Asp Gly Ile Lys Phe Met Gly Gly Gly Gly Glu	
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Ser Cys Ser Leu Ile Ala Glu Gly Leu Ser Thr Ala Leu Gln Leu Phe	
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Asp Asp Phe Lys Lys Met Arg Glu Gln Ile Gly Gln Thr His Arg Val	
130 135 140	
tgc ctc ctc atc tgc aac tca ccc cca tac ttg ttg cct gct gtt gag	480
Cys Leu Leu Ile Cys Asn Ser Pro Pro Tyr Leu Leu Pro Ala Val Glu	
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Ser Thr Thr Tyr Ser Gly Cys Thr Thr Glu Asn Leu Val Gln Pro Asp	
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Trp Gly Ser Gly Gly Ser Thr Ser Pro Leu Val Ser Pro Arg Lys Leu	
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ggaaggaaga gaggtagaca gatacaag atg aaa tcc tgt caa aaa atg gaa	172
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gga aaa cca gaa aat gag agt gaa cca aag cat gag gaa gag cca aag	220
Gly Lys Pro Glu Asn Glu Ser Glu Pro Lys His Glu Glu Glu Pro Lys	
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cct gag gaa aag cca gaa gag gag gag aag cta gag gag gag gcc aaa	268
Pro Glu Glu Lys Pro Glu Glu Glu Glu Lys Leu Glu Glu Glu Ala Lys	
25 30 35 40	
gca aaa gga act ttt aga gaa agg ctg att caa tct ctc cag gag ttt	316
Ala Lys Gly Thr Phe Arg Glu Arg Leu Ile Gln Ser Leu Gln Glu Phe	
45 50 55	
aaa gaa gat ata cac aac agg cat tta agc aat gaa gat atg ttt aga	364
Lys Glu Asp Ile His Asn Arg His Leu Ser Asn Glu Asp Met Phe Arg	
60 65 70	
gaa gtg gat gaa ata gat gag ata agg aga gtc aga aac aaa ctt ata	412
Glu Val Asp Glu Ile Asp Glu Ile Arg Arg Val Arg Asn Lys Leu Ile	
75 80 85	
gtg atg cgt tgg aag gta acg aac cct cct acc cca ttt aaa tta gag	460
Val Met Arg Trp Lys Val Thr Asn Pro Pro Thr Pro Phe Lys Leu Glu	
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105 110 115	

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Met Met Gly Leu Thr Glu	
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ggg gtg ttc ctg att ctg tct ggc act cag ttc aca ctg gga att ctg	160
Gly Val Phe Leu Ile Leu Ser Gly Thr Gln Phe Thr Leu Gly Ile Leu	
10 15 20	
gtc aat tgt ttc att gag ttg gtc aat ggt agc agc tgg ttc aag acc	208
Val Asn Cys Phe Ile Glu Leu Val Asn Gly Ser Ser Trp Phe Lys Thr	
25 30 35	

aag aga atg tct ttg tct gac ttc atc atc acc acc ctg gca ctc ttg	256
Lys Arg Met Ser Leu Ser Asp Phe Ile Ile Thr Thr Leu Ala Leu Leu	
40 45 50	
agg atc att ctg ctg tgt att atc ttg act gat agt ttt tta ata gaa	304
Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr Asp Ser Phe Leu Ile Glu	
55 60 65 70	
ttc tct ccc aac aca cat gat tca ggg ata ata atg caa att att gat	352
Phe Ser Pro Asn Thr His Asp Ser Gly Ile Ile Met Gln Ile Ile Asp	
75 80 85	
gtt tcc tgg aca ttt aca aac cat ctg agc att tgg ctt gcc acc tgt	400
Val Ser Trp Thr Phe Thr Asn His Leu Ser Ile Trp Leu Ala Thr Cys	
90 95 100	
ctt ggt gtc ctc tac tgc ctg aaa atc gcc agt ttc tct cac ccc aca	448
Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala Ser Phe Ser His Pro Thr	
105 110 115	
ttc ctc tgg ctc aag tgg aga gtt tct agg gtg atg gta tgg atg ctg	496
Phe Leu Trp Leu Lys Trp Arg Val Ser Arg Val Met Val Trp Met Leu	
120 125 130	
ttg ggt gca ctg ctc tta tcc tgt ggt agt acc gca tct ctg atc aat	544
Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser Thr Ala Ser Leu Ile Asn	
135 140 145 150	
gag ttt aag ctc tat tct gtc ttt agg gga att gag gcc acc agg aat	592
Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly Ile Glu Ala Thr Arg Asn	
155 160 165	
gtg act gaa cac ttc aga aag aag agg agt gag tat tat ctg atc cat	640
Val Thr Glu His Phe Arg Lys Lys Arg Ser Glu Tyr Tyr Leu Ile His	
170 175 180	
gtt ctt ggg act ctg tgg tac ctg cct ccc tta att gtg tcc ctg gcc	688
Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro Leu Ile Val Ser Leu Ala	
185 190 195	
tcc tac tct ttg ctc atc ttc tcc ctg ggg agg cac aca cgg cag atg	736
Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met	
200 205 210	
ctg caa aat ggg aca agc tcc aga gat cca acc act gag gcc cac aag	784
Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro Thr Thr Glu Ala His Lys	
215 220 225 230	
agg gcc atc aga atc atc ctt tcc ttc ttc ttt ctc ttc tta ctt tac	832
Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe Phe Leu Phe Leu Leu Tyr	
235 240 245	
ttt ctt gct ttc tta att gca tca ttt ggt aat ttc cta cca aaa acc	880
Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly Asn Phe Leu Pro Lys Thr	
250 255 260	
aag atg gct aag atg att ggc gaa gta atg aca atg ttt tat cct gct	928

Lys Met Ala Lys Met Ile Gly Glu Val Met Thr Met Phe Tyr Pro Ala  
 265 270 275

ggc cac tca ttt att ctc att ctg ggg aac agt aag ctg aag cag aca 976  
 Gly His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr  
 280 285 290

ttt gta gtg atg ctc cgg tgt gag tct ggt cat ctg aag cct gga tcc 1024  
 Phe Val Val Met Leu Arg Cys Glu Ser Gly His Leu Lys Pro Gly Ser  
 295 300 305 310

aag gga ccc att ttc tct tag 1045  
 Lys Gly Pro Ile Phe Ser \*  
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 <222> (86)..(310)

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 Met Val Leu Leu Glu Pro Lys Pro Trp  
 1 5

ctg gaa ctg atg ctg ctg tgg tgg tca ggg ttc agt gag cag gag gaa 160  
 Leu Glu Leu Met Leu Leu Trp Trp Ser Gly Phe Ser Glu Gln Glu Glu  
 10 15 20 25

gga ctt ggt gtt tac ccc ttg ttt acc cct ttc ctt ggc ttc ctt cca 208  
 Gly Leu Gly Val Tyr Pro Leu Phe Thr Pro Phe Leu Gly Phe Leu Pro  
 30 35 40

tgc agg cca ccc tgt gac ccc gtg gtg gcc ccc tct gga acc aag agc 256  
 Cys Arg Pro Pro Cys Asp Pro Val Val Ala Pro Ser Gly Thr Lys Ser  
 45 50 55

tgc cga ctt cca gca gca cac aca gga tca gtg ctg ggg cca tct gtg 304  
 Cys Arg Leu Pro Ala Ala His Thr Gly Ser Val Leu Gly Pro Ser Val  
 60 65 70

cac tga ccaaagcctc tgctggcctc accagaccaa ggccagtgtg tgcttcaggg 360

His \*  
75

agccttggat cctccaggct gccaacagaa acaccggccc tctcggcagc agcccatcc 420  
ttccacccct gcaactgggtc ctgaaaagcc cattttgggg ccgttgctat ttagccaacc 480  
tgccctccct tgctctcctg tgattttctca ctattccggc tgcagctcgc tgggagaaac 540  
acttgagagt cttttgtgct ccacacccat gtacttaaaa taccaggcct ataggtcatt 600  
tcaatgaggg aatttggctc ataacacgtg tgccccgagg cnagnatcct acttctgcag 660  
atgctggcca agaagggctg tgtcccagcc gccatggggg ggggccacag agagggcagg 720  
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cagtatcaag 790

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tctaag atg agg gac atg gct att aag gtc aag cca aac tat act aaa 108  
Met Arg Asp Met Ala Ile Lys Val Lys Pro Asn Tyr Thr Lys  
1 5 10  
agt agt ata ggg cag cag tta aaa tta tct ttt gaa aat caa gta tta 156  
Ser Ser Ile Gly Gln Gln Leu Lys Leu Ser Phe Glu Asn Gln Val Leu  
15 20 25 30  
cct ggt ttc ttc tgt cac aac aga ata gct ggt tac cta gtc agt cac 204  
Pro Gly Phe Phe Cys His Asn Arg Ile Ala Gly Tyr Leu Val Ser His  
35 40 45  
agt tgc cct tgc ctt ccc ttg tta gtc cct gga ggt act tga gtggaac 253  
Ser Cys Pro Cys Leu Pro Leu Leu Val Pro Gly Gly Thr \*  
50 55 60  
agaaggtaga attagcaaca gctcaatcac tttaggtagc atttctcctg aattctgctg 313  
ccaaatcctc aggggtctatg gattggttga aatagtaaaa tcacacatag tgatttcttg 373  
cacagcgtaa aggcgtttta ttttagtgta tagtgaacaa agaaggaaaa ctgggtcata 433

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 <213> Homo sapiens

<220>  
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 <222> (117)..(911)

<400> 358

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ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggacc      116
atg ggg gct ggg gcc agt gct gag gag aag cac tcc agg gag ctg gaa      164
Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
  1             5             10             15

aag aag ctg aaa gag gac gct gag aag gat gct cga acc gtg aag ctg      212
Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
          20             25             30

ctg ctt ctg ggt gcc ggt gag tcc ggg aag agc acc atc gtc aag cag      260
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
          35             40             45

atg aag att atc cac cag gac ggg tac tcg ctg gaa gag tgc ctc gag      308
Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
          50             55             60

ttt atc gcc atc atc tac ggc aac acg ttg cag tcc atc ctg gcc atc      356
Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
          65             70             75             80

gta cgc gcc atg acc aca ctc aac atc cag tac gga gac tct gca cgc      404
Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
          85             90             95

cag gac gac gcc cgg aag ctg atg cac atg gca gac act atc gag gag      452
Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
          100             105             110

ggc acg atg ccc aag gag atg tcg gac atc atc cag cgg ctg tgg aag      500
Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
          115             120             125

gac tcc ggt atc cag gcc tgt ttt gag cgc gcc tcg gag tac cag ctc      548
Asp Ser Gly Ile Gln Ala Cys Phe Glu Arg Ala Ser Glu Tyr Gln Leu
          130             135             140

aac gac tcg gcg ggc tac tac ctc tcc gac ctg gag cgc ctg gta acc      596
Asn Asp Ser Ala Gly Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
          145             150             155             160

ccg ggc tac gtg ccc acc gag cag gac gtg ctg cgc tcg cga gtc aag      644
Pro Gly Tyr Val Pro Thr Glu Gln Asp Val Leu Arg Ser Arg Val Lys

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165	170	175	
acc act ggc atc atc gag acg cag ttc tcc ttc aag gat ctc aac ttc			692
Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe			
180	185	190	
cgg atg ttc gat gtg ggc ggg cag cgc tcc gag cgc aag aag tgg atc			740
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile			
195	200	205	
cac tgc ttc gag ggc gtg acc tgc atc atc ttc atc gcg gcg ctg agc			788
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser			
210	215	220	
gcc cta cga cat ggt gct agt gga gga cga cga agt gaa ccg cat gca			836
Ala Leu Arg His Gly Ala Ser Gly Gly Arg Arg Ser Glu Pro His Ala			
225	230	235	240
cga gag cct gca cct gtt caa cag cat ctg caa cca ccg cta ctt cgc			884
Arg Glu Pro Ala Pro Val Gln Gln His Leu Gln Pro Pro Leu Leu Arg			
245	250	255	
cac gac gtc cat cgt gct ctt cct taa caaga aggacgtctt cttcgagaag			936
His Asp Val His Arg Ala Leu Pro *			
260	265		
atcaagaagg cgcacctcag catctgtttc ccggactacg atggacccaa cacctacgag			996
gacgccggca actacatcaa ggtgcagttc ctcgagctca acatgcggcg cgacgtgaag			1056
gagatctatt cccacatgac gtgcgccacc gacacgcaga acgtcaaatt tgtcttcgac			1116
gctgtcaccg acatcatcat caaggagaac ctcaaagact gtggcctctt ctgagcacca			1176
aatctttgct tatagatcca cagccagggc ctgtgctgca gtcgggggaca aggagcttcc			1236
gtctggcaag ggaagctgag agccatggct gaactatcag ggacaaaggc ccatgtcccc			1296
acatccctgc tccctccttc ctcatccagc accaaatctt tgcttatgct ccacagccag			1356
ggcctgtgct gcagtcgggg acaaggagct tccgtactgg caaggccggg gcacaatttg			1416
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aaaaaaaa			1483

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 <213> Homo sapiens  
  
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 <222> (1)..(441)

<400> 359

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Met Lys Pro Thr Leu Ile Ser Val Leu Val Ile Ile Phe Ile Leu Arg  
1 5 10 15

gga aca aga gcc cag aga gtg act cag ccc gag aag ctc ctc tct gtc 96  
Gly Thr Arg Ala Gln Arg Val Thr Gln Pro Glu Lys Leu Leu Ser Val  
20 25 30

ttt aaa ggg gcc cca gtg gag ctg aag tgc aac tat tcc tat tct ggg 144  
Phe Lys Gly Ala Pro Val Glu Leu Lys Cys Asn Tyr Ser Tyr Ser Gly  
35 40 45

agt cct gaa ctc ttc tgg tat gtc cag tac tcc aga caa cgc ctc cag 192  
Ser Pro Glu Leu Phe Trp Tyr Val Gln Tyr Ser Arg Gln Arg Leu Gln  
50 55 60

tta ctc ttg aga cac atc tct aga gag agc atc aaa ggc ttc act gct 240  
Leu Leu Leu Arg His Ile Ser Arg Glu Ser Ile Lys Gly Phe Thr Ala  
65 70 75 80

gac ctt aac aaa ggc gag aca tct ttc cac ctg aag aaa cca ttt gct 288  
Asp Leu Asn Lys Gly Glu Thr Ser Phe His Leu Lys Lys Pro Phe Ala  
85 90 95

caa gag gaa gac tca gcc atg tat tac tgt gct cta agt ggc aca gta 336  
Gln Glu Glu Asp Ser Ala Met Tyr Tyr Cys Ala Leu Ser Gly Thr Val  
100 105 110

gct ggt ttt gca agg aag cag aac aca aac cct tta aat aca gga aat 384  
Ala Gly Phe Ala Arg Lys Gln Asn Thr Asn Pro Leu Asn Thr Gly Asn  
115 120 125

att tct ttg caa act ctc tgt atg gcc aca gca ggg cat tct ttc tcc 432  
Ile Ser Leu Gln Thr Leu Cys Met Ala Thr Ala Gly His Ser Phe Ser  
130 135 140

aga aat taa tattgag tttatctcgt agatattata tcactactca tcagctagcc 488  
Arg Asn \*  
145

atacaccac ctcacaattt tgtccaaaaa attctcatca tttaccctgc ctaaattaa 548

tttaaaaaata gtaaactgat tcatttcgtc tagcagcact ggacacacac cttcgaaata 608

aaaactacct tgcactgcac aaaaaacaaa aacaaaaaca cattgccggc cgccccctta 668

ttcccctcag tcagggtac cctaccttcc acctcatccg ctcatt 714

<210> 360

<211> 3154

<212> DNA

<213> Homo sapiens

<220>  
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 <222> (278)..(1483)

<400> 360

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ggtgccgcag ctcgtccatg ttcaccgaca tggcgcgggc gcgcgggggccc cggcgtctcc	180
ggccgggacgc agacgcgggg ctgctgctcgt agcgggggccc cggatccccg agtggcggcc	240
ggagcctcga aaagagattc tcagcgctga ttttgag atg atg ggc ttg gga aac	295
Met Met Gly Leu Gly Asn	
1 5	
ggg cgt cgc agc atg aag tgc ccg ccc ctc gtg ctg gcc gcc ctg gtg	343
Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu Val	
10 15 20	
gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc cgg	391
Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser Arg	
25 30 35	
agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc cgc	439
Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val Arg	
40 45 50	
agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag ttc	487
Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu Phe	
55 60 65 70	
cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag tcc	535
Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser	
75 80 85	
agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac gaa	583
Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu	
90 95 100	
aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc cga	631
Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg	
105 110 115	
gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg ctg	679
Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu	
120 125 130	
cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag agg	727
Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg	
135 140 145 150	
aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag gtg	775
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu Val	
155 160 165	

aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg aat Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly Asn 170 175 180	823
gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga cag Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg Gln 185 190 195	871
cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca ggc Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala Gly 200 205 210	919
ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt aac Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly Asn 215 220 225 230	967
agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat tca Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp Ser 235 240 245	1015
aag aga caa gtt gag aaa gag gaa acc aat gag atc cag gtg gtg aat Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val Asn 250 255 260	1063
gag gag cct cag agg gac agg ctg ccg cag gag cca ggc cgg gag cag Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu Gln 265 270 275	1111
gtg gtg gaa gac aga cct gta ggt gga aga ggc ttc ggg gga gcc gga Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala Gly 280 285 290	1159
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gaa aat cca gag atg gag ggc cct gag cga gac cag ctt gtc atc ccc Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro 315 320 325	1255
gac gga cag gag gag gag cag gaa gct gcc ggg gaa ggg aga aac cag Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln 330 335 340	1303
cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa gca Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala 345 350 355	1351
gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga aac Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn 360 365 370	1399
ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat tta Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu 375 380 385 390	1447

ctt gat cag cgt gaa aag cgg aat cat aca ctc tga attg aactggaatc	1497
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *	
395 400	
acatattttca caacaggggcc gaagagatga ctataaaatg ttcattgaggg actgaataact	1557
gaaaactgtg aaatgtacta aataaaatgt acatctgaag atgattattg tgaaatttta	1617
gtatgcactt tgtgtaggaa aaaatggaat ggtcttttaa acagcttttg ggggggtact	1677
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tcgaaggata tatacagtgt tagaaattag gactgtttag aaaaacagga atacaatggg	2457
tgtttttatc atagtgtaca catttagctt gtggtaaatg actcacaaaa ctgattttta	2517
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tgcaaataac tggccacatc attaatgact gacttcccag taaggctctc taaggggtaa	2697
gtaggaggat ccacaggatt tgagatgcta agggcccaga gatcgtttga tccaaccctc	2757
ttattttcag aggggaaaat ggggcctaga agttacagag catctagctg gtgcgctggc	2817
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aggccctgtt tgcaattcac gttgccacct ccaacttaaa cattcttcat atgtgatgtc	2937
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tactttcata ctcttctaag tctcttcca gcctcacttt gactcctcct tgggggtgat	3057
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3154

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<400> 361

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atgtcctc atg ata ttt gaa tta cac aga tat acc tta tat ctg ctt atg	170
Met Ile Phe Glu Leu His Arg Tyr Thr Leu Tyr Leu Leu Met	
1 5 10	
tac tgt ata tac atc tta gtt tta tat att aat cat aag att ttt tca	218
Tyr Cys Ile Tyr Ile Leu Val Leu Tyr Ile Asn His Lys Ile Phe Ser	
15 20 25 30	
ccc ttc ctc ctc caa gaa caa att ttt acc ccc ttc aaa gca ata tgg	266
Pro Phe Leu Leu Gln Glu Gln Ile Phe Thr Pro Phe Lys Ala Ile Trp	
35 40 45	
ccc cac tgt tcc att gct tta agg gaa ata cca tgt aag cct cta tta	314
Pro His Cys Ser Ile Ala Leu Arg Glu Ile Pro Cys Lys Pro Leu Leu	
50 55 60	
tct acc aag ctc tga gcaggctctt cacatagttt cattaactca tcaaaaccct	369
Ser Thr Lys Leu *	
65	
gcttcctgat ctctaattct tttcctcatt ttggtaccaa caaacatgac cttcagtgga	429
gatattttgtt tagcaaaaga gattacctat ttttttctcc aaccagttgt tgatgccatg	489
aatttctatt aagaaaagcc tggatagttc tttcaaattt gccgaaacac aacttgacct	549
ttttttgtgt gtgcgcc	566

<210> 362  
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<212> DNA  
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<220>

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 <222> (364)..(588)

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Met Val Lys Lys Ile Glu Ile Ser Gln Tyr Ala Lys Tyr Ile Cys	
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Ser Phe Leu Trp Gln Asn Gln Asp Glu Glu Thr Ser Cys Gly Asp Leu	
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Val Leu Trp Phe Cys Met Lys Thr Val Lys Val Ser Ser Ser Arg Asn	
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His Ile Val Trp Thr Tyr Asn Thr Thr Ser Ala Val Thr Val Lys Ser	
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Thr Ile Arg Arg Leu Lys Gln Leu Lys Asp Gln *	
65 70 75	
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